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U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New Amendment Renewal Variance Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: [42.800592, -112.809722]

SW: [42.799192, -112.809637]

NE: [42.800549, -112.807507]

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

SE: [42.799129, -112.807467]

Previous Permit Number(s): 15-349-103rm

7. MEANS OF MOVEMENT

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No
Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

N/A

9. REGULATED ARTICLE

Scientific Name: Triticum aestivum

Common Name: Wheat

Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne - Route d'Ennezat Boone Ames, IA 63720	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proZmVp1] **from** [Zea mays] - [Maize Viviparous1 gene promoter. Tissue specific expression (embryo and aleurone of cereal maize kernels) of the gene downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

3) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):**

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsSALT] **from** [Oryza sativa] - [Rice saltT gene promoter. Inducible expression of the gene downstream its sequence in salty growing conditions]

intron: [intOsSALT] **from** [Oryza sativa] - [Partial sequence of the saltT promoter (inducible in salty growing condition) from rice, that is not transcribed (located before the ATG sequence). Ensures a good transcription of the gene inserted downstream its sequence.]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

4) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01782

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGDAS1] **from** [Triticum aestivum] - [Glutamine Dependent Asparagine Synthetase. Aspartate synthetase dependant to glutamine concentration. Reaction= ATP + L-aspartate + L-glutamine + H(2)O ; AMP + diphosphate + L-asparagine + L-glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

6) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

7) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

8) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)**Gene of interest**

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [NtNPK1] **from** [Nicotiana tabacum] - [Mitogen Activated Protein kinase kinase kinase. Mitogen-activated protein kinase kinase kinase signal transduction pathway]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

10) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01822

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]
 intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]
 gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]
 terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]
 Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

11) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01823

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

14) Phenotypic Designation Name:

Identifying Line(s):

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Construct(s):	T 01830
Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	
Phenotype(s)	
AP - [Enhanced nitrogen use]	
Genotype(s)	
Gene silencer promoter: [proOsPRO0110] from [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]	
intron: [intZmSH1] from [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
intron: [intOsTubL] from [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
terminator: [terAtSac66] from [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]	
Selectable Marker Terminal Inverted Repeat: [ZmDs5'Ac] from [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	
promoter: [proVirSc4] from [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]	
intron: [intAtFAD2] from [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]	
gene: [EcNPTII] from [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]	
terminator: [terAtNOS] from [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]	
Terminal Inverted Repeat: [ZmDs3'Ac] from [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	

15) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01832**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

17) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

18) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmKnotted1] **from** [Zea Mays] - [Maize knotted1 gene promoter. Specific expression in the apical meristem]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

19) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

20) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsLRK1] **from** [Oryza sativa] - [LRK1 regulates rice branch number by enhancing cellular proliferation]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

22) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDEP1] **from** [Oryza sativa] - [PEBP (phosphatidylethanolamine-binding protein) like domain protein sharing some homology with the N terminus of GS3]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

23) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

24) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTin3A] **from** [Brachypodium distachyon] - [Protein involved in tiller development]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

25) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTkw2] **from** [Brachypodium distachyon] - [Thousand Kernel Weight 2. EST annotated "Large Tegument protein", candidate gene under yield QTL]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

26) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01985

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)**Gene of interest**

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

27) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaPAMT] **from** [Triticum aestivum] - [Protein Arginine N-MethylTransferase. Catalyzes the addition of a methyl group to an arginine residue]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

28) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01987

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMFSA] **from** [Triticum aestivum] - [Major Facilitator Superfamily Antiporter. Membrane protein involved as single polypeptide secondary carriers, transporting a diverse range of substrates]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

29) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01988

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMPase] **from** [Triticum aestivum] - [Metallopeptidase. Peptidase with metal cofactor: Catalysis of the hydrolysis of peptide bonds by a mechanism in which water acts as a nucleophile, one or two metal ions hold the water molecule in place, and charged amino acid side chains are ligands for the metal ions.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

30) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrbu3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrbu3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaZFP] **from** [Triticum aestivum] - [Zinc finger protein. Transcription factor related to nitrogen metabolism. Close relative of wheat Zinc Finger Protein1 gene]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

31) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01991

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaT6PS] **from** [Triticum aestivum] - [Trehalose-6-phosphate synthase. Trehalose-6-phosphate synthase involved in sugar metabolism. Reaction: UDP-glucose + D-glucose 6-phosphate ; UDP + alpha,alpha-trehalose 6-phosphate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

32) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02003

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

33) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02004

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved fungal disease resistance

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrb3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrb3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

34) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

35) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

36) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02051

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsNAC10] **from** [Oryza sativa] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity. NAC family transcription factor involved in stress tolerance response]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

37) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02094

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation

reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [HvSUT1] **from** [Hordeum vulgare] - [sucrose transporter]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

38) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02110

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaCYCB2] **from** [Triticum aestivum] - [Cyclin B2 is a member of the B-type cyclins and are essential components of the cell cycle regulatory machinery.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin

phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

40) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' pregin of the califlower mosaic virus,]promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to α-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

42) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02134

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' preregion of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

43) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02135

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

44) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02137

Mode of Transformation: Agrobacterium tumefaciens disarmed

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Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH₃ =>; Gln)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac tranposase is present]

45) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02154

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

46) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02155

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

47) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmAspAT1] **from** [Zea mays] - [Aspartate AminoTransferasel. Aspartate aminotransferase catalyzes the reversible interconversions of glutamate and aspartate, and their 2-keto analogs: Glutamate + oxaloacetate (OAA) ; 2-oxoglutarate + aspartate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

48) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumLOG] **from** [Agrobacterium tumefaciens] - [Lysine decarboxylase]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

50) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaBril] **from** [Triticum aestivum] - [Brassinosteroid-insensitive1. Brassinosteroid LRR receptor kinase involved in brassinosteroid signal transduction]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtCKX3] **from** [Arabidopsis thaliana] - [Involved in degradation of cytokinins]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsSCI2] **from** [Oryza sativa] - [Rice Subtilisin_chymotrypsin_inhibitor2 promoter. Inducible expression of the gene downstream its sequence under abiotic stress (salt, drought, ABA, cold)]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtTPS1] **from** [Arabidopsis thaliana] - [Enzyme of the threahose synthase pathway - osmoprotectant/ signaling molecule]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

54) Phenotypic Designation Name:

Identifying Line(s):**Construct(s):** T 02268**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATHRD] **from** [Arabidopsis thaliana] - [The HARDY protein is a transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

55) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02269**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ALSAP] **from** [Allocasuarina littoralis] - [Stress Associated Protein. Probable Ubiquitin ligase]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

57) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02304

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

58) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaARF22] **from** [Triticum aestivum] - [Transcription factor involved in pericarp development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

59) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSHN2] **from** [Arabidopsis thaliana] - [AP2 type transcription factor is involved in cuticular wax accumulation and in stomatal density]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

60) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02334

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsAT] **from** [Oryza sativa] - [Aminotransferase. catalyzes the transfer of an amino group between an amino acid and an α-keto acid]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [protoActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

61) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02335**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]gene: [OsHisTpter] **from** [Oryza sativa] - [Histidine AA transporter. amino acid transporter]terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

62) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02336

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmAGAT2] **from** [Zea mays] - [Conversion of glyoxylate into glycine]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

63) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02337

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmANAC075] **from** [Zea mays] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity involved in drought stress]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region

(terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

64) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02339

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbFd_NADP_Reductase] **from** [Sorghum bicolor] - [Ferredoxin-NADP reductase. belongs to the family of oxidoreductases involved in the transfer of electrons]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

65) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02342

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

Signal peptide: [ctpRca] **from** [Zea mays] - [Chloroplastid transit peptide from Rubisco Activase gene]

gene: [BlnAGK] **from** [Brevibacillus laterosporus] - [Enzyme involved in Arginine biosynthesis]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green

fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaWali5] **from** [Triticum aestivum] - [Wali5 protein is a transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaBamy2] **from** [Triticum aestivum] - [The bamylose protein is a putative amylase]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal

kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

69) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

70) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02347

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a

Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSAP5] **from** [Arabidopsis thaliana] - [Stress Associated protein 5]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s):

T 02349

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsZnFG18] **from** [Oryza sativa] - [ZnFg CCCH domain-containing protein 18. Zinc

finger domain containing transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

Gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

73) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02350

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmDof1] **from** [Zea mays] - [Dof1 domain containing transcription factor. Dof proteins share a unique and highly conserved DNA binding domain with one C2-C2 zinc finger motif. Dof proteins can function as transcriptional activators or repressors of tissue-specific and light-regulated gene expression in plants (carbon metabolism)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

74) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaPPI_FKBP] **from** [Triticum aestivum] - [Peptidyl-prolyl cis-trans isomerase, FKBP-type family protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

75) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02352

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [HvA1] **from** [Hordeum vulgare] - [Chaperone like protein. Member of the Late Embryogenesis Abundant (LEA) protein family. Chaperone like protein linked to drought tolerance]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

76) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02353

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmASR] **from** [Zea mays] - [ABA Stress Ripening induced protein. ASR proteins are induced by abscisic acid (ABA), stress and ripening. First described in tomato, at least seven genes have been found in maize. ASR1 is one of the 7 genes isolated so far. ASR protein have a key role in the mechanism conducting to drought and salt resistance via ABA and sugar signalization]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbPEPC] **from** [Sorghum bicolor] - [PhosphoEnol Pyruvate Carboxylase. C4 photosynthetic carbon assimilation cycle enzyme. Reaction: PEP + CO₂ --->; OxaloAcetate + Pi]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

77) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02355

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [EcBetA] **from** [E. Coli] - [The Choline Dehydrogenase is an enzyme that catalyzes the chemical reaction from the substrates choline and acceptor, whereas its two products are betaine aldehyde and reduced acceptor.]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsrubii3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubii3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ThVP] **from** [Thellungielle halophila] - [Thellungielle halophila H(+)-pyrophosphatase. vacuolar H+-pyrophosphatase, enzyme (EC 3.6.1.1) that catalyzes the conversion of one molecule of pyrophosphate to two phosphate ions]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinothricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

78) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsNAC5] **from** [Oryza sativa] - [NAC family transcription factor. NAC family transcriptional factor putatively involved in kernel filling]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsLEA3.1] **from** [Oryza sativa] - [Chaperone like protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and Galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

80) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02367

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AnNADP_GDHA] **from** [Aspergillus niger] - [The NADP glutamate dehydrogenase A converts 2-oxo-glutarate into L-glutamate by incorporating NH₃ (EC:1,41,4)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

81) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02368

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmEF_Tu] **from** [Zea mays] - [EF-Tu mediates the entry of the aminoacyl tRNA into a free site of the ribosome]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

82) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02386

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [TaMEG1b] **from** [Triticum aestivum] - [Maternally Expressed Gene1. Wheat endosperm transfert cell-specific gene with a maternal parent of origin pattern expression.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

83) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02423

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

84) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ScTPS1+ScTPS2_fusion] **from** [Saccharomyces cerevisiae] - [Regulation of synthesis of trehalose]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from

rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinotricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

85) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [OsSAP] **from** [Oryza sativa] - [senescence-associated rhodanese-like domain containing protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	IA County: Boone	

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Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	<p>IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
2) [AgraServ]	<p>ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
3) [Agro-Tech Research Farm]	<p>ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
4) [Qualls Ag Laboratory]	<p>WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	15-ID-Ta01	
Location GPS Coordinates:	[42.804648], [-112.790011]	
Release Site History:	This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
2) AgraServ NUE	<p>ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	
Location Unique ID:	16-ID-Ta-02	
Location GPS Coordinates:	[42.800000], [-112.809722] [42.799000], [-112.809637] [42.800000], [-112.807507] [42.799129], [-112.807467]	
Release Site History:	This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
3) Agro-Tech Research Farm	<p>ID County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	16-ND-Ta01	
Location GPS Coordinates:	[48.172554], [-101.001077] [48.178800], [-101.000472] [48.156788], [-100.978399]	
Release Site History:	This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
4) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	16-WA-Ta01	
Location GPS Coordinates:	[47.151634], [-119.560611]	

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Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS

Production Design

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[The purpose of the introduction is to evaluate the performance or produce seed for research purpose only. Plants will be grown under various environment with various level of fertilisation or various level of watering. The performance will be determined by collecting various phenotyping data as the grain yield. The release site will be spatially isolated by no less than 130 feet from sexually compatible species. The release site will be surrounded by border and/or buffer area. All equipment used in the release site will be thoroughly cleaned at the release site. After harvest, the remaining material will incorporate to the soil and left for devitalization by the elements.]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only". Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment. Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use. Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site. All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

["Regulated wheat will be planted only at the field site specified in the permit. Field sites will be well-defined with stakes and GPS coordinates. A buffer area of no less than 13 feet will separate wheat regulated under this permit and any other planted agricultural material. The field site, border rows and buffer area will be monitored for volunteers for the four successive growing seasons after harvest. Volunteers will be removed prior to flowering and destroyed. A minimum of one monitoring every 4 weeks is performed at the field site. Any volunteer plants will be destroyed by any one of the following methods : mechanical grinding or other methods to incorporate the plant into the soil or chemical treatment. The monitoring area is left fallow or planted with a distinct and non-sexually compatible crop. The soil preparation and planting of the crop in the monitoring area is made independently from the rest of the field."]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[Seed or other material capable of propagation will be devitalized by autoclaving, burning or incineration, mechanical grinding or crushing, herbicide treatment, or returning to the field site and burying at the field site. Seed not used in the field trial will be returned to facility for storage or destruction.]

14. ATTACHMENTS

CBI	CBI-Deleted/Non-CBI
	Biogemma Wheat Design Protocol 2016 (3/22/2016 @ 10:56 AM)

15. ADDITIONAL INFORMATION

16. COURTESY JUSTIFICATION

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WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, William 'Chris' Anderson, hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b) (6)

18. DATE

March 22, 2016

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New
- Amendment
- Renewal
- Variance
- Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: []
 SW: []
 NE: []

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SE: []

Previous Permit Number(s): 15-349-103rm**7. MEANS OF MOVEMENT**

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No
Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

N/A

9. REGULATED ARTICLE**Scientific Name:** Triticum aestivum**Common Name:** Wheat**Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:**

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:The genetically engineered lines covered in this permit were created and developed at Biogemma,
Site de la Garenne, route d'Ennezat, 63720 Chappes, France.**Processes, Procedures, and Safeguards Description:**

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne - Route d'Ennezat Boone Ames, IA 63720	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**3) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s):

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**4) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01782**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

6) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

7) **Phenotypic Designation Name:**

Identifying Line(s):

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

8) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

10) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01822**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.
Improved yield under low nitrogen supply**Phenotype(s)**

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

11) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01823**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**12) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

14) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01830

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

 promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene: [] **from** [] - []

 terminator: [] **from** [] - []

 Terminal Inverted Repeat: [] **from** [] - []

15) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01832

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
 promoter: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

17) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

18) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**19) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

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Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

20) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**22) Phenotypic Designation Name:**

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**23) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

24) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

25) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

26) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01985

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

27) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]  
Terminal Inverted Repeat: [           ] from [           ] - [           ]
```

28) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01987**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]
```

Selectable Marker

```
Terminal Inverted Repeat: [           ] from [           ] - [           ]  
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

29) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01988**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

30) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

31) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s):

T 01991

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**32) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02003**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved fungal disease resistance

Phenotype(s)

FR - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

33) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02004

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

34) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

35) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

36) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02051**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

37) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02094**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []

```
gene: [      ] from [      ] - [  
]  
terminator: [      ] from [      ] - [  
]  
promoter: [      ] from [      ] - [  
]  
intron: [      ] from [      ] - [  
]  
gene: [      ] from [      ] - [  
]  
terminator: [      ] from [      ] - [  
]  
  
Selectable Marker  
Terminal Inverted Repeat: [      ] from [      ] - [  
]  
]  
promoter: [      ] from [      ] - [  
]  
intron: [      ] from [      ] - [  
]  
]  
gene: [      ] from [      ] - [  
]  
]  
terminator: [      ] from [      ] - [  
]  
]  
Terminal Inverted Repeat: [      ] from [      ] - [  
]  
]
```

38) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02110**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

40) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

42) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02134**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

43) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02135**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**44) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02137**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

[]

gene: [] **from** [] - []

terminator: [] **from** [] - []

[]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

45) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02154**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

46) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02155**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

47) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

48) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

]

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

50) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

54) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02268

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

[]

55) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02269

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

57) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02304**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

58) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02324**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

59) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02333**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

60) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02334**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

```
promoter: [           ] from [           ] - [  
          ]  
gene: [     ] from [           ] - [  
          ]  
terminator: [       ] from [           ] - [  
          ]  
promoter: [           ] from [           ] - [  
          ]  
intron: [       ] from [           ] - [  
          ]  
gene: [     ] from [           ] - [  
          ]  
  
terminator: [       ] from [           ] - [  
          ]  
Terminal Inverted Repeat: [       ] from [           ] - [  
          ]
```

61) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02335**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

62) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02336**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

63) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02337**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

64) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02339**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

65) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02342**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

Signal peptide: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

69) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

70) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02347**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

71) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02348**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02349

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

```
terminator: [ ] from [ ] - [ ]  
promoter: [ ] from [ ] - [ ]  
intron: [ ] from [ ] - [ ]  
gene: [ ] from [ ] - [ ]  
  
terminator: [ ] from [ ] - [ ]  
Terminal Inverted Repeat: [ ] from [ ] - [ ]
```

73) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02350**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] from [] - []

intron: [] from [] - []

gene: [] from [] - []

terminator: [] from [] - []

Selectable Marker

Terminal Inverted Repeat: [] from [] - []

promoter: [] from [] - []

```

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

promoter: [          ] from [           ] - [
]

intron: [          ] from [           ] - [
]

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

Terminal Inverted Repeat: [          ] from [           ] - [
]

```

74) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]

intron: [] **from** [] - [
]

gene: [] **from** [] - [
]

terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]

promoter: [] **from** [] - [
]

```
gene: [      ] from [           ] - [  
          ]  
  
terminator: [      ] from [           ] - [  
          ]  
  
promoter: [      ] from [           ] - [  
          ]  
  
intron: [      ] from [           ] - [  
          ]  
  
gene: [      ] from [           ] - [  
          ]  
  
  
terminator: [      ] from [           ] - [  
          ]  
  
Terminal Inverted Repeat: [      ] from [           ] - [  
          ]
```

75) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02352**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]intron: [] **from** [] - [
]gene: [] **from** [] - [
]terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]promoter: [] **from** [] - [
]

```
]

gene: [      ] from [           ] - [      ]

terminator: [      ] from [           ] - [      ]

promoter: [      ] from [           ] - [      ]

intron: [      ] from [           ] - [      ]

gene: [      ] from [           ] - [      ]

terminator: [      ] from [           ] - [      ]

Terminal Inverted Repeat: [      ] from [           ] - [      ]
```

76) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02353**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [      ] from [           ] - [      ]
```



```
intron: [      ] from [           ] - [      ]
```



```
gene: [      ] from [           ] - [      ]
```



```
terminator: [      ] from [           ] - [      ]
```



```
promoter: [      ] from [           ] - [      ]
```



```
intron: [      ] from [           ] - [      ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

77) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02355**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

78) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

80) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02367**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

81) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02368**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

82) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02386**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

83) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02423**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

84) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

85) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

]

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
2) []	ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
3) []	ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
4) []	WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres	1) [] [] Day Telephone: []
Location Unique ID:	15-ID-Ta01	
Location GPS Coordinates:	[], []	
Release Site History:	This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years	
Critical Habitat Involved?:	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
2) AgraServ NUE	ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres	
Location Unique ID:	16-ID-Ta-02	
Location GPS Coordinates:	[], [] [], [] [], [] [], []	
Release Site History:	This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.	
Critical Habitat Involved?:	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
3) Agro-Tech Research Farm	ND County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres	1) [] [] Day Telephone: []
Location Unique ID:	16-ND-Ta01	
Location GPS Coordinates:	[], [] [], [] [], []	
Release Site History:	This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years	
Critical Habitat Involved?:	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
4) Qualls Ag Lab	WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres	1) [] [] Day Telephone: []
Location Unique ID:	16-WA-Ta01	
Location GPS Coordinates:	[], []	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS**Production Design**

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[

]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only".

Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment.

Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use.

Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site.

All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

[

]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[

]

14. ATTACHMENTS**Attachments**

Biogemma Wheat Design Protocol 2016 (3/22/2016 @ 10:56 AM)

15. ADDITIONAL INFORMATION**16. COURTESY JUSTIFICATION**

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, (b)(6), hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b)(6)

18. DATE

March 22, 2016

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New Amendment Renewal Variance Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: 42.800592, -112.809722

SW: 42.799192, -112.809637

NE: 42.800549, -112.807507

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

SE: 42.799129, -112.807467

Previous Permit Number(s): 15-349-103rm

7. MEANS OF MOVEMENT

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No
Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

N/A

9. REGULATED ARTICLE

Scientific Name: Triticum aestivum

Common Name: Wheat

Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne - Route d'Ennezat Boone Ames, IA 63720	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proZmVp1] **from** [Zea mays] - [Maize Viviparous1 gene promoter. Tissue specific expression (embryo and aleurone of cereal maize kernels) of the gene downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

3) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):**

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsSALT] **from** [Oryza sativa] - [Rice saltT gene promoter. Inducible expression of the gene downstream its sequence in salty growing conditions]

intron: [intOsSALT] **from** [Oryza sativa] - [Partial sequence of the saltT promoter (inducible in salty growing condition) from rice, that is not transcribed (located before the ATG sequence). Ensures a good transcription of the gene inserted downstream its sequence.]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

4) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01782

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGDAS1] **from** [Triticum aestivum] - [Glutamine Dependent Asparagine Synthetase. Aspartate synthetase dependant to glutamine concentration. Reaction= ATP + L-aspartate + L-glutamine + H(2)O ; AMP + diphosphate + L-asparagine + L-glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

6) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

7) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

8) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)**Gene of interest**

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [NtNPK1] **from** [Nicotiana tabacum] - [Mitogen Activated Protein kinase kinase kinase. Mitogen-activated protein kinase kinase kinase signal transduction pathway]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

10) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01822

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]
 intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]
 gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]
 terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]
 Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

11) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01823

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

14) Phenotypic Designation Name:

Identifying Line(s):

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Construct(s):	T 01830
Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	
Phenotype(s)	
AP - [Enhanced nitrogen use]	
Genotype(s)	
Gene silencer promoter: [proOsPRO0110] from [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]	
intron: [intZmSH1] from [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
intron: [intOsTubL] from [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
terminator: [terAtSac66] from [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]	
Selectable Marker Terminal Inverted Repeat: [ZmDs5'Ac] from [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	
promoter: [proVirSc4] from [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]	
intron: [intAtFAD2] from [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]	
gene: [EcNPTII] from [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]	
terminator: [terAtNOS] from [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]	
Terminal Inverted Repeat: [ZmDs3'Ac] from [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	

15) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01832**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

17) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

18) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmKnotted1] **from** [Zea Mays] - [Maize knotted1 gene promoter. Specific expression in the apical meristem]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

19) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

20) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsLRK1] **from** [Oryza sativa] - [LRK1 regulates rice branch number by enhancing cellular proliferation]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

22) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDEP1] **from** [Oryza sativa] - [PEBP (phosphatidylethanolamine-binding protein) like domain protein sharing some homology with the N terminus of GS3]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

23) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

24) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTin3A] **from** [Brachypodium distachyon] - [Protein involved in tiller development]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

25) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTkw2] **from** [Brachypodium distachyon] - [Thousand Kernel Weight 2. EST annotated "Large Tegument protein", candidate gene under yield QTL]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

26) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01985

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)**Gene of interest**

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

27) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaPAMT] **from** [Triticum aestivum] - [Protein Arginine N-MethylTransferase. Catalyzes the addition of a methyl group to an arginine residue]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

28) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01987

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMFSA] **from** [Triticum aestivum] - [Major Facilitator Superfamily Antiporter. Membrane protein involved as single polypeptide secondary carriers, transporting a diverse range of substrates]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

29) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01988

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMPase] **from** [Triticum aestivum] - [Metallopeptidase. Peptidase with metal cofactor: Catalysis of the hydrolysis of peptide bonds by a mechanism in which water acts as a nucleophile, one or two metal ions hold the water molecule in place, and charged amino acid side chains are ligands for the metal ions.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

30) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrbu3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrbu3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaZFP] **from** [Triticum aestivum] - [Zinc finger protein. Transcription factor related to nitrogen metabolism. Close relative of wheat Zinc Finger Protein1 gene]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

31) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01991

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaT6PS] **from** [Triticum aestivum] - [Trehalose-6-phosphate synthase. Trehalose-6-phosphate synthase involved in sugar metabolism. Reaction: UDP-glucose + D-glucose 6-phosphate ; UDP + alpha,alpha-trehalose 6-phosphate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

32) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02003

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

33) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02004

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved fungal disease resistance

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrb3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrb3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

34) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

35) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

36) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02051

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsNAC10] **from** [Oryza sativa] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity. NAC family transcription factor involved in stress tolerance response]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

37) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02094

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation

reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [HvSUT1] **from** [Hordeum vulgare] - [sucrose transporter]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

38) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02110

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaCYCB2] **from** [Triticum aestivum] - [Cyclin B2 is a member of the B-type cyclins and are essential components of the cell cycle regulatory machinery.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin

phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

40) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' pregin of the califlower mosaic virus,]promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to α-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

42) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02134

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' preregion of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

43) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02135

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

44) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02137

Mode of Transformation: Agrobacterium tumefaciens disarmed

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH₃ =>; Gln)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac tranposase is present]

45) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02154

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

46) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02155

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

47) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmAspAT1] **from** [Zea mays] - [Aspartate AminoTransferasel. Aspartate aminotransferase catalyzes the reversible interconversions of glutamate and aspartate, and their 2-keto analogs: Glutamate + oxaloacetate (OAA) ; 2-oxoglutarate + aspartate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

48) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumLOG] **from** [Agrobacterium tumefaciens] - [Lysine decarboxylase]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

50) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaBril] **from** [Triticum aestivum] - [Brassinosteroid-insensitive1. Brassinosteroid LRR receptor kinase involved in brassinosteroid signal transduction]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtCKX3] **from** [Arabidopsis thaliana] - [Involved in degradation of cytokinins]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsSCI2] **from** [Oryza sativa] - [Rice Subtilisin_chymotrypsin_inhibitor2 promoter. Inducible expression of the gene downstream its sequence under abiotic stress (salt, drought, ABA, cold)]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtTPS1] **from** [Arabidopsis thaliana] - [Enzyme of the threahose synthase pathway - osmoprotectant/ signaling molecule]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

54) Phenotypic Designation Name:

Identifying Line(s):**Construct(s):** T 02268**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATHRD] **from** [Arabidopsis thaliana] - [The HARDY protein is a transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

55) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02269**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ALSAP] **from** [Allocasuarina littoralis] - [Stress Associated Protein. Probable Ubiquitin ligase]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

57) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02304

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

58) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaARF22] **from** [Triticum aestivum] - [Transcription factor involved in pericarp development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

59) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

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AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSHN2] **from** [Arabidopsis thaliana] - [AP2 type transcription factor is involved in cuticular wax accumulation and in stomatal density]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

60) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02334

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsAT] **from** [Oryza sativa] - [Aminotransferase. catalyzes the transfer of an amino group between an amino acid and an α-keto acid]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [protoActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

61) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02335

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsHisTpter] **from** [Oryza sativa] - [Histidine AA transporter. amino acid transporter]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

62) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02336**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]gene: [ZmAGAT2] **from** [Zea mays] - [Conversion of glyoxylate into glycine]terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

63) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02337

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmANAC075] **from** [Zea mays] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity involved in drought stress]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region

(terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

64) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02339

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbFd_NADP_Reductase] **from** [Sorghum bicolor] - [Ferredoxin-NADP reductase. belongs to the family of oxidoreductases involved in the transfer of electrons]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

65) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02342

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

Signal peptide: [ctpRca] **from** [Zea mays] - [Chloroplastid transit peptide from Rubisco Activase gene]

gene: [BlnAGK] **from** [Brevibacillus laterosporus] - [Enzyme involved in Arginine biosynthesis]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green

fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaWali5] **from** [Triticum aestivum] - [Wali5 protein is a transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaBamy2] **from** [Triticum aestivum] - [The bamylose protein is a putative amylase]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal

kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

69) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

70) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02347

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a

Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSAP5] **from** [Arabidopsis thaliana] - [Stress Associated protein 5]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s):

T 02349

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsZnFG18] **from** [Oryza sativa] - [ZnFg CCCH domain-containing protein 18. Zinc

finger domain containing transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

Gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

73) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02350

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmDof1] **from** [Zea mays] - [Dof1 domain containing transcription factor. Dof proteins share a unique and highly conserved DNA binding domain with one C2-C2 zinc finger motif. Dof proteins can function as transcriptional activators or repressors of tissue-specific and light-regulated gene expression in plants (carbon metabolism)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

74) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaPPI_FKBP] **from** [Triticum aestivum] - [Peptidyl-prolyl cis-trans isomerase, FKBP-type family protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

75) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02352

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [HvA1] **from** [Hordeum vulgare] - [Chaperone like protein. Member of the Late Embryogenesis Abundant (LEA) protein family. Chaperone like protein linked to drought tolerance]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

76) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02353

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmASR] **from** [Zea mays] - [ABA Stress Ripening induced protein. ASR proteins are induced by abscisic acid (ABA), stress and ripening. First described in tomato, at least seven genes have been found in maize. ASR1 is one of the 7 genes isolated so far. ASR protein have a key role in the mechanism conducting to drought and salt resistance via ABA and sugar signalization]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbPEPC] **from** [Sorghum bicolor] - [PhosphoEnol Pyruvate Carboxylase. C4 photosynthetic carbon assimilation cycle enzyme. Reaction: PEP + CO₂ --->; OxaloAcetate + Pi]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

77) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02355

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [EcBetA] **from** [E. Coli] - [The Choline Dehydrogenase is an enzyme that catalyzes the chemical reaction from the substrates choline and acceptor, whereas its two products are betaine aldehyde and reduced acceptor.]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsrubii3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubii3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ThVP] **from** [Theellungielle halophila] - [Theellungielle halophila H(+)-pyrophosphatase. vacuolar H+-pyrophosphatase, enzyme (EC 3.6.1.1) that catalyzes the conversion of one molecule of pyrophosphate to two phosphate ions]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinothricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

78) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsNAC5] **from** [Oryza sativa] - [NAC family transcription factor. NAC family transcriptional factor putatively involved in kernel filling]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsLEA3.1] **from** [Oryza sativa] - [Chaperone like protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and Galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

80) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02367

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AnNADP_GDHA] **from** [Aspergillus niger] - [The NADP glutamate dehydrogenase A converts 2-oxo-glutarate into L-glutamate by incorporating NH₃ (EC:1,41,4)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

81) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02368

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmEF_Tu] **from** [Zea mays] - [EF-Tu mediates the entry of the aminoacyl tRNA into a free site of the ribosome]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

82) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02386

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [TaMEG1b] **from** [Triticum aestivum] - [Maternally Expressed Gene1. Wheat endosperm transfert cell-specific gene with a maternal parent of origin pattern expression.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

83) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02423

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

84) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ScTPS1+ScTPS2_fusion] **from** [Saccharomyces cerevisiae] - [Regulation of synthesis of trehalose]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from

rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinotricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

85) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [OsSAP] **from** [Oryza sativa] - [senescence-associated rhodanese-like domain containing protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	<p>IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) [b] (6) Day Telephone: [b] (6)</p>
2) [AgraServ]	<p>ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
3) [Agro-Tech Research Farm]	<p>ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
4) [Qualls Ag Laboratory]	<p>WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	15-ID-Ta01	
Location GPS Coordinates:	[42.804648], [-112.790011]	
Release Site History:	This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
2) AgraServ NUE	<p>ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	
Location Unique ID:	16-ID-Ta-02	
Location GPS Coordinates:	[42.800000], [-112.809722] [42.799000], [-112.809637] [42.800000], [-112.807507] [42.799129], [-112.807467]	
Release Site History:	This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
3) Agro-Tech Research Farm	<p>ID County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	16-ND-Ta01	
Location GPS Coordinates:	[48.172554], [-101.001077] [48.178800], [-101.000472] [48.156788], [-100.978399]	
Release Site History:	This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
4) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	16-WA-Ta01	
Location GPS Coordinates:	[47.151634], [-119.560611]	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS

Production Design

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[The purpose of the introduction is to evaluate the performance or produce seed for research purpose only. Plants will be grown under various environment with various level of fertilisation or various level of watering. The performance will be determined by collecting various phenotyping data as the grain yield. The release site will be spatially isolated by no less than 130 feet from sexually compatible species. The release site will be surrounded by border and/or buffer area. All equipment used in the release site will be thoroughly cleaned at the release site. After harvest, the remaining material will incorporate to the soil and left for devitalization by the elements.]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only". Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment. Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use. Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site. All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

["Regulated wheat will be planted only at the field site specified in the permit. Field sites will be well-defined with stakes and GPS coordinates. A buffer area of no less than 13 feet will separate wheat regulated under this permit and any other planted agricultural material. The field site, border rows and buffer area will be monitored for volunteers for the four successive growing seasons after harvest. Volunteers will be removed prior to flowering and destroyed. A minimum of one monitoring every 4 weeks is performed at the field site. Any volunteer plants will be destroyed by any one of the following methods : mechanical grinding or other methods to incorporate the plant into the soil or chemical treatment. The monitoring area is left fallow or planted with a distinct and non-sexually compatible crop. The soil preparation and planting of the crop in the monitoring area is made independently from the rest of the field."]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[Seed or other material capable of propagation will be devitalized by autoclaving, burning or incineration, mechanical grinding or crushing, herbicide treatment, or returning to the field site and burying at the field site. Seed not used in the field trial will be returned to facility for storage or destruction.]

14. ATTACHMENTS

CBI	CBI-Deleted/Non-CBI
	Biogemma Wheat Design Protocol 2016 (3/22/2016 @ 10:56 AM)

15. ADDITIONAL INFORMATION

16. COURTESY JUSTIFICATION

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, (b)(6) hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b)(6)

18. DATE

March 22, 2016

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New Amendment Renewal Variance Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: 42.800592, -112.809722

SW: 42.799192, -112.809637

NE: 42.800549, -112.807507

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

SE: 42.799129, -112.807467

Previous Permit Number(s): 15-349-103rm**7. MEANS OF MOVEMENT**

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No
Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

N/A

9. REGULATED ARTICLE**Scientific Name:** Triticum aestivum**Common Name:** Wheat**Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:**

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne - Route d'Ennezat Boone Ames, IA 63720	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**3) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s):

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**4) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01782**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

6) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

7) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

8) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

10) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01822**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.
Improved yield under low nitrogen supply**Phenotype(s)**

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

11) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01823**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**12) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

14) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01830

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

 promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene: [] **from** [] - []

 terminator: [] **from** [] - []

 Terminal Inverted Repeat: [] **from** [] - []

15) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01832

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
 promoter: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

17) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

18) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**19) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

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Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

20) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**22) Phenotypic Designation Name:**

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**23) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

24) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

25) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

26) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01985

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []

[]

gene: [] **from** [] - []

[]

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

27) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]  
Terminal Inverted Repeat: [           ] from [           ] - [           ]
```

28) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01987**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]
```

Selectable Marker

```
Terminal Inverted Repeat: [           ] from [           ] - [           ]  
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

29) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01988**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

30) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

31) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s):

T 01991

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**32) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02003**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved fungal disease resistance

Phenotype(s)

FR - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

33) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02004

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

34) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

35) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

36) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02051**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

37) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02094**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []

```
gene: [      ] from [      ] - [  
]  
terminator: [      ] from [      ] - [  
]  
promoter: [      ] from [      ] - [  
]  
intron: [      ] from [      ] - [  
]  
gene: [      ] from [      ] - [  
]  
terminator: [      ] from [      ] - [  
]  
  
Selectable Marker  
Terminal Inverted Repeat: [      ] from [      ] - [  
]  
]  
promoter: [      ] from [      ] - [  
]  
intron: [      ] from [      ] - [  
]  
]  
gene: [      ] from [      ] - [  
]  
]  
terminator: [      ] from [      ] - [  
]  
]  
Terminal Inverted Repeat: [      ] from [      ] - [  
]  
]
```

38) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02110**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

39) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02123**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

40) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

42) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02134**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

43) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02135**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**44) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02137**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

[]

gene: [] **from** [] - []

terminator: [] **from** [] - []

[]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

45) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02154**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

46) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02155**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

47) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

48) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

]

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

50) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

54) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02268

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

55) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02269

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

57) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02304**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

58) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02324**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

59) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02333**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

60) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02334**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

61) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02335**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

62) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02336**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

63) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02337**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

64) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02339**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

65) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02342**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

Signal peptide: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

69) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

70) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02347**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02349

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

```
terminator: [ ] from [ ] - [ ]  
promoter: [ ] from [ ] - [ ]  
intron: [ ] from [ ] - [ ]  
gene: [ ] from [ ] - [ ]  
  
terminator: [ ] from [ ] - [ ]  
Terminal Inverted Repeat: [ ] from [ ] - [ ]
```

73) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02350**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] from [] - []

intron: [] from [] - []

gene: [] from [] - []

terminator: [] from [] - []

Selectable Marker

Terminal Inverted Repeat: [] from [] - []

promoter: [] from [] - []

```

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

promoter: [          ] from [           ] - [
]

intron: [          ] from [           ] - [
]

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

Terminal Inverted Repeat: [          ] from [           ] - [
]

```

74) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]

intron: [] **from** [] - [
]

gene: [] **from** [] - [
]

terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]

promoter: [] **from** [] - [
]

```
gene: [      ] from [           ] - [  
          ]  
  
terminator: [      ] from [           ] - [  
          ]  
  
promoter: [      ] from [           ] - [  
          ]  
  
intron: [      ] from [           ] - [  
          ]  
  
gene: [      ] from [           ] - [  
          ]  
  
  
terminator: [      ] from [           ] - [  
          ]  
  
Terminal Inverted Repeat: [      ] from [           ] - [  
          ]
```

75) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02352**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]intron: [] **from** [] - [
]gene: [] **from** [] - [
]terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]promoter: [] **from** [] - [
]

```
]

gene: [      ] from [           ] - [      ]

terminator: [      ] from [           ] - [      ]

promoter: [      ] from [           ] - [      ]

intron: [      ] from [           ] - [      ]

gene: [      ] from [           ] - [      ]

terminator: [      ] from [           ] - [      ]

Terminal Inverted Repeat: [      ] from [           ] - [      ]
```

76) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02353**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [      ] from [           ] - [      ]  
intron: [      ] from [           ] - [      ]  
gene: [      ] from [           ] - [      ]  
terminator: [      ] from [           ] - [      ]  
promoter: [      ] from [           ] - [      ]  
intron: [      ] from [           ] - [      ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

77) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02355**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

78) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

80) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02367

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

81) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02368**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

82) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02386**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

83) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02423**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

84) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

85) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

]

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
2) []	ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
3) []	ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
4) []	WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 15-ID-Ta01		
Location GPS Coordinates: [], []		
Release Site History: This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
2) AgraServ NUE	<p>ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	
Location Unique ID: 16-ID-Ta-02		
Location GPS Coordinates: [], [] [], [] [], [] [], []		
Release Site History: This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
3) Agro-Tech Research Farm	<p>ND County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 16-ND-Ta01		
Location GPS Coordinates: [], [] [], [] [], []		
Release Site History: This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
4) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 16-WA-Ta01		
Location GPS Coordinates: [], []		

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Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS**Production Design**

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[

]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only".

Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment.

Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use.

Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site.

All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

[

]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[

]

14. ATTACHMENTS**Attachments**

Biogemma Wheat Design Protocol 2016 (3/22/2016 @ 10:56 AM)

15. ADDITIONAL INFORMATION**16. COURTESY JUSTIFICATION**

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, (b)(6) hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b)(6)

18. DATE

March 22, 2016

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New Amendment Renewal Variance Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: [42.800592, -112.809722]

SW: [42.799192, -112.809637]

NE: [42.800549, -112.807507]

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

SE: [42.799129, -112.807467]
=====

The amendment for application #15-349-103rm-a2 is being made because the null-segregants from two different constructs were planted without prior permission. These constructs are Phenotypic Designation #86 (T01398) and Phenotypic Designation #87 (T01736) on the application. Both of these constructs are planted at two locations, as follows: 16-ID-Ta-02 (Power County, Idaho) and 16-ND-Ta01 (McHenry County, ND). These constructs have been used at those locations in past years, so there are no changes to our design protocols.

Previous Permit Number(s): 15-349-103rm-a1

7. MEANS OF MOVEMENT

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No

Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

N/A

9. REGULATED ARTICLE

Scientific Name: Triticum aestivum

Common Name: Wheat

Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne Route De Ennezat Chappes, Puy de Dome 63720 France	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proZmVp1] **from** [Zea mays] - [Maize Viviparous1 gene promoter. Tissue specific expression (embryo and aleurone of cereal maize kernels) of the gene downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

3) Phenotypic Designation Name:

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Identifying Line(s):**Construct(s):**

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsSALT] **from** [Oryza sativa] - [Rice saltT gene promoter. Inducible expression of the gene downstream its sequence in salty growing conditions]

intron: [intOsSALT] **from** [Oryza sativa] - [Partial sequence of the saltT promoter (inducible in salty growing condition) from rice, that is not transcribed (located before the ATG sequence). Ensures a good transcription of the gene inserted downstream its sequence.]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

4) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01782

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGDAS1] **from** [Triticum aestivum] - [Glutamine Dependent Asparagine Synthetase. Aspartate synthetase dependant to glutamine concentration. Reaction= ATP + L-aspartate + L-glutamine + H(2)O ; AMP + diphosphate + L-asparagine + L-glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

6) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

7) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

8) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)**Gene of interest**

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [NtNPK1] **from** [Nicotiana tabacum] - [Mitogen Activated Protein kinase kinase kinase. Mitogen-activated protein kinase kinase kinase signal transduction pathway]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

10) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01822

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]
 intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]
 gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]
 terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]
 Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

11) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01823

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

14) Phenotypic Designation Name:

Identifying Line(s):

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Construct(s):	T 01830
Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	
Phenotype(s)	
AP - [Enhanced nitrogen use]	
Genotype(s)	
Gene silencer promoter: [proOsPRO0110] from [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]	
intron: [intZmSH1] from [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
intron: [intOsTubL] from [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
terminator: [terAtSac66] from [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]	
Selectable Marker Terminal Inverted Repeat: [ZmDs5'Ac] from [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	
promoter: [proVirSc4] from [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]	
intron: [intAtFAD2] from [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]	
gene: [EcNPTII] from [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]	
terminator: [terAtNOS] from [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]	
Terminal Inverted Repeat: [ZmDs3'Ac] from [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	

15) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01832**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

17) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

18) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmKnotted1] **from** [Zea Mays] - [Maize knotted1 gene promoter. Specific expression in the apical meristem]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

19) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

20) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsLRK1] **from** [Oryza sativa] - [LRK1 regulates rice branch number by enhancing cellular proliferation]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

22) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDEP1] **from** [Oryza sativa] - [PEBP (phosphatidylethanolamine-binding protein) like domain protein sharing some homology with the N terminus of GS3]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

23) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

24) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTin3A] **from** [Brachypodium distachyon] - [Protein involved in tiller development]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

25) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTkw2] **from** [Brachypodium distachyon] - [Thousand Kernel Weight 2. EST annotated "Large Tegument protein", candidate gene under yield QTL]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

26) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01985

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)**Gene of interest**

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

27) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaPAMT] **from** [Triticum aestivum] - [Protein Arginine N-MethylTransferase. Catalyzes the addition of a methyl group to an arginine residue]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

28) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01987

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMFSA] **from** [Triticum aestivum] - [Major Facilitator Superfamily Antiporter. Membrane protein involved as single polypeptide secondary carriers, transporting a diverse range of substrates]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

29) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01988

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMPase] **from** [Triticum aestivum] - [Metallopeptidase. Peptidase with metal cofactor: Catalysis of the hydrolysis of peptide bonds by a mechanism in which water acts as a nucleophile, one or two metal ions hold the water molecule in place, and charged amino acid side chains are ligands for the metal ions.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

30) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrbu3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrbu3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaZFP] **from** [Triticum aestivum] - [Zinc finger protein. Transcription factor related to nitrogen metabolism. Close relative of wheat Zinc Finger Protein1 gene]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

31) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01991

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaT6PS] **from** [Triticum aestivum] - [Trehalose-6-phosphate synthase. Trehalose-6-phosphate synthase involved in sugar metabolism. Reaction: UDP-glucose + D-glucose 6-phosphate ; UDP + alpha,alpha-trehalose 6-phosphate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

32) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02003

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

33) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02004

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved fungal disease resistance

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrb3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrb3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

34) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

35) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

36) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02051

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsNAC10] **from** [Oryza sativa] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity. NAC family transcription factor involved in stress tolerance response]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

37) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02094

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation

reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [HvSUT1] **from** [Hordeum vulgare] - [sucrose transporter]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

38) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02110

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaCYCB2] **from** [Triticum aestivum] - [Cyclin B2 is a member of the B-type cyclins and are essential components of the cell cycle regulatory machinery.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin

phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

40) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' pregin of the califlower mosaic virus,]promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to α-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

42) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02134

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' preregion of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

43) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02135

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

44) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02137

Mode of Transformation: Agrobacterium tumefaciens disarmed

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH₃ =>; Gln)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

45) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02154

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

46) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02155

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

47) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmAspAT1] **from** [Zea mays] - [Aspartate AminoTransferasel. Aspartate aminotransferase catalyzes the reversible interconversions of glutamate and aspartate, and their 2-keto analogs: Glutamate + oxaloacetate (OAA) ; 2-oxoglutarate + aspartate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

48) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumLOG] **from** [Agrobacterium tumefaciens] - [Lysine decarboxylase]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

50) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaBril] **from** [Triticum aestivum] - [Brassinosteroid-insensitive1. Brassinosteroid LRR receptor kinase involved in brassinosteroid signal transduction]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtCKX3] **from** [Arabidopsis thaliana] - [Involved in degradation of cytokinins]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsSCI2] **from** [Oryza sativa] - [Rice Subtilisin_chymotrypsin_inhibitor2 promoter. Inducible expression of the gene downstream its sequence under abiotic stress (salt, drought, ABA, cold)]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.

Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtTPS1] **from** [Arabidopsis thaliana] - [Enzyme of the threahose synthase pathway - osmoprotectant/ signaling molecule]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

54) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 02268**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATHRD] **from** [Arabidopsis thaliana] - [The HARDY protein is a transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

55) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02269**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ALSAP] **from** [Allocasuarina littoralis] - [Stress Associated Protein. Probable Ubiquitin ligase]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

57) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02304

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

58) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaARF22] **from** [Triticum aestivum] - [Transcription factor involved in pericarp development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

59) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSHN2] **from** [Arabidopsis thaliana] - [AP2 type transcription factor is involved in cuticular wax accumulation and in stomatal density]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

60) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02334

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsAT] **from** [Oryza sativa] - [Aminotransferase. catalyzes the transfer of an amino group between an amino acid and an α-keto acid]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [protoActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

61) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02335

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsHisTpter] **from** [Oryza sativa] - [Histidine AA transporter. amino acid transporter]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

62) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02336

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmAGAT2] **from** [Zea mays] - [Conversion of glyoxylate into glycine]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

63) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02337

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmANAC075] **from** [Zea mays] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity involved in drought stress]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region

(terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

64) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02339

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbFd_NADP_Reductase] **from** [Sorghum bicolor] - [Ferredoxin-NADP reductase. belongs to the family of oxidoreductases involved in the transfer of electrons]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

65) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02342

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

Signal peptide: [ctpRca] **from** [Zea mays] - [Chloroplastid transit peptide from Rubisco Activase gene]

gene: [BlnAGK] **from** [Brevibacillus laterosporus] - [Enzyme involved in Arginine biosynthesis]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green

fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaWali5] **from** [Triticum aestivum] - [Wali5 protein is a transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaBamy2] **from** [Triticum aestivum] - [The bamylose protein is a putative amylase]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal

kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

69) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intrон: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

intrон: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

70) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02347

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a

Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSAP5] **from** [Arabidopsis thaliana] - [Stress Associated protein 5]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s):

T 02349

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsZnFG18] **from** [Oryza sativa] - [ZnFg CCCH domain-containing protein 18. Zinc

finger domain containing transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

73) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02350

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmDof1] **from** [Zea mays] - [Dof1 domain containing transcription factor. Dof proteins share a unique and highly conserved DNA binding domain with one C2-C2 zinc finger motif. Dof proteins can function as transcriptional activators or repressors of tissue-specific and light-regulated gene expression in plants (carbon metabolism)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

74) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaPPI_FKBP] **from** [Triticum aestivum] - [Peptidyl-prolyl cis-trans isomerase, FKBP-type family protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

75) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02352

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [HvAl] **from** [Hordeum vulgare] - [Chaperone like protein. Member of the Late Embryogenesis Abundant (LEA) protein family. Chaperone like protein linked to drought tolerance]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

76) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02353

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmASR] **from** [Zea mays] - [ABA Stress Ripening induced protein. ASR proteins are induced by abscisic acid (ABA), stress and ripening. First described in tomato, at least seven genes have been found in maize. ASR1 is one of the 7 genes isolated so far. ASR protein have a key role in the mechanism conducting to drought and salt resistance via ABA and sugar signalization]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbPEPC] **from** [Sorghum bicolor] - [PhosphoEnol Pyruvate Carboxylase. C4 photosynthetic carbon assimilation cycle enzyme. Reaction: PEP + CO₂ --->; OxaloAcetate + Pi]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

77) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02355

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [EcBetA] **from** [E. Coli] - [The Choline Dehydrogenase is an enzyme that catalyzes the chemical reaction from the substrates choline and acceptor, whereas its two products are betaine aldehyde and reduced acceptor.]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsrubii3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubii3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ThVP] **from** [Theellungielle halophila] - [Theellungielle halophila H(+)-pyrophosphatase. vacuolar H+-pyrophosphatase, enzyme (EC 3.6.1.1) that catalyzes the conversion of one molecule of pyrophosphate to two phosphate ions]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinothricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

78) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsNAC5] **from** [Oryza sativa] - [NAC family transcription factor. NAC family transcriptional factor putatively involved in kernel filling]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsLEA3.1] **from** [Oryza sativa] - [Chaperone like protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and Galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

80) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02367

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AnNADP_GDHA] **from** [Aspergillus niger] - [The NADP glutamate dehydrogenase A converts 2-oxo-glutarate into L-glutamate by incorporating NH₃ (EC:1,41,4)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

81) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02368

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmEF_Tu] **from** [Zea mays] - [EF-Tu mediates the entry of the aminoacyl tRNA into a free site of the ribosome]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

82) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02386

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [TaMEG1b] **from** [Triticum aestivum] - [Maternally Expressed Gene1. Wheat endosperm transfert cell-specific gene with a maternal parent of origin pattern expression.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

83) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02423

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

84) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ScTPS1+ScTPS2_fusion] **from** [Saccharomyces cerevisiae] - [Regulation of synthesis of trehalose]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from

rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinotricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

85) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [OsSAP] **from** [Oryza sativa] - [senescence-associated rhodanese-like domain containing protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

86) Phenotypic Designation Name: T01398

Identifying Line(s): null-segregant bulk only

Construct(s): pHMG-SPA2B--JTT.gb

Mode of Transformation: Agrobacterium tumefaciens, disarmed

Phenotype Description: PQ - [storage protein altered]

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

PQ - Storage protein altered

Genotype(s)

Selectable Marker

5`UTR: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

3'UTR: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Gene(s) of Interest

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

Gene: [TaSPA2] **from** [Triticum aestivum] - [SPA Transcription factor 2 involved in storage protein accumulation in wheat endosperm]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

87) Phenotypic Designation Name: T01736

Identifying Line(s): bulk of null-segregants only.

Construct(s): pBIOS1675

Mode of Transformation:	Agrobacterium tumefaciens, disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved yield under low nitrogen supply

Phenotype(s)

AP - Nitrogen utilization efficiency increase

Genotype(s)

Selectable Marker

5`UTR: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

Promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [5'end non coding region of SCSV. Constitutive expression of the gene downstream its sequence]

Intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [EcNPTII] **from** [Streptomyces hygroscopicus] - [Coding sequence of the aminophotransferase gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group of kanamycin]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

3`UTR: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Gene(s) of Interest

Promoter: [proOsAnt1] **from** [Oryza sativa] - [Promoter of rice antiquin 1. Root specific promoter slightly inducible by abiotic stress]

Gene: [HvALaAT] **from** [Hordeum vulgare] - [Alanine aminotransferase 2 transferring the amine group from glutamate on pyruvate to form alanine (reversible reaction)]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	<p>IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
2) [AgraServ]	<p>ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
3) [Agro-Tech Research Farm]	<p>ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
4) [Qualls Ag Laboratory]	<p>WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
Location Unique ID:	15-ID-Ta01	
Location GPS Coordinates:	[42.804648], [-112.790011]	
Release Site History:	This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
2) AgraServ NUE	<p>ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	
Location Unique ID:	16-ID-Ta-02	
Location GPS Coordinates:	[42.800000], [-112.809722] [42.799000], [-112.809637] [42.800000], [-112.807507] [42.799129], [-112.807467]	
Release Site History:	This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
3) Agro-Tech Research Farm	<p>ID County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
Location Unique ID:	16-ND-Ta01	
Location GPS Coordinates:	[48.172554], [-101.001077] [48.178800], [-101.000472] [48.156788], [-100.978399]	
Release Site History:	This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
4) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
Location Unique ID:	16-WA-Ta01	
Location GPS Coordinates:	[47.151634], [-119.560611]	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS

Production Design

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[The purpose of the introduction is to evaluate the performance or produce seed for research purpose only. Plants will be grown under various environment with various level of fertilisation or various level of watering. The performance will be determined by collecting various phenotyping data as the grain yield. The release site will be spatially isolated by no less than 130 feet from sexually compatible species. The release site will be surrounded by border and/or buffer area. All equipment used in the release site will be thoroughly cleaned at the release site. After harvest, the remaining material will incorporate to the soil and left for devitalization by the elements].

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only". Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment. Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use. Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site. All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

["Regulated wheat will be planted only at the field site specified in the permit. Field sites will be well-defined with stakes and GPS coordinates. A buffer area of no less than 13 feet will separate wheat regulated under this permit and any other planted agricultural material. The field site, border rows and buffer area will be monitored for volunteers for the four successive growing seasons after harvest. Volunteers will be removed prior to flowering and destroyed. A minimum of one monitoring every 4 weeks is performed at the field site. Any volunteer plants will be destroyed by any one of the following methods : mechanical grinding or other methods to incorporate the plant into the soil or chemical treatment. The monitoring area is left fallow or planted with a distinct and non-sexually compatible crop. The soil preparation and planting of the crop in the monitoring area is made independently from the rest of the field."]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[Seed or other material capable of propagation will be devitalized by autoclaving, burning or incineration, mechanical grinding or crushing, herbicide treatment, or returning to the field site and burying at the field site. Seed not used in the field trial will be returned to facility for storage or destruction.]

14. ATTACHMENTS

CBI	CBI-Deleted/Non-CBI
	Biogemma Wheat Design Protocol 2016 (5/6/2016 @ 01:35 PM)

15. ADDITIONAL INFORMATION

16. COURTESY JUSTIFICATION

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, (b)(6), hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b)(6)

18. DATE

May 6, 2016

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New
- Amendment
- Renewal
- Variance
- Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: []
 SW: []
 NE: []

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

SE: []

The amendment for application #15-349-103rm-a2 is being made because the null-segregants from two different constructs were planted without prior permission. These constructs are Phenotypic Designation #86 (T01398) and Phenotypic Designation #87 (T01736) on the application. Both of these constructs are planted at two locations, as follows: 16-ID-Ta-02 (Power County, Idaho) and 16-ND-Ta01 (McHenry County, ND). These constructs have been used at those locations in past years, so there are no changes to our design protocols.

Previous Permit Number(s): 15-349-103rm-a1**7. MEANS OF MOVEMENT**

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATIONHave you previously applied for variance(s) that you wish to apply to this permit? Yes No**Variance Number(s):****If so, describe in a brief summary how the variance will be applied:**

N/A

9. REGULATED ARTICLE**Scientific Name:** Triticum aestivum**Common Name:** Wheat**Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:**

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne Route De Ennezat Chappes, Puy de Dome 63720 France	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**3) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s):

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**4) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01782**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

6) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

7) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

8) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

10) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01822**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.
Improved yield under low nitrogen supply**Phenotype(s)**

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

11) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01823**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**12) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

14) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01830

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

 promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene: [] **from** [] - []

 terminator: [] **from** [] - []

 Terminal Inverted Repeat: [] **from** [] - []

15) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01832

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene fragment: [] **from** [] - []
 intron: [] **from** [] - []
 gene fragment: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

17) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01921**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

18) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**19) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

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Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

20) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**22) Phenotypic Designation Name:**

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**23) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

24) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

25) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

26) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01985

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

27) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]  
Terminal Inverted Repeat: [           ] from [           ] - [           ]
```

28) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01987

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]
```

Selectable Marker

```
Terminal Inverted Repeat: [           ] from [           ] - [           ]  
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

29) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01988**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

30) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

31) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s):

T 01991

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**32) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02003**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved fungal disease resistance

Phenotype(s)

FR - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

33) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02004

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

34) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

35) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

36) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02051**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

37) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02094**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []

```
gene: [      ] from [      ] - [  
]  
terminator: [      ] from [      ] - [  
]  
promoter: [      ] from [      ] - [  
]  
intron: [      ] from [      ] - [  
]  
gene: [      ] from [      ] - [  
]  
terminator: [      ] from [      ] - [  
]  
  
Selectable Marker  
Terminal Inverted Repeat: [      ] from [      ] - [  
]  
]  
promoter: [      ] from [      ] - [  
]  
intron: [      ] from [      ] - [  
]  
]  
gene: [      ] from [      ] - [  
]  
]  
terminator: [      ] from [      ] - [  
]  
]  
Terminal Inverted Repeat: [      ] from [      ] - [  
]  
]
```

38) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02110**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

40) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

42) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02134**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

43) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02135**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**44) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02137**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

[]

gene: [] **from** [] - []

terminator: [] **from** [] - []

[]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

45) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02154**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

46) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02155**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

47) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

48) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

]

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

50) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

51) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

54) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02268

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

[]

55) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02269

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

57) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02304**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

58) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

59) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

60) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02334**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

```
promoter: [           ] from [           ] - [  
          ]  
gene: [     ] from [           ] - [  
          ]  
terminator: [       ] from [           ] - [  
          ]  
promoter: [           ] from [           ] - [  
          ]  
intron: [       ] from [           ] - [  
          ]  
gene: [     ] from [           ] - [  
          ]  
  
terminator: [       ] from [           ] - [  
          ]  
Terminal Inverted Repeat: [       ] from [           ] - [  
          ]
```

61) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02335**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

62) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02336**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

63) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02337**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

64) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02339**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

65) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02342**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

Signal peptide: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

68) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

69) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

```
promoter: [ ] from [ ] - [ ]  
intron: [ ] from [ ] - [ ]  
gene: [ ] from [ ] - [ ]  
  
terminator: [ ] from [ ] - [ ]  
Terminal Inverted Repeat: [ ] from [ ] - [ ]
```

70) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02347**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] from [] - []

intron: [] from [] - []

gene: [] from [] - []

terminator: [] from [] - []

Selectable Marker

Terminal Inverted Repeat: [] from [] - []

promoter: [] from [] - []

gene: [] from [] - []

terminator: [] from [] - []

promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

72) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02349**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []

```
terminator: [ ] from [ ] - [ ]  
promoter: [ ] from [ ] - [ ]  
intron: [ ] from [ ] - [ ]  
gene: [ ] from [ ] - [ ]  
  
terminator: [ ] from [ ] - [ ]  
Terminal Inverted Repeat: [ ] from [ ] - [ ]
```

73) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02350**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] from [] - []

intron: [] from [] - []

gene: [] from [] - []

terminator: [] from [] - []

Selectable Marker

Terminal Inverted Repeat: [] from [] - []

promoter: [] from [] - []

```

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

promoter: [          ] from [           ] - [
]

intron: [          ] from [           ] - [
]

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

Terminal Inverted Repeat: [          ] from [           ] - [
]

```

74) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]

intron: [] **from** [] - [
]

gene: [] **from** [] - [
]

terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]

promoter: [] **from** [] - [
]

```
gene: [      ] from [           ] - [  
          ]  
  
terminator: [      ] from [           ] - [  
          ]  
  
promoter: [      ] from [           ] - [  
          ]  
  
intron: [      ] from [           ] - [  
          ]  
  
gene: [      ] from [           ] - [  
          ]  
  
  
terminator: [      ] from [           ] - [  
          ]  
  
Terminal Inverted Repeat: [      ] from [           ] - [  
          ]
```

75) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02352**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]intron: [] **from** [] - [
]gene: [] **from** [] - [
]terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]promoter: [] **from** [] - [
]

```
]

gene: [      ] from [           ] - [      ]

terminator: [      ] from [           ] - [      ]

promoter: [      ] from [           ] - [      ]

intron: [      ] from [           ] - [      ]

gene: [      ] from [           ] - [      ]

terminator: [      ] from [           ] - [      ]

Terminal Inverted Repeat: [      ] from [           ] - [      ]
```

76) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02353**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [      ] from [           ] - [      ]

intron: [      ] from [           ] - [      ]

gene: [      ] from [           ] - [      ]

terminator: [      ] from [           ] - [      ]

promoter: [      ] from [           ] - [      ]

intron: [      ] from [           ] - [      ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

77) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02355**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

78) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

80) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02367

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

81) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02368**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

82) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02386**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

83) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02423**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

84) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

85) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02542**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

86) Phenotypic Designation Name: T01398**Identifying Line(s):** null-segregant bulk only

Construct(s): pHMG-SPA2B--JTT.gb

Mode of Transformation: Agrobacterium tumefaciens, disarmed

Phenotype Description: PQ - []

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

PQ - Storage protein altered

Genotype(s)

Selectable Marker

5'UTR: [] **from** [] - []

Promoter: [] **from** [] - []

Intron: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

3'UTR: [] **from** [] - []

Gene(s) of Interest

Promoter: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

87) Phenotypic Designation Name: T01736

Identifying Line(s): bulk of null-segregants only.

Construct(s): pBIOS1675

Mode of Transformation: Agrobacterium tumefaciens, disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - Nitrogen utilization efficiency increase

Genotype(s)

Selectable Marker

5`UTR: [] **from** [] - []

Promoter: [] **from** [] - []

Intron: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

3`UTR: [] **from** [] - []

Gene(s) of Interest

Promoter: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
2) []	ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
3) []	ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
4) []	WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 15-ID-Ta01		
Location GPS Coordinates: [], []		
Release Site History: This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
2) AgraServ NUE	<p>ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	
Location Unique ID: 16-ID-Ta-02		
Location GPS Coordinates: [], [] [], [] [], [] [], []		
Release Site History: This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
3) Agro-Tech Research Farm	<p>ND County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 16-ND-Ta01		
Location GPS Coordinates: [], [] [], [] [], []		
Release Site History: This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
4) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 16-WA-Ta01		
Location GPS Coordinates: [], []		

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Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS**Production Design**

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[

].

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only".

Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment.

Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use.

Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site.

All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

[

]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[

]

14. ATTACHMENTS**Attachments**

Biogemma Wheat Design Protocol 2016 (5/6/2016 @ 01:35 PM)

15. ADDITIONAL INFORMATION**16. COURTESY JUSTIFICATION**

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, (b)(6), hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b)(6)

18. DATE

May 6, 2016

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New Amendment Renewal Variance Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: [42.800592, -112.809722]

SW: [42.799192, -112.809637]

NE: [42.800549, -112.807507]

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

SE: [42.799129, -112.807467]

Previous Permit Number(s): 15-349-103rm-a1

7. MEANS OF MOVEMENT

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No
Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

N/A

9. REGULATED ARTICLE

Scientific Name: Triticum aestivum

Common Name: Wheat

Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne Route De Ennezat Chappes, Puy de Dome 63720 France	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proZmVp1] **from** [Zea mays] - [Maize Viviparous1 gene promoter. Tissue specific expression (embryo and aleurone of cereal maize kernels) of the gene downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

3) Phenotypic Designation Name:

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Identifying Line(s):**Construct(s):**

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsSALT] **from** [Oryza sativa] - [Rice saltT gene promoter. Inducible expression of the gene downstream its sequence in salty growing conditions]

intron: [intOsSALT] **from** [Oryza sativa] - [Partial sequence of the saltT promoter (inducible in salty growing condition) from rice, that is not transcribed (located before the ATG sequence). Ensures a good transcription of the gene inserted downstream its sequence.]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

4) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01782

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGDAS1] **from** [Triticum aestivum] - [Glutamine Dependent Asparagine Synthetase. Aspartate synthetase dependant to glutamine concentration. Reaction= ATP + L-aspartate + L-glutamine + H(2)O ; AMP + diphosphate + L-asparagine + L-glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

6) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

7) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

8) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)**Gene of interest**

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [NtNPK1] **from** [Nicotiana tabacum] - [Mitogen Activated Protein kinase kinase kinase. Mitogen-activated protein kinase kinase kinase signal transduction pathway]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

10) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01822

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]
 intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]
 gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]
 terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]
 Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

11) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01823

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oryza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

14) Phenotypic Designation Name:

Identifying Line(s):

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Construct(s):	T 01830
Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	
Phenotype(s)	
AP - [Enhanced nitrogen use]	
Genotype(s)	
Gene silencer promoter: [proOsPRO0110] from [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]	
intron: [intZmSH1] from [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
intron: [intOsTubL] from [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
terminator: [terAtSac66] from [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]	
Selectable Marker Terminal Inverted Repeat: [ZmDs5'Ac] from [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	
promoter: [proVirSc4] from [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]	
intron: [intAtFAD2] from [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]	
gene: [EcNPTII] from [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]	
terminator: [terAtNOS] from [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]	
Terminal Inverted Repeat: [ZmDs3'Ac] from [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	

15) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01832**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

17) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

18) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmKnotted1] **from** [Zea Mays] - [Maize knotted1 gene promoter. Specific expression in the apical meristem]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

19) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

20) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsLRK1] **from** [Oryza sativa] - [LRK1 regulates rice branch number by enhancing cellular proliferation]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

22) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDEP1] **from** [Oryza sativa] - [PEBP (phosphatidylethanolamine-binding protein) like domain protein sharing some homology with the N terminus of GS3]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

23) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

24) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTin3A] **from** [Brachypodium distachyon] - [Protein involved in tiller development]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

25) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTkw2] **from** [Brachypodium distachyon] - [Thousand Kernel Weight 2. EST annotated "Large Tegument protein", candidate gene under yield QTL]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

26) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01985

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - [Yield increased]

Genotype(s)**Gene of interest**

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

27) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaPAMT] **from** [Triticum aestivum] - [Protein Arginine N-MethylTransferase. Catalyzes the addition of a methyl group to an arginine residue]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

28) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01987

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMFSA] **from** [Triticum aestivum] - [Major Facilitator Superfamily Antiporter. Membrane protein involved as single polypeptide secondary carriers, transporting a diverse range of substrates]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

29) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01988

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMPase] **from** [Triticum aestivum] - [Metallopeptidase. Peptidase with metal cofactor: Catalysis of the hydrolysis of peptide bonds by a mechanism in which water acts as a nucleophile, one or two metal ions hold the water molecule in place, and charged amino acid side chains are ligands for the metal ions.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

30) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrbu3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrbu3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaZFP] **from** [Triticum aestivum] - [Zinc finger protein. Transcription factor related to nitrogen metabolism. Close relative of wheat Zinc Finger Protein1 gene]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

31) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01991

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaT6PS] **from** [Triticum aestivum] - [Trehalose-6-phosphate synthase. Trehalose-6-phosphate synthase involved in sugar metabolism. Reaction: UDP-glucose + D-glucose 6-phosphate ; UDP + alpha,alpha-trehalose 6-phosphate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

32) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02003

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

33) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02004

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved fungal disease resistance

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrb3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrb3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

34) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

35) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

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Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

36) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02051

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsNAC10] **from** [Oryza sativa] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity. NAC family transcription factor involved in stress tolerance response]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

37) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02094

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation

reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [HvSUT1] **from** [Hordeum vulgare] - [sucrose transporter]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

38) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02110

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaCYCB2] **from** [Triticum aestivum] - [Cyclin B2 is a member of the B-type cyclins and are essential components of the cell cycle regulatory machinery.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin

phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

40) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

41) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02133

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' pregin of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to α-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

42) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02134

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' preregion of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

43) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02135

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

44) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02137

Mode of Transformation: Agrobacterium tumefaciens disarmed

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Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH₃ =>; Gln)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

45) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02154

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

46) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02155

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

47) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmAspAT1] **from** [Zea mays] - [Aspartate AminoTransferasel. Aspartate aminotransferase catalyzes the reversible interconversions of glutamate and aspartate, and their 2-keto analogs: Glutamate + oxaloacetate (OAA) ; 2-oxoglutarate + aspartate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

48) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumLOG] **from** [Agrobacterium tumefaciens] - [Lysine decarboxylase]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

50) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaBril] **from** [Triticum aestivum] - [Brassinosteroid-insensitive1. Brassinosteroid LRR receptor kinase involved in brassinosteroid signal transduction]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtCKX3] **from** [Arabidopsis thaliana] - [Involved in degradation of cytokinins]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsSCI2] **from** [Oryza sativa] - [Rice Subtilisin_chymotrypsin_inhibitor2 promoter. Inducible expression of the gene downstream its sequence under abiotic stress (salt, drought, ABA, cold)]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.

Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtTPS1] **from** [Arabidopsis thaliana] - [Enzyme of the threahose synthase pathway - osmoprotectant/ signaling molecule]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

54) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 02268**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATHRD] **from** [Arabidopsis thaliana] - [The HARDY protein is a transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

55) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02269**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ALSAP] **from** [Allocasuarina littoralis] - [Stress Associated Protein. Probable Ubiquitin ligase]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

57) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02304

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

58) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaARF22] **from** [Triticum aestivum] - [Transcription factor involved in pericarp development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

59) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSHN2] **from** [Arabidopsis thaliana] - [AP2 type transcription factor is involved in cuticular wax accumulation and in stomatal density]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

60) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02334

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsAT] **from** [Oryza sativa] - [Aminotransferase. catalyzes the transfer of an amino group between an amino acid and an α-keto acid]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [protoActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

61) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02335

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsHisTpter] **from** [Oryza sativa] - [Histidine AA transporter. amino acid transporter]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

62) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02336

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmAGAT2] **from** [Zea mays] - [Conversion of glyoxylate into glycine]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

63) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02337

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmANAC075] **from** [Zea mays] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity involved in drought stress]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region

(terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

64) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02339

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbFd_NADP_Reductase] **from** [Sorghum bicolor] - [Ferredoxin-NADP reductase. belongs to the family of oxidoreductases involved in the transfer of electrons]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

65) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02342

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

Signal peptide: [ctpRca] **from** [Zea mays] - [Chloroplastid transit peptide from Rubisco Activase gene]

gene: [BlnAGK] **from** [Brevibacillus laterosporus] - [Enzyme involved in Arginine biosynthesis]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green

fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaWali5] **from** [Triticum aestivum] - [Wali5 protein is a transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaBamy2] **from** [Triticum aestivum] - [The bamylose protein is a putative amylase]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal

kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

69) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

70) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02347

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a

Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSAP5] **from** [Arabidopsis thaliana] - [Stress Associated protein 5]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s):

T 02349

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsZnFG18] **from** [Oryza sativa] - [ZnFg CCCH domain-containing protein 18. Zinc

finger domain containing transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

Gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

73) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02350

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmDof1] **from** [Zea mays] - [Dof1 domain containing transcription factor. Dof proteins share a unique and highly conserved DNA binding domain with one C2-C2 zinc finger motif. Dof proteins can function as transcriptional activators or repressors of tissue-specific and light-regulated gene expression in plants (carbon metabolism)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

74) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaPPI_FKBP] **from** [Triticum aestivum] - [Peptidyl-prolyl cis-trans isomerase, FKBP-type family protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

75) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02352

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [HvAl] **from** [Hordeum vulgare] - [Chaperone like protein. Member of the Late Embryogenesis Abundant (LEA) protein family. Chaperone like protein linked to drought tolerance]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

76) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02353

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmASR] **from** [Zea mays] - [ABA Stress Ripening induced protein. ASR proteins are induced by abscisic acid (ABA), stress and ripening. First described in tomato, at least seven genes have been found in maize. ASR1 is one of the 7 genes isolated so far. ASR protein have a key role in the mechanism conducting to drought and salt resistance via ABA and sugar signalization]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbPEPC] **from** [Sorghum bicolor] - [PhosphoEnol Pyruvate Carboxylase. C4 photosynthetic carbon assimilation cycle enzyme. Reaction: PEP + CO₂ --->; OxaloAcetate + Pi]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

77) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02355

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [EcBetA] **from** [E. Coli] - [The Choline Dehydrogenase is an enzyme that catalyzes the chemical reaction from the substrates choline and acceptor, whereas its two products are betaine aldehyde and reduced acceptor.]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsrubii3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubii3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ThVP] **from** [Theellungielle halophila] - [Theellungielle halophila H(+)-pyrophosphatase. vacuolar H+-pyrophosphatase, enzyme (EC 3.6.1.1) that catalyzes the conversion of one molecule of pyrophosphate to two phosphate ions]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinothricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

78) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsNAC5] **from** [Oryza sativa] - [NAC family transcription factor. NAC family transcriptional factor putatively involved in kernel filling]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsLEA3.1] **from** [Oryza sativa] - [Chaperone like protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and Galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

80) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02367

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AnNADP_GDHA] **from** [Aspergillus niger] - [The NADP glutamate dehydrogenase A converts 2-oxo-glutarate into L-glutamate by incorporating NH₃ (EC:1,41,4)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

81) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02368

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmEF_Tu] **from** [Zea mays] - [EF-Tu mediates the entry of the aminoacyl tRNA into a free site of the ribosome]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

82) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02386

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [TaMEG1b] **from** [Triticum aestivum] - [Maternally Expressed Gene1. Wheat endosperm transfert cell-specific gene with a maternal parent of origin pattern expression.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

83) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02423

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

84) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ScTPS1+ScTPS2_fusion] **from** [Saccharomyces cerevisiae] - [Regulation of synthesis of trehalose]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from

rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinotricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

85) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [OsSAP] **from** [Oryza sativa] - [senescence-associated rhodanese-like domain containing protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

86) Phenotypic Designation Name: T01398

Identifying Line(s): null-segregant bulk only

Construct(s): pHMG-SPA2B--JTT.gb

Mode of Transformation: Agrobacterium tumefaciens, disarmed

Phenotype Description: PQ - [storage protein altered]

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

PQ - Storage protein altered

Genotype(s)

Selectable Marker

5`UTR: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

3'UTR: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Gene(s) of Interest

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

Gene: [TaSPA2] **from** [Triticum aestivum] - [SPA Transcription factor 2 involved in storage protein accumulation in wheat endosperm]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

87) Phenotypic Designation Name: T01736

Identifying Line(s): bulk of null-segregants only.

Construct(s): pBIOS1675

Mode of Transformation:	Agrobacterium tumefaciens, disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved yield under low nitrogen supply

Phenotype(s)

AP - Nitrogen utilization efficiency increase

Genotype(s)

Selectable Marker

5`UTR: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

Promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [5'end non coding region of SCSV. Constitutive expression of the gene downstream its sequence]

Intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [EcNPTII] **from** [Streptomyces hygroscopicus] - [Coding sequence of the aminophotransferase gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group of kanamycin]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

3`UTR: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Gene(s) of Interest

Promoter: [proOsAnt1] **from** [Oryza sativa] - [Promoter of rice antiquin 1. Root specific promoter slightly inducible by abiotic stress]

Gene: [HvALaAT] **from** [Hordeum vulgare] - [Alanine aminotransferase 2 transferring the amine group from glutamate on pyruvate to form alanine (reversible reaction)]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	<p>IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
2) [AgraServ]	<p>ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
3) [Agro-Tech Research Farm]	<p>ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
4) [Qualls Ag Laboratory]	<p>WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID: 15-ID-Ta01		
Location GPS Coordinates: [42.804648], [-112.790011]		
Release Site History: This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years		
Critical Habitat Involved? ____ Yes <input checked="" type="checkbox"/> No		
2) AgraServ NUE	<p>ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	
Location Unique ID: 16-ID-Ta-02		
Location GPS Coordinates: [42.800000], [-112.809722] [42.799000], [-112.809637] [42.800000], [-112.807507] [42.799129], [-112.807467]		
Release Site History: This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.		
Critical Habitat Involved? ____ Yes <input checked="" type="checkbox"/> No		
3) Agro-Tech Research Farm	<p>ID County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID: 16-ND-Ta01		
Location GPS Coordinates: [48.172554], [-101.001077] [48.178800], [-101.000472] [48.156788], [-100.978399]		
Release Site History: This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years		
Critical Habitat Involved? ____ Yes <input checked="" type="checkbox"/> No		
4) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID: 16-WA-Ta01		
Location GPS Coordinates: [47.151634], [-119.560611]		

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS

Production Design

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[The purpose of the introduction is to evaluate the performance or produce seed for research purpose only. Plants will be grown under various environment with various level of fertilisation or various level of watering. The performance will be determined by collecting various phenotyping data as the grain yield. The release site will be spatially isolated by no less than 130 feet from sexually compatible species. The release site will be surrounded by border and/or buffer area. All equipment used in the release site will be thoroughly cleaned at the release site. After harvest, the remaining material will incorporate to the soil and left for devitalization by the elements.]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only". Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment. Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use. Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site. All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

["Regulated wheat will be planted only at the field site specified in the permit. Field sites will be well-defined with stakes and GPS coordinates. A buffer area of no less than 13 feet will separate wheat regulated under this permit and any other planted agricultural material. The field site, border rows and buffer area will be monitored for volunteers for the four successive growing seasons after harvest. Volunteers will be removed prior to flowering and destroyed. A minimum of one monitoring every 4 weeks is performed at the field site. Any volunteer plants will be destroyed by any one of the following methods : mechanical grinding or other methods to incorporate the plant into the soil or chemical treatment. The monitoring area is left fallow or planted with a distinct and non-sexually compatible crop. The soil preparation and planting of the crop in the monitoring area is made independently from the rest of the field."]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[Seed or other material capable of propagation will be devitalized by autoclaving, burning or incineration, mechanical grinding or crushing, herbicide treatment, or returning to the field site and burying at the field site. Seed not used in the field trial will be returned to facility for storage or destruction.]

14. ATTACHMENTS

CBI	CBI-Deleted/Non-CBI
	Biogemma Wheat Design Protocol 2016 (5/6/2016 @ 01:35 PM)

15. ADDITIONAL INFORMATION

16. COURTESY JUSTIFICATION

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, (b)(6), hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b)(6)

18. DATE

May 6, 2016

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New
- Amendment
- Renewal
- Variance
- Amendment, Renewal and/or Variance

Amendment/Renewal Description:

We are doing a wheat study concerning Nitrogen Use Efficiency. The GM wheat 'varieties' in this trial all have constructs with putative nitrogen use efficiency (modifying) genes in them. The field that we originally selected (for this Permit) in Power County, Idaho has too high of a residual nitrogen content, so we have to move this experiment to a different field, still in Power County, Idaho, although it is about one kilometer away from the original field. The new GPS coordinates for the four corners of the 'new' field are:

NW: []
 SW: []
 NE: []

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

SE: []

Previous Permit Number(s): 15-349-103rm-a1**7. MEANS OF MOVEMENT**

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No
Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

N/A

9. REGULATED ARTICLE**Scientific Name:** Triticum aestivum**Common Name:** Wheat**Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:**

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:The genetically engineered lines covered in this permit were created and developed at Biogemma,
Site de la Garenne, route d'Ennezat, 63720 Chappes, France.**Processes, Procedures, and Safeguards Description:**

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard.

At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne Route De Ennezat Chappes, Puy de Dome 63720 France	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**3) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s):

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**4) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01782**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

6) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

7) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

8) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

10) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01822**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.
Improved yield under low nitrogen supply**Phenotype(s)**

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

11) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01823**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**12) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

14) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01830

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 intron: [] **from** [] - []

 gene fragment: [] **from** [] - []

 terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

 promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene: [] **from** [] - []

 terminator: [] **from** [] - []

 Terminal Inverted Repeat: [] **from** [] - []

15) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01832

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer
 promoter: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

16) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01920**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

17) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01921**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

18) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**19) Phenotypic Designation Name:****Identifying Line(s):**

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

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Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

20) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**22) Phenotypic Designation Name:**

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Identifying Line(s):**Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**23) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

24) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

introns: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

25) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

26) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01985

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

27) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]  
Terminal Inverted Repeat: [           ] from [           ] - [           ]
```

28) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01987**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]  
gene: [           ] from [           ] - [           ]  
terminator: [           ] from [           ] - [           ]
```

Selectable Marker

```
Terminal Inverted Repeat: [           ] from [           ] - [           ]  
promoter: [           ] from [           ] - [           ]  
intron: [           ] from [           ] - [           ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

29) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01988**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []
intron: [] **from** [] - []gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

30) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

31) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s):

T 01991

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**32) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02003**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved fungal disease resistance

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

33) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02004

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

34) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

35) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

36) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02051**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

37) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02094**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []

```

gene: [      ] from [      ] - [
]

terminator: [      ] from [      ] - [
]

promoter: [      ] from [      ] - [
]

intron: [      ] from [      ] - [
]

gene: [      ] from [      ] - [
]

terminator: [      ] from [      ] - [
]

Selectable Marker
Terminal Inverted Repeat: [      ] from [      ] - [
]

promoter: [      ] from [      ] - [
]

intron: [      ] from [      ] - [
]

gene: [      ] from [      ] - [
]

terminator: [      ] from [      ] - [
]

Terminal Inverted Repeat: [      ] from [      ] - [
]

```

38) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02110

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

40) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

42) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02134**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

Enhancer: [] **from** [] - []

]

promoter: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

]

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

43) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02135**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:**

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited water and nitrogen supply

Phenotype(s)

AP - []

Genotype(s)Gene of interest
promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []**44) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 02137**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

[]

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

45) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02154**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

46) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02155**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

47) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

48) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

]

intron: [] **from** [] - []

]

gene: [] **from** [] - []

]

terminator: [] **from** [] - []

]

Terminal Inverted Repeat: [] **from** [] - []

]

50) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

51) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

54) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02268

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

55) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02269

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []

Selectable Marker
 Terminal Inverted Repeat: [] **from** [] - []
 promoter: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

57) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02304**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

58) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

59) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

60) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02334**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

```
promoter: [           ] from [           ] - [  
          ]  
gene: [     ] from [           ] - [  
          ]  
terminator: [       ] from [           ] - [  
          ]  
promoter: [           ] from [           ] - [  
          ]  
intron: [       ] from [           ] - [  
          ]  
gene: [     ] from [           ] - [  
          ]  
  
terminator: [       ] from [           ] - [  
          ]  
Terminal Inverted Repeat: [       ] from [           ] - [  
          ]
```

61) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02335**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

62) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02336**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

63) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02337**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

64) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02339**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

65) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02342**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - []

Genotype(s)Gene silencer
promoter: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []intron: [] **from** [] - []gene fragment: [] **from** [] - []terminator: [] **from** [] - []Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

Signal peptide: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

]

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

]

promoter: [] **from** [] - []

intron: [] **from** [] - []

]

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

68) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

69) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene silencer

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

intron: [] **from** [] - []

gene fragment: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

70) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02347**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

promoter: [] **from** [] - []
 intron: [] **from** [] - []
 gene: [] **from** [] - []
 terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
 promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

72) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02349**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []

```
terminator: [ ] from [ ] - [ ]  
promoter: [ ] from [ ] - [ ]  
intron: [ ] from [ ] - [ ]  
gene: [ ] from [ ] - [ ]  
  
terminator: [ ] from [ ] - [ ]  
Terminal Inverted Repeat: [ ] from [ ] - [ ]
```

73) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02350**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] from [] - []

intron: [] from [] - []

gene: [] from [] - []

terminator: [] from [] - []

Selectable Marker

Terminal Inverted Repeat: [] from [] - []

promoter: [] from [] - []

```

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

promoter: [          ] from [           ] - [
]

intron: [          ] from [           ] - [
]

gene: [      ] from [           ] - [
]

terminator: [          ] from [           ] - [
]

Terminal Inverted Repeat: [          ] from [           ] - [
]

```

74) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]

intron: [] **from** [] - [
]

gene: [] **from** [] - [
]

terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]

promoter: [] **from** [] - [
]

```
gene: [      ] from [           ] - [  
          ]  
  
terminator: [      ] from [           ] - [  
          ]  
  
promoter: [      ] from [           ] - [  
          ]  
  
intron: [      ] from [           ] - [  
          ]  
  
gene: [      ] from [           ] - [  
          ]  
  
  
terminator: [      ] from [           ] - [  
          ]  
  
Terminal Inverted Repeat: [      ] from [           ] - [  
          ]
```

75) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02352**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - [
]intron: [] **from** [] - [
]gene: [] **from** [] - [
]terminator: [] **from** [] - [
]

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - [
]promoter: [] **from** [] - [
]

```
        ]  
gene: [      ] from [           ] - [  
          ]  
  
terminator: [       ] from [           ] - [  
          ]  
  
promoter: [       ] from [           ] - [  
          ]  
  
intron: [       ] from [           ] - [  
          ]  
  
gene: [      ] from [           ] - [  
          ]  
  
  
terminator: [       ] from [           ] - [  
          ]  
  
Terminal Inverted Repeat: [       ] from [           ] - [  
          ]
```

76) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02353**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

```
promoter: [       ] from [           ] - [  
          ]  
  
intron: [       ] from [           ] - [  
          ]  
  
gene: [      ] from [           ] - [  
          ]  
  
  
terminator: [       ] from [           ] - [  
          ]  
  
promoter: [       ] from [           ] - [  
          ]  
  
intron: [       ] from [           ] - [  
          ]
```

gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

77) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02355**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []

Selectable Marker
Terminal Inverted Repeat: [] **from** [] - []
promoter: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []
terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

78) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []
intron: [] **from** [] - []
gene: [] **from** [] - []

terminator: [] **from** [] - []
Terminal Inverted Repeat: [] **from** [] - []

80) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02367**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest
promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

81) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02368**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

82) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02386**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []Terminal Inverted Repeat: [] **from** [] - []

]

83) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02423**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []promoter: [] **from** [] - []gene: [] **from** [] - []terminator: [] **from** [] - []promoter: [] **from** [] - []intron: [] **from** [] - []gene: [] **from** [] - []

terminator: [] **from** [] - []

Terminal Inverted Repeat: [] **from** [] - []

]

]

84) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

Gene of interest

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

Selectable Marker

Terminal Inverted Repeat: [] **from** [] - []

promoter: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []

promoter: [] **from** [] - []

intron: [] **from** [] - []

gene: [] **from** [] - []

terminator: [] **from** [] - []
 Terminal Inverted Repeat: [] **from** [] - []

85) Phenotypic Designation Name:
Identifying Line(s):
Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - []

Genotype(s)

 Gene of interest
 promoter: [] **from** [] - []

]

 gene: [] **from** [] - []

 terminator: [] **from** [] - []

Selectable Marker

 Terminal Inverted Repeat: [] **from** [] - []
]

 promoter: [] **from** [] - []

 intron: [] **from** [] - []

 gene: [] **from** [] - []

 terminator: [] **from** [] - []

 Terminal Inverted Repeat: [] **from** [] - []

86) Phenotypic Designation Name: T01398

Identifying Line(s): null-segregant bulk only

Construct(s): pHMG-SPA2B--JTT.gb

Mode of Transformation: Agrobacterium tumefaciens, disarmed

Phenotype Description: PQ - []

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

PQ - Storage protein altered

Genotype(s)

Selectable Marker

5'UTR: [] **from** [] - []

Promoter: [] **from** [] - []

Intron: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

3'UTR: [] **from** [] - []

Gene(s) of Interest

Promoter: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

87) Phenotypic Designation Name: T01736

Identifying Line(s): bulk of null-segregants only.

Construct(s): pBIOS1675

Mode of Transformation: Agrobacterium tumefaciens, disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - Nitrogen utilization efficiency increase

Genotype(s)

Selectable Marker

5`UTR: [] **from** [] - []

Promoter: [] **from** [] - []

Intron: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

3`UTR: [] **from** [] - []

Gene(s) of Interest

Promoter: [] **from** [] - []

Gene: [] **from** [] - []

Terminator: [] **from** [] - []

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) []	IA County: Boone Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 3000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
2) []	ID County: Power Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
3) []	ND County: McHenry Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []
4) []	WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds Inspected by BRS or PPQ? Unknown Previous Permit No.:	1) [] [] Day Telephone: []

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 15-ID-Ta01		
Location GPS Coordinates: [], []		
Release Site History: This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
2) AgraServ NUE	<p>ID County/Province: Power Proposed Release Start Date: 4/05/2016 Proposed Release End Date: 4/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	
Location Unique ID: 16-ID-Ta-02		
Location GPS Coordinates: [], [] [], [] [], [] [], []		
Release Site History: This field was fallow in 2015, planted to flax in 2014, and has been in a crop rotation of wheat, potatoes, alfalfa, corn and sugarbeet for 12 or more years before that. Therefore, we won't be changing the cropping system by conducting these wheat trials.		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
3) Agro-Tech Research Farm	<p>ND County/Province: McHenry Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 16-ND-Ta01		
Location GPS Coordinates: [], [] [], [] [], []		
Release Site History: This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years		
Critical Habitat Involved?: <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No		
4) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/05/2016 Proposed Release End Date: 04/05/2017 No. of Releases: 2 Quantity: 10 acres</p>	<p>1) [] [] Day Telephone: []</p>
Location Unique ID: 16-WA-Ta01		
Location GPS Coordinates: [], []		

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site History:

this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years

Critical Habitat Involved?:

Yes No

13. DESIGN PROTOCOLS**Production Design**

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[

]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only".

Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment.

Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use.

Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site.

All regulated material movement between the facility and the field release must be packed at least in 2 closed containers.

"

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

[

]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[

]

14. ATTACHMENTS**Attachments**

Biogemma Wheat Design Protocol 2016 (5/6/2016 @ 01:35 PM)

15. ADDITIONAL INFORMATION**16. COURTESY JUSTIFICATION**

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

I, (b)(6), hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON

(b)(6)

18. DATE

May 6, 2016

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New Amendment Renewal Variance Amendment, Renewal and/or Variance

Amendment/Renewal Description:

Previous Permit Number(s):

7. MEANS OF MOVEMENT

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No

Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

N/A

9. REGULATED ARTICLE**Scientific Name:** Triticum aestivum**Common Name:** Wheat**Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:**

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard. At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne - Route d'Ennezat Boone Ames, IA 63720	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proZmVp1] **from** [Zea mays] - [Maize Viviparous1 gene promoter. Tissue specific expression (embryo and aleurone of cereal maize kernels) of the gene downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

3) Phenotypic Designation Name:

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Identifying Line(s):**Construct(s):**

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsSALT] **from** [Oryza sativa] - [Rice saltT gene promoter. Inducible expression of the gene downstream its sequence in salty growing conditions]

intron: [intOsSALT] **from** [Oryza sativa] - [Partial sequence of the saltT promoter (inducible in salty growing condition) from rice, that is not transcribed (located before the ATG sequence). Ensures a good transcription of the gene inserted downstream its sequence.]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

4) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01782

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGDAS1] **from** [Triticum aestivum] - [Glutamine Dependent Asparagine Synthetase. Aspartate synthetase dependant to glutamine concentration. Reaction= ATP + L-aspartate + L-glutamine + H(2)O ; AMP + diphosphate + L-asparagine + L-glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

6) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

7) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oriza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

8) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)**Gene of interest**

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [NtNPK1] **from** [Nicotiana tabacum] - [Mitogen Activated Protein kinase kinase kinase. Mitogen-activated protein kinase kinase kinase signal transduction pathway]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

10) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01822

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]
 intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]
 gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]
 terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]
 Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

11) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01823

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oriza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

14) Phenotypic Designation Name:

Identifying Line(s):

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Construct(s):	T 01830
Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	
Phenotype(s)	
AP - [Enhanced nitrogen use]	
Genotype(s)	
Gene silencer promoter: [proOsPRO0110] from [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]	
intron: [intZmSH1] from [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
intron: [intOsTubL] from [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
terminator: [terAtSac66] from [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]	
Selectable Marker Terminal Inverted Repeat: [ZmDs5'Ac] from [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	
promoter: [proVirSc4] from [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]	
intron: [intAtFAD2] from [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]	
gene: [EcNPTII] from [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]	
terminator: [terAtNOS] from [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]	
Terminal Inverted Repeat: [ZmDs3'Ac] from [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	

15) Phenotypic Designation Name:

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Identifying Line(s):**Construct(s):** T 01832**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

16) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01920

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

17) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

18) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmKnotted1] **from** [Zea Mays] - [Maize knotted1 gene promoter. Specific expression in the apical meristem]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

19) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

20) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsLRK1] **from** [Oryza sativa] - [LRK1 regulates rice branch number by enhancing cellular proliferation]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

22) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDEP1] **from** [Oryza sativa] - [PEBP (phosphatidylethanolamine-binding protein) like domain protein sharing some homology with the N terminus of GS3]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

23) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

24) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTin3A] **from** [Brachypodium distachyon] - [Protein involved in tiller development]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

25) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTkw2] **from** [Brachypodium distachyon] - [Thousand Kernel Weight 2. EST annotated "Large Tegument protein", candidate gene under yield QTL]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

26) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01985

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)**Gene of interest**

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

27) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaPAMT] **from** [Triticum aestivum] - [Protein Arginine N-MethylTransferase. Catalyzes the addition of a methyl group to an arginine residue]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

28) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01987

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMFSA] **from** [Triticum aestivum] - [Major Facilitator Superfamily Antiporter. Membrane protein involved as single polypeptide secondary carriers, transporting a diverse range of substrates]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

29) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01988

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMPase] **from** [Triticum aestivum] - [Metallopeptidase. Peptidase with metal cofactor: Catalysis of the hydrolysis of peptide bonds by a mechanism in which water acts as a nucleophile, one or two metal ions hold the water molecule in place, and charged amino acid side chains are ligands for the metal ions.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

30) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrbu3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrbu3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaZFP] **from** [Triticum aestivum] - [Zinc finger protein. Transcription factor related to nitrogen metabolism. Close relative of wheat Zinc Finger Protein1 gene]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

31) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01991

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaT6PS] **from** [Triticum aestivum] - [Trehalose-6-phosphate synthase. Trehalose-6-phosphate synthase involved in sugar metabolism. Reaction: UDP-glucose + D-glucose 6-phosphate ; UDP + alpha,alpha-trehalose 6-phosphate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

32) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02003

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

33) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02004

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved fungal disease resistance

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrb3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrb3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

34) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

35) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

36) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02051

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsNAC10] **from** [Oryza sativa] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity. NAC family transcription factor involved in stress tolerance response]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

37) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02094

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation

reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [HvSUT1] **from** [Hordeum vulgare] - [sucrose transporter]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

38) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02110

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaCYCB2] **from** [Triticum aestivum] - [Cyclin B2 is a member of the B-type cyclins and are essential components of the cell cycle regulatory machinery.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin

phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

40) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

41) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02133**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' pregin of the califlower mosaic virus,]promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to α-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

42) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02134

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' preregion of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

43) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02135

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

44) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02137

Mode of Transformation: Agrobacterium tumefaciens disarmed

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Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH₃ =>; Gln)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

45) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02154

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

46) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02155

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

47) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmAspAT1] **from** [Zea mays] - [Aspartate AminoTransferasel. Aspartate aminotransferase catalyzes the reversible interconversions of glutamate and aspartate, and their 2-keto analogs: Glutamate + oxaloacetate (OAA) ; 2-oxoglutarate + aspartate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

48) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumLOG] **from** [Agrobacterium tumefaciens] - [Lysine decarboxylase]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

50) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaBril] **from** [Triticum aestivum] - [Brassinosteroid-insensitive1. Brassinosteroid LRR receptor kinase involved in brassinosteroid signal transduction]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtCKX3] **from** [Arabidopsis thaliana] - [Involved in degradation of cytokinins]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsSCI2] **from** [Oryza sativa] - [Rice Subtilisin_chymotrypsin_inhibitor2 promoter. Inducible expression of the gene downstream its sequence under abiotic stress (salt, drought, ABA, cold)]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtTPS1] **from** [Arabidopsis thaliana] - [Enzyme of the threahose synthase pathway - osmoprotectant/ signaling molecule]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

54) Phenotypic Designation Name:

Identifying Line(s):**Construct(s):** T 02268**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATHRD] **from** [Arabidopsis thaliana] - [The HARDY protein is a transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

55) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02269**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ALSAP] **from** [Allocasuarina littoralis] - [Stress Associated Protein. Probable Ubiquitin ligase]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

57) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02304

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

58) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaARF22] **from** [Triticum aestivum] - [Transcription factor involved in pericarp development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

59) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSHN2] **from** [Arabidopsis thaliana] - [AP2 type transcription factor is involved in cuticular wax accumulation and in stomatal density]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

60) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02334

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsAT] **from** [Oryza sativa] - [Aminotransferase. catalyzes the transfer of an amino group between an amino acid and an a-keto acid]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [protoActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

61) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02335

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsHisTpter] **from** [Oryza sativa] - [Histidine AA transporter. amino acid transporter]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

62) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02336

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmAGAT2] **from** [Zea mays] - [Conversion of glyoxylate into glycine]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

63) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02337

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmANAC075] **from** [Zea mays] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity involved in drought stress]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region

(terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

64) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02339

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbFd_NADP_Reductase] **from** [Sorghum bicolor] - [Ferredoxin-NADP reductase. belongs to the family of oxidoreductases involved in the transfer of electrons]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

65) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02342

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

Signal peptide: [ctpRca] **from** [Zea mays] - [Chloroplastid transit peptide from Rubisco Activase gene]

gene: [BlnAGK] **from** [Brevibacillus laterosporus] - [Enzyme involved in Arginine biosynthesis]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green

fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaWali5] **from** [Triticum aestivum] - [Wali5 protein is a transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaBamy2] **from** [Triticum aestivum] - [The bamylose protein is a putative amylase]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal

kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

69) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

70) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02347

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a

Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSAP5] **from** [Arabidopsis thaliana] - [Stress Associated protein 5]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s):

T 02349

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsZnFG18] **from** [Oryza sativa] - [ZnFg CCCH domain-containing protein 18. Zinc

finger domain containing transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

73) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02350

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmDof1] **from** [Zea mays] - [Dof1 domain containing transcription factor. Dof proteins share a unique and highly conserved DNA binding domain with one C2-C2 zinc finger motif. Dof proteins can function as transcriptional activators or repressors of tissue-specific and light-regulated gene expression in plants (carbon metabolism)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

74) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaPPI_FKBP] **from** [Triticum aestivum] - [Peptidyl-prolyl cis-trans isomerase, FKBP-type family protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

75) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02352

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [HvA1] **from** [Hordeum vulgare] - [Chaperone like protein. Member of the Late Embryogenesis Abundant (LEA) protein family. Chaperone like protein linked to drought tolerance]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

76) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02353

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmASR] **from** [Zea mays] - [ABA Stress Ripening induced protein. ASR proteins are induced by abscisic acid (ABA), stress and ripening. First described in tomato, at least seven genes have been found in maize. ASR1 is one of the 7 genes isolated so far. ASR protein have a key role in the mechanism conducting to drought and salt resistance via ABA and sugar signalization]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbPEPC] **from** [Sorghum bicolor] - [PhosphoEnol Pyruvate Carboxylase. C4 photosynthetic carbon assimilation cycle enzyme. Reaction: PEP + CO₂ --->; OxaloAcetate + Pi]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

77) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02355

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [EcBetA] **from** [E. Coli] - [The Choline Dehydrogenase is an enzyme that catalyzes the chemical reaction from the substrates choline and acceptor, whereas its two products are betaine aldehyde and reduced acceptor.]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsrub3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrub3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ThVP] **from** [Theellungielle halophila] - [Theellungielle halophila H(+)-pyrophosphatase. vacuolar H+-pyrophosphatase, enzyme (EC 3.6.1.1) that catalyzes the conversion of one molecule of pyrophosphate to two phosphate ions]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinothricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

78) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsNAC5] **from** [Oryza sativa] - [NAC family transcription factor. NAC family transcriptional factor putatively involved in kernel filling]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsLEA3.1] **from** [Oryza sativa] - [Chaperone like protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtGOLS1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and Galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

80) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02367

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AnNADP_GDHA] **from** [Aspergillus niger] - [The NADP glutamate dehydrogenase A converts 2-oxo-glutarate into L-glutamate by incorporating NH₃ (EC:1,41,4)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

81) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02368

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmEF_Tu] **from** [Zea mays] - [EF-Tu mediates the entry of the aminoacyl tRNA into a free site of the ribosome]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

82) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02386

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [TaMEG1b] **from** [Triticum aestivum] - [Maternally Expressed Gene1. Wheat endosperm transfert cell-specific gene with a maternal parent of origin pattern expression.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

83) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02423

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

84) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ScTPS1+ScTPS2_fusion] **from** [Yeast] - [Regulation of synthesis of trehalose]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

85) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [OsSAP] **from** [Oryza sativa] - [senescence-associated rhodanese-like domain containing protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	<p>IA County: Boone Proposed Start Date: 04/18/2016 Proposed End Date: 04/18/2017 Quantity: 3000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
2) [AgraServ]	<p>ID County: Power Proposed Start Date: 04/15/2016 Proposed End Date: 04/15/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
3) [Agro-Tech Research Farm]	<p>ND County: McHenry Proposed Start Date: 04/15/2016 Proposed End Date: 04/15/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>
4) [Qualls Ag Laboratory]	<p>WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) [b] (6) Day Telephone: [b] (6)</p>

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/20/2016 Proposed Release End Date: 04/20/2017 No. of Releases: 2 Quantity: 10 Acres</p>	<p>1) [b] (b) [b] Day Telephone: [b] (b) [b]</p>
Location Unique ID:	15-ID-Ta01	
Location GPS Coordinates:	[42.804648], [-112.790011]	
Release Site History:	This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years	
Critical Habitat Involved?	____ Yes <input checked="" type="checkbox"/> No	
2) Agro-Tech Research Farm	<p>ND County/Province: McHenry Proposed Release Start Date: 04/20/2016 Proposed Release End Date: 04/20/2017 No. of Releases: 2 Quantity: 10 Acres</p>	<p>1) [b] (b) [b] Day Telephone: [b] (b) [b]</p>
Location Unique ID:	16-ND-Ta01	
Location GPS Coordinates:	[48.172554], [-101.001077] [48.178800], [-101.000472] [48.156788], [-100.978399]	
Release Site History:	This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years	
Critical Habitat Involved?	____ Yes <input checked="" type="checkbox"/> No	
3) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/08/2016 Proposed Release End Date: 04/08/2017 No. of Releases: 2 Quantity: 10 Acres</p>	<p>1) [b] (b) [b] Day Telephone: [b] (b) [b]</p>
Location Unique ID:	16-WA-Ta01	
Location GPS Coordinates:	[47.151634], [-119.560611]	
Release Site History:	this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years	
Critical Habitat Involved?	____ Yes <input checked="" type="checkbox"/> No	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

13. DESIGN PROTOCOLS

Production Design

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[The purpose of the introduction is to evaluate the performance or produce seed for research purpose only. Plants will be grown under various environment with various level of fertilisation or various level of watering. The performance will be determined by collecting various phenotyping data as the grain yield. The release site will be spatially isolated by no less than 130 feet from sexually compatible species. The release site will be surrounded by border and/or buffer area. All equipment used in the release site will be thoroughly cleaned at the release site. After harvest, the remaining material will incorporate to the soil and left for devitalization by the elements.]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only". Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment. Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use. Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site. All regulated material movement between the facility and the field release must be packed at least in 2 closed containers."

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

["Regulated wheat will be planted only at the field site specified in the permit. Field sites will be well-defined with stakes and GPS coordinates. A buffer area of no less than 13 feet will separate wheat regulated under this permit and any other planted agricultural material. The field site, border rows and buffer area will be monitored for volunteers for the four successive growing seasons after harvest. Volunteers will be removed prior to flowering and destroyed. A minimum of one monitoring every 4 weeks is performed at the field site. Any volunteer plants will be destroyed by any one of the following methods : mechanical grinding or other methods to incorporate the plant into the soil or chemical treatment. The monitoring area is left fallow or planted with a distinct and non-sexually compatible crop. The soil preparation and planting of the crop in the monitoring area is made independently from the rest of the field."]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[Seed or other material capable of propagation will be devitalized by autoclaving, burning or incineration, mechanical grinding or crushing, herbicide treatment, or returning to the field site and burying at the field site. Seed not used in the field trial will be returned to facility for storage or destruction.]

14. ATTACHMENTS

CBI	CBI-Deleted/Non-CBI
	Biogemma Wheat Design Protocols (12/15/2015 @ 11:48 AM)

15. ADDITIONAL INFORMATION

16. COURTESY JUSTIFICATION

I, William 'Chris' Anderson, hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON	18. DATE
William 'Chris' Anderson	January 19, 2016

The collection of this information is authorized by the Plant Protection Act of 2000. The information will be used to determine eligibility to receive all types of permits. No permit will be issued until this application has been approved.

U.S. DEPARTMENT OF AGRICULTURE
ANIMAL AND PLANT HEALTH INSPECTION SERVICE
BIOTECHNOLOGY REGULATORY SERVICE

APPLICATIONS FOR PERMIT OR COURTESY PERMIT UNDER 7 CFR 340

(Genetically Engineered Organisms or Products)

1. NAME, ADDRESS, TELEPHONE, AND EMAIL OF APPLICANT

Name: (b) (6)
 Position:
 Organization: Biogemma USA Corp
 Organization Unique ID:
 Address: 2331 230th Street
 Ames, IA 50014
 County/Province:
 Township/Island:
 Day Telephone: (b) (6)
 FAX:
 Alternate:
 Email 1: (b) (6) @biogemma.com
 Email 2:

2. INTRODUCTION TYPE

- Importation
- Interstate Movement
- Interstate Movement and Release
- Release

3. PERMIT TYPE

- Standard
- Permit
- Courtesy
- Permit

4. PURPOSE OF PERMIT

- Industrial Product
- Pharmaceutical Product
- Phytoremediation
- Traditional

5. CONFIDENTIAL BUSINESS INFORMATION VERIFICATION (CBI)

Does this application contain CBI? Yes No

CBI Justification:

Confidential Business Information Justification FOR Importation, Interstate Movement AND Release Notifications (Reference 06-AP-111) The freedom of Information Act (FOIA) specifically exempts federal agencies from releasing information that are trade secrets AND commercial OR financial information obtained from a person as privileged OR confidential 5.U.S.C.552 (b) (4). Exemption 4 applies WHERE the disclosure of information would likely cause substantial harm TO the competitive Position of the person from whom the information was obtained,OR WHERE, IN the CASE of voluntarily submitted information, the submitter would be less likely IN the future TO share data with agency voluntarily.Disclosure of this information would cause substantial harm TO Biogemma by allowing OTHER companies TO unfairly compete with Biogemma. We must keep confidential certain traits which Biogemma has selected TO be of significant agronomic importance which, IF imported TO A new corn seed hybrid, would represent A competitive advantage IN the market place. Disclosure of this information would reveal TO competitors Biogemmas marketing strategy which identifies target s of potential commercial opportunity. IN addition, this information would enable their competitors TO duplicate the research AND products without incurring substantial sums of money AND many years of research AND development expended by Biogemma. Lastly, we must keep research information strictly confidential because IN many cases, patent have NOT been filed OR patents are pending AND have NOT been published. Genes AND regulatory sequences. Biogemmas technology consists of vectors transferred into plants. These vectors comprise genes FOR the expression of traits AND regulatory sequences such as promoters, leaders, enhancers AND terminators. Disclosure of the nature of these vectors will directly provide their competitors with the knowledge of the precise genetic sequences that Biogemma has found effective. Disclosure of this information may also reveal the specific modifications made by Biogemma TO enhance the usefulness of the gene AND would provide their competitors commercially valuable knowledge about the usefulness of the gene discovered by Biogemma AND its partners. It is Biogemmas commercial interest that their intellectual property is NOT jeopardized by disclosure of this information.

6. REQUEST TYPE

- New Amendment Renewal Variance Amendment, Renewal and/or Variance

Amendment/Renewal Description:

Previous Permit Number(s):

7. MEANS OF MOVEMENT

Regulated article will be moved by common carrier Air or ground, or both.

8. VARIANCE VERIFICATION

Have you previously applied for variance(s) that you wish to apply to this permit? Yes No

Variance Number(s):

If so, describe in a brief summary how the variance will be applied:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

N/A

9. REGULATED ARTICLE**Scientific Name:** Triticum aestivum**Common Name:** Wheat**Any biological material (e.g., culture medium, or host material) accompanying the regulated Article during movement:**

No additional biological material will be included with the regulated material during movement.

Country and locality where the donor organism, recipient organism, and vector or vector agent were collected, developed, and produced:

The genetically engineered lines covered in this permit were created and developed at Biogemma, Site de la Garenne, route d'Ennezat, 63720 Chappes, France.

Processes, Procedures, and Safeguards Description:

"The facility where the genetically engineered lines were created and developed is a controlled-access building. The greenhouse facilities to produce seeds is covered by an agreement (S2 confinement level) and is a controlled access facility via security badges. All regulated and non engineered seed lots are labeled with a unique code. Regulated material is kept separated physically from non engineered seed. Seeds are moved from the point of origin to the destination location using three containment levels. The primary container is a seed envelope closed by a clip, which is then put inside a cardboard box sealed with a cap. A third containment is then used, using either a double or triple wall corrugated cardboard. At destination, regulated wheat is stored in locked and secured areas, where only trained persons are authorized to access. All regulated seeds are stored separately from any other seeds in order to prevent mixing. The entire facility at Biogemma USA Corp (Ames, IA) is locked and alarmed during non-working hours."

10. ARTICLE SUPPLIER AND/OR DEVELOPER

<u>Name</u>	<u>Location</u>	<u>Contact Information</u>
(b) (6)	Site de la Garenne - Route d'Ennezat Boone Ames, IA 63720	Day Telephone: (b) (6) FAX: Email:

11. PHENOTYPES/GENOTYPE**1) Phenotypic Designation Name:****Identifying Line(s):****Construct(s):** T 01677**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]gene fragment: [TaNLP_partial] **from** [Triticum aestivum] - [Nin-like protein 7. Transcription factor similar to nodule inception genes in dicots]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]**Selectable Marker**Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

2) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01768**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proZmVp1] **from** [Zea mays] - [Maize Viviparous1 gene promoter. Tissue specific expression (embryo and aleurone of cereal maize kernels) of the gene downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [TaGID1_partial] **from** [Triticum aestivum] - [Gibberellin Insensitive Dwarf1. Giberellin receptor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

3) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):**

T 01781

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under low nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsSALT] **from** [Oryza sativa] - [Rice saltT gene promoter. Inducible expression of the gene downstream its sequence in salty growing conditions]

intron: [intOsSALT] **from** [Oryza sativa] - [Partial sequence of the saltT promoter (inducible in salty growing condition) from rice, that is not transcribed (located before the ATG sequence). Ensures a good transcription of the gene inserted downstream its sequence.]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

4) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01782

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

5) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01783

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGDAS1] **from** [Triticum aestivum] - [Glutamine Dependent Asparagine Synthetase. Aspartate synthetase dependant to glutamine concentration. Reaction= ATP + L-aspartate + L-glutamine + H(2)O ; AMP + diphosphate + L-asparagine + L-glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

6) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01786

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

7) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01789

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oriza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

8) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01790

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)**Gene of interest**

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

9) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01792

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [NtNPK1] **from** [Nicotiana tabacum] - [Mitogen Activated Protein kinase kinase kinase. Mitogen-activated protein kinase kinase kinase signal transduction pathway]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

10) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01822

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TmMYB] **from** [Triticum monococcum] - [MYB transcription factor. Nitrogen responsive transcription factor]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]
 intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]
 gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]
 terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]
 Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

11) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01823

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [VaP5CS] **from** [Vigna aconitifolia] - [Delta-1-pyrroline-5-carboxylate synthetase. Catalyzes the first step of the proline synthesis: L-glutamate + ATP + NADPH ; ADP + L-glutamate ?-semialdehyde + NADP+ + phosphate. The mothbean enzyme has both gamma-glutamyl kinase and glutamic-gamma-semialdehyde dehydrogenase activities]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01825

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [OsHSDH] **from** [Oriza sativa] - [HomoSerine DeHydrogenase. homoserine dehydrogenase catalyses reaction from homoserine to aspartate. Reaction: L-homoserine + NAD(P)+ ; L-aspartate 4-semialdehyde + NAD(P)H + H+]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

13) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01826

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaCS] **from** [Triticum aestivum] - [Cysteine synthase. Cysteine synthase involved in amino acid synthesis. Reaction: O-acetyl-L-serine + hydrogen sulfide ; L-cysteine + acetate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

14) Phenotypic Designation Name:

Identifying Line(s):

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Construct(s):	T 01830
Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description:	Improved yield under low nitrogen supply
A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	
Phenotype(s)	
AP - [Enhanced nitrogen use]	
Genotype(s)	
Gene silencer promoter: [proOsPRO0110] from [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]	
intron: [intZmSH1] from [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
intron: [intOsTubL] from [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]	
gene fragment: [Ta6SFT_5'+3' UTR partial] from [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the 5' and 3' UTR]	
terminator: [terAtSac66] from [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]	
Selectable Marker	
Terminal Inverted Repeat: [ZmDs5'Ac] from [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	
promoter: [proVirSc4] from [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]	
intron: [intAtFAD2] from [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]	
gene: [EcNPTII] from [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]	
terminator: [terAtNOS] from [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]	
Terminal Inverted Repeat: [ZmDs3'Ac] from [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]	

15) Phenotypic Designation Name:

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Identifying Line(s):**Construct(s):** T 01832**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene silencer

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

intron: [intOsTubL] **from** [Oryza sativa] - [Rice Tubulin gene intron, is used as spacer for the production of the hairpin structure in the RNA interference approach]

gene fragment: [Ta6SFT_CDS partial] **from** [Triticum aestivum] - [Sucrose:fructan 6-fructosyl transferase. Transfers a fructosyl group from sucrose to various acceptors including oligofructans, thus elongating fructan chains. RNAi approach targeting the coding sequence]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

16) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01920

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

17) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01921

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvNAR2.3] **from** [Hordeum vulgare] - [Nitrate assimilation-related gene. Nitrate transporter associated protein necessary for nitrate transporter activity]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [HvNRT2.1] **from** [Hordeum vulgare] - [Nitrate transporter2.1.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

18) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01922

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmKnotted1] **from** [Zea Mays] - [Maize knotted1 gene promoter. Specific expression in the apical meristem]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

19) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01923

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

20) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01930

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsLRK1] **from** [Oryza sativa] - [LRK1 regulates rice branch number by enhancing cellular proliferation]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

21) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01935**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene silencer

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]gene fragment: [TaGW2_partial] **from** [Triticum aestivum] - [Grain Width 2. GW2 encodes for a RING-type E3 ubiquitin ligase, acts as a negative regulator of grain size]terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

22) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01946**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDEP1] **from** [Oryza sativa] - [PEBP (phosphatidylethanolamine-binding protein) like domain protein sharing some homology with the N terminus of GS3]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

23) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 01953**Mode of Transformation:** Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

introns: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

24) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01956

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTin3A] **from** [Brachypodium distachyon] - [Protein involved in tiller development]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

25) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 01972

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [BdTkw2] **from** [Brachypodium distachyon] - [Thousand Kernel Weight 2. EST annotated "Large Tegument protein", candidate gene under yield QTL]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

26) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):**

T 01985

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield

Phenotype(s)

AP - [Yield increased]

Genotype(s)**Gene of interest**

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

27) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01986

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaPAMT] **from** [Triticum aestivum] - [Protein Arginine N-MethylTransferase. Catalyzes the addition of a methyl group to an arginine residue]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

28) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01987

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMFSA] **from** [Triticum aestivum] - [Major Facilitator Superfamily Antiporter. Membrane protein involved as single polypeptide secondary carriers, transporting a diverse range of substrates]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover

virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

29) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01988

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaMPase] **from** [Triticum aestivum] - [Metallopeptidase. Peptidase with metal cofactor: Catalysis of the hydrolysis of peptide bonds by a mechanism in which water acts as a nucleophile, one or two metal ions hold the water molecule in place, and charged amino acid side chains are ligands for the metal ions.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

30) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01989

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrbu3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrbu3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaZFP] **from** [Triticum aestivum] - [Zinc finger protein. Transcription factor related to nitrogen metabolism. Close relative of wheat Zinc Finger Protein1 gene]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

31) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 01991

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under low nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [TaT6PS] **from** [Triticum aestivum] - [Trehalose-6-phosphate synthase. Trehalose-6-phosphate synthase involved in sugar metabolism. Reaction: UDP-glucose + D-glucose 6-phosphate ; UDP + alpha,alpha-trehalose 6-phosphate]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

32) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02003

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene dowstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

33) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02004

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved fungal disease resistance

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrb3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrb3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

34) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02029

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

35) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02036

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AnNrtB] **from** [Aspergillus niger] - [Nitrate transporter belonging to the super family of Major Facilitator]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

36) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02051

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [OsNAC10] **from** [Oryza sativa] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity. NAC family transcription factor involved in stress tolerance response]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsWAK91] **from** [Oryza sativa] - [Kinase involved in signal transduction]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

gene: [Os33KD] **from** [Oryza sativa] - [Protein involved in pathogen response]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

37) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02094

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation

reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [HvSUT1] **from** [Hordeum vulgare] - [sucrose transporter]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [ZmIncW2] **from** [Zea mays] - [Cell Wall INvertase2. Cell wall invertase, hydrolyses sucrose into glucose and fructose]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [ZmBt2] **from** [Zea mays] - [ADP glucose pyrophosphorylase small sub-unit, enzyme involved in starch biosynthesis]

terminator: [terVirCaMV] **from** [Cauliflower Mosaic Virus] - [3'end non coding region (terminator) of the gene encoding the 35S transcript.]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

38) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02110

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

inttron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [OsDwf4] **from** [Oryza sativa] - [Brassinosteroid C-22 hydroxylase. Cytochrome P450 Monooxygenase Protein. Brassinosteroid C-22 hydroxylase (mediates C-22 hydroxylation reactions in brassinosteroid synthesis)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaCYCB2] **from** [Triticum aestivum] - [Cyclin B2 is a member of the B-type cyclins and are essential components of the cell cycle regulatory machinery.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

inttron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First inttron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

39) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02123

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin

phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

40) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02124

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular

construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

41) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02133

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' pregin of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to α-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

42) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02134

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

Enhancer: [proVirCaMV35S Enhancer] **from** [cauliflower mosaic virus] - [promoter enhancing fragment from the 5' preregion of the califlower mosaic virus,]

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

43) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02135

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use and drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

44) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02137

Mode of Transformation: Agrobacterium tumefaciens disarmed

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved yield under limited nitrogen supply

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH₃ =>; Gln)]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the

expression cassette of the selective marker. Only active when corn Ac transposase is present]

45) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02154

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

46) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02155

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited water and nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsAnt1] **from** [Oryza sativa] - [Rice antiquitin 1 gene promoter. Root specific promoter slightly inducible by abiotic stress]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [HvALaAT2] **from** [Hordeum vulgare] - [Alanine AminoTransferase2 protein. Alanine aminotransferase 2 catalyzes the transfer of an amino group from alanine to a-ketoglutarate, the products of this reversible transamination reaction being pyruvate and glutamate]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

47) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02157

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmAspAT1] **from** [Zea mays] - [Aspartate AminoTransferasel. Aspartate aminotransferase catalyzes the reversible interconversions of glutamate and aspartate, and their 2-keto analogs: Glutamate + oxaloacetate (OAA) ; 2-oxoglutarate + aspartate]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

48) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02176

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proPvSARK] **from** [Phaseolus vulgaris] - [Bean Senescence-Associated-Receptor-Kinase gene promoter induced during leaf senescence.]

gene: [AtumLOG] **from** [Agrobacterium tumefaciens] - [Lysine decarboxylase]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

introns: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

49) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02185

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

50) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02190

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [TaBril] **from** [Triticum aestivum] - [Brassinosteroid-insensitive1. Brassinosteroid LRR receptor kinase involved in brassinosteroid signal transduction]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter.
Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtCKX3] **from** [Arabidopsis thaliana] - [Involved in degradation of cytokinins]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycine phosphotransferase II. Neomycine phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

51) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02206

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsSCI2] **from** [Oryza sativa] - [Rice Subtilisin_chymotrypsin_inhibitor2 promoter. Inducible expression of the gene downstream its sequence under abiotic stress (salt, drought, ABA, cold)]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

52) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02207

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [AtumIPT] **from** [Agrobacterium tumefaciens] - [Isopentenyltransferase. Isopentenyltransferase involved in cytokinin synthesis. Reaction: dimethylallyl diphosphate + AMP ; diphosphate + N6-(dimethylallyl)adenosine 5'-phosphate]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

53) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02267

Mode of Transformation:	Agrobacterium tumefaciens disarmed
Phenotype Description: A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.	Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtTPS1] **from** [Arabidopsis thaliana] - [Enzyme of the threahose synthase pathway - osmoprotectant/ signaling molecule]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

54) Phenotypic Designation Name:

Identifying Line(s):**Construct(s):** T 02268**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter.
Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATHRD] **from** [Arabidopsis thaliana] - [The HARDY protein is a transcription factor]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

55) Phenotypic Designation Name:**Identifying Line(s):****Construct(s):** T 02269**Mode of Transformation:** Agrobacterium tumefaciens disarmed**Phenotype Description:** Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubI3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubI3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ALSAP] **from** [Allocasuarina littoralis] - [Stress Associated Protein. Probable Ubiquitin ligase]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

56) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02275

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [AtGols1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

57) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02304

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ZmFd_GOGAT] **from** [Zea mays] - [Ferredoxin-Glutamate Synthase (chloroplastic). Involved in Nitrate (ammonium) assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsPRO0110] **from** [Oryza sativa] - [Rice RCC3 gene promoter. Root-specific expression of the gene fused downstream its sequence]

gene: [ZmGS2] **from** [Zea mays] - [Glutamine synthetase 2 (chloroplastic). Involved in Nitrate (ammonium) assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

58) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02324

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [TaARF22] **from** [Triticum aestivum] - [Transcription factor involved in pericarp development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

59) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02333

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSHN2] **from** [Arabidopsis thaliana] - [AP2 type transcription factor is involved in cuticular wax accumulation and in stomatal density]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

60) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02334

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsAT] **from** [Oryza sativa] - [Aminotransferase. catalyzes the transfer of an amino group between an amino acid and an a-keto acid]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [protoActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

61) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02335

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsHisTpter] **from** [Oryza sativa] - [Histidine AA transporter. amino acid transporter]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

62) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02336

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmAGAT2] **from** [Zea mays] - [Conversion of glyoxylate into glycine]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

63) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02337

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmANAC075] **from** [Zea mays] - [NAM, ATAF, and CUC (NAC) transcription factor with transactivation activity involved in drought stress]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region

(terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

64) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02339

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbFd_NADP_Reductase] **from** [Sorghum bicolor] - [Ferredoxin-NADP reductase. belongs to the family of oxidoreductases involved in the transfer of electrons]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

65) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02342

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved fungal disease resistance

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

FR - [Fungus resistance]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [TaAlaGAT_partial] **from** [Triticum aestivum] - [The alanine glyoxylate aminotransferase 2 catalyzes the reaction from both substrates L-alanine and glyoxylate and products the pyruvate and glycine.]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

66) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02343

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

Signal peptide: [ctpRca] **from** [Zea mays] - [Chloroplastid transit peptide from Rubisco Activase gene]

gene: [BlnAGK] **from** [Brevibacillus laterosporus] - [Enzyme involved in Arginine biosynthesis]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green

fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

67) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02344

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaWali5] **from** [Triticum aestivum] - [Wali5 protein is a transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

68) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02345

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaBamy2] **from** [Triticum aestivum] - [The bamylose protein is a putative amylase]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal

kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

69) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02346

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene silencer

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

intron: [intStLS1] **from** [Solanum tuberosum] - [Intron from the Potato light-inducible tissue-specific LS1 gene. Used to help generating a hairpin structure for RNAi repression of gene activity]

gene fragment: [OsMADS26_partial] **from** [Oryza sativa] - [MADS box transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

70) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02347

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSRK2C] **from** [Arabidopsis thaliana] - [SNF1-related protein kinase 2. SNF1-related protein kinases 2 (SnRK2s) are plant-specific enzymes involved in environmental stress signaling and abscisic acid-regulated plant development]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a

Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinotrichin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

71) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02348

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtSAP5] **from** [Arabidopsis thaliana] - [Stress Associated protein 5]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinotricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

72) Phenotypic Designation Name:

Identifying Line(s):

Construct(s):

T 02349

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsZnFG18] **from** [Oryza sativa] - [ZnFg CCCH domain-containing protein 18. Zinc

finger domain containing transcription factor]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

73) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02350

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmDof1] **from** [Zea mays] - [Dof1 domain containing transcription factor. Dof proteins share a unique and highly conserved DNA binding domain with one C2-C2 zinc finger motif. Dof proteins can function as transcriptional activators or repressors of tissue-specific and light-regulated gene expression in plants (carbon metabolism)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

74) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02351

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [TaPPI_FKBP] **from** [Triticum aestivum] - [Peptidyl-prolyl cis-trans isomerase, FKBP-type family protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

75) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02352

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [HvA1] **from** [Hordeum vulgare] - [Chaperone like protein. Member of the Late Embryogenesis Abundant (LEA) protein family. Chaperone like protein linked to drought tolerance]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

76) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02353

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proOsrubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ZmASR] **from** [Zea mays] - [ABA Stress Ripening induced protein. ASR proteins are induced by abscisic acid (ABA), stress and ripening. First described in tomato, at least seven genes have been found in maize. ASR1 is one of the 7 genes isolated so far. ASR protein have a key role in the mechanism conducting to drought and salt resistance via ABA and sugar signalization]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [SbPEPC] **from** [Sorghum bicolor] - [PhosphoEnol Pyruvate Carboxylase. C4 photosynthetic carbon assimilation cycle enzyme. Reaction: PEP + CO₂ --->; OxaloAcetate + Pi]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

77) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02355

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [EcBetA] **from** [E. Coli] - [The Choline Dehydrogenase is an enzyme that catalyzes the chemical reaction from the substrates choline and acceptor, whereas its two products are betaine aldehyde and reduced acceptor.]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

promoter: [proOsrbubi3] **from** [Oryza sativa] - [Rice rubi3 polyubiquitin gene promoter. Constitutive expression of the gene downstream its sequence. In transgenic maize plants, this promoter was shown to increase the level of expression comparing to the native maize ubiquitin promoter]

intron: [intOsrbubi3] **from** [Oryza sativa] - [First intron of the rubi3 poly-ubiquitin gene from rice. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream in its sequence]

gene: [ThVP] **from** [Theellungielle halophila] - [Theellungielle halophila H(+)-pyrophosphatase. vacuolar H+-pyrophosphatase, enzyme (EC 3.6.1.1) that catalyzes the conversion of one molecule of pyrophosphate to two phosphate ions]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinothricin or demethylphosphinothricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

78) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02356

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsNAC5] **from** [Oryza sativa] - [NAC family transcription factor. NAC family transcriptional factor putatively involved in kernel filling]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [OsLEA3.1] **from** [Oryza sativa] - [Chaperone like protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

Promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

Intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

Gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

Terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

79) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02360

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AtGOLS1] **from** [Arabidopsis thaliana] - [Galactinol synthase. First enzyme in the biosynthetic pathway of raffinose saccharides (UDP-galactose + myo-inositol ->; galactinol + UDP)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ATRS2] **from** [Arabidopsis thaliana] - [Raffinose synthase. Raffinose synthase catalyzes the synthesis of raffinose from Suc and Galactinol]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

80) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02367

Mode of Transformation:

Agrobacterium tumefaciens disarmed

Phenotype Description:

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Improved Yield under limited water supply.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [AnNADP_GDHA] **from** [Aspergillus niger] - [The NADP glutamate dehydrogenase A converts 2-oxo-glutarate into L-glutamate by incorporating NH₃ (EC:1,41,4)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac tranposase is present]

81) Phenotypic Designation Name:**Identifying Line(s):**

Construct(s): T 02368

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proZmUbi] **from** [Zea mays] - [Maize house keeping gene expressed constitutively. Constitutive expression of the gene downstream its sequence]

intron: [intZmUbi] **from** [Zea mays] - [First intron of maize ubiquitin 1 gene. House keeping gene expressed constitutively. Enhances promoter activity]

gene: [ZmEF_Tu] **from** [Zea mays] - [EF-Tu mediates the entry of the aminoacyl tRNA into a free site of the ribosome]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat]

from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

82) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02386

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Yield increased]

Genotype(s)

Gene of interest

promoter: [proZmBETL9] **from** [Zea mays] - [Maize basal endosperm transfer layer gene 9 promoter. Specific expression in the basal endosperm transfer layer of the gene fused downstream its sequence]

gene: [TaMEG1b] **from** [Triticum aestivum] - [Maternally Expressed Gene1. Wheat endosperm transfert cell-specific gene with a maternal parent of origin pattern expression.]

terminator: [terAtSac66] **from** [Arabidopsis thaliana] - [3'end non coding region (terminator) of the endopolygalacturonase gene 1 from Arabidopsis]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [protoHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intoOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

83) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02423

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [ZmGS1.3] **from** [Zea mays] - [Glutamine synthetase. Glutamine synthetase involved in nitrate assimilation (Glu + NH3 =>; Gln)]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

promoter: [proZmRbcS] **from** [Zea mays] - [Maize rubisco gene promoter. Constitutive expression of the gene downstream its sequence]

gene: [TaGOGAT] **from** [Triticum aestivum] - [NADH-Glutamate synthase. Glutamate synthase involved in nitrate assimilation (2-OG + Gln =>; 2 Glu)]

terminator: [terSoUbi4] **from** [Saccharum officinarum] - [3'end non coding region (terminator) of the ubiquitin4 gene from Saccharum officinarum]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

84) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02454

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved Yield under limited water supply.

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Drought tolerance increased]

Genotype(s)

Gene of interest

promoter: [proHvDhn4s] **from** [Hordeum vulgare] - [Barley dehydrin 4 promoter. Inducible expression of the gene downstream its sequence in abiotic conditions]

intron: [intZmSH1] **from** [Zea mays] - [First intron of the sucrose synthase (shrunken 1) gene from maize. Plays a role of enhancer in the molecular construction, increases the level of transcription of the gene downstream its sequence]

gene: [ScTPS1+ScTPS2_fusion] **from** [Yeast] - [Regulation of synthesis of trehalose]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [3' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proTaHMWG] **from** [Triticum aestivum] - [Wheat high molecular weight glutenin 1D-1 gene promoter. Tissue specific expression (endosperm and aleurone of cereal kernels) of the gene downstream its sequence]

gene: [AeGFP] **from** [Aequorea victoria] - [Green Fluorescent protein. Green fluorescent protein from Jellyfish]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

promoter: [proOsActin] **from** [Oryza sativa] - [Rice actin1 gene promoter. Constitutive expression of the gene downstream its sequence]

intron: [intOsActin] **from** [Oryza sativa] - [First intron of the actin1 gene from rice. Plays a role of enhancer in the molecular construction, increase the level of

transcription of the gene downstream its sequence]

gene: [ShBar] **from** [Streptomyces hygroscopicus] - [Phosphinothricin Acetyl Transferase. The bar gene encodes for a modifying enzyme which acetylates phosphinotricin or demethylphosphinopthricin. Its expression confers to the plant the resistance to the herbicide glufosinate ammonium.]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

85) Phenotypic Designation Name:

Identifying Line(s):

Construct(s): T 02542

Mode of Transformation: Agrobacterium tumefaciens disarmed

Phenotype Description: Improved yield under limited nitrogen supply

A description of the anticipated or actual expression of the altered genetic material in the regulated article and how that expression differs from the expression in the non-modified parental organism.

Phenotype(s)

AP - [Enhanced nitrogen use]

Genotype(s)

Gene of interest

promoter: [proSvPEPC] **from** [Sorghum vulgare] - [Sorghum phosphoenolpyruvate carboxylase gene promoter. Specific expression in the cytosol of mesophyll cells of the gene downstream its sequence.]

gene: [OsSAP] **from** [Oryza sativa] - [senescence-associated rhodanese-like domain containing protein]

terminator: [terZmHSP] **from** [Zea mays] - [3'end non coding region (terminator) of a Heat shock factor gene from maize]

Selectable Marker

Terminal Inverted Repeat: [ZmDs5'Ac] **from** [Zea mays] - [5' Terminal inverted repeat from the corn Dissociation element. Used in conjunction with ZmDs3'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

promoter: [proVirSc4] **from** [Subterranean Clover Stunt Virus] - [Subterranean clover virus gene 4 promoter. Constitutive expression of the gene downstream its sequence]

intron: [intAtFAD2] **from** [Arabidopsis thaliana] - [First intron of the FAD2 gene for microsomal omega-6 desaturase from Arabidopsis. Plays a role of enhancer in the molecular construction, increase the level of transcription of the gene downstream its sequence]

gene: [EcNPTII] **from** [Escherichia coli] - [Neomycin phosphotransferase II. Neomycin phosphotransferase II, an aminophosphotransferase (APH) gene. The APH protein inactivates kanamycin by phosphorylating a hydroxyl group]

terminator: [terAtNOS] **from** [Agrobacterium tumefaciens] - [3'end non coding region (terminator) of the nopaline synthase gene from pTi plasmid of Agrobacterium tumefaciens]

Terminal Inverted Repeat: [ZmDs3'Ac] **from** [Zea mays] - [5' Terminal inverted repeat

from the corn Dissociation element. Used in conjunction with ZmDs5'Ac to excise the expression cassette of the selective marker. Only active when corn Ac transposase is present]

12. INTRODUCTION**Point of Origin**

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	IA County: Boone	

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Destination

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) [Biogemma USA Corp]	<p>IA County: Boone Proposed Start Date: 04/18/2016 Proposed End Date: 04/18/2017 Quantity: 3000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) (b)(6) [REDACTED] Day Telephone: (b)(6) [REDACTED]</p>
2) [AgraServ]	<p>ID County: Power Proposed Start Date: 04/15/2016 Proposed End Date: 04/15/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) (b)(6) Day Telephone: (b)(6) [REDACTED]</p>
3) [Agro-Tech Research Farm]	<p>ND County: McHenry Proposed Start Date: 04/15/2016 Proposed End Date: 04/15/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) (b)(6) Day Telephone: (b)(6) [REDACTED]</p>
4) [Qualls Ag Laboratory]	<p>WA County: Grant Proposed Start Date: 04/05/2016 Proposed End Date: 04/05/2017 Quantity: 1000 Kilograms Seeds</p> <p>Inspected by BRS or PPQ? Unknown Previous Permit No.:</p>	<p>1) (b)(6) Day Telephone: (b)(6) [REDACTED]</p>

WARNING: Any use of ePermits to make materially false, fictitious, or fraudulent statements or representations is subject to civil penalties of up to \$250,000 (7 U.S.C. § 7734(b)) or punishable by a fine of not more than \$10,000, or imprisonment of not more than 5 years, or both (18 U.S.C. §1001).

Release Site

<u>Location Name & Description</u>	<u>Location Address</u>	<u>Contact(s)</u>
1) AgraServ	<p>ID County/Province: Power Proposed Release Start Date: 04/20/2016 Proposed Release End Date: 04/20/2017 No. of Releases: 2 Quantity: 10 Acres</p>	<p>1) (b)(6) Day Telephone: (b)(6) [REDACTED] 38]</p>
Location Unique ID:	15-ID-Ta01	
Location GPS Coordinates:	[42.804648], [-112.790011]	
Release Site History:	This field has been cropped to a rotation of wheat, sugar beet, potatoes, flax, and alfalfa for the past 15-20 years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
2) Agro-Tech Research Farm	<p>ND County/Province: McHenry Proposed Release Start Date: 04/20/2016 Proposed Release End Date: 04/20/2017 No. of Releases: 2 Quantity: 10 Acres</p>	<p>1) (b)(6) Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	16-ND-Ta01	
Location GPS Coordinates:	[48.172554], [-101.001077] [48.178800], [-101.000472] [48.156788], [-100.978399]	
Release Site History:	This field has been cropped to commercial wheat, barley, soybean, and sunflower for the past 20-plus years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	
3) Qualls Ag Lab	<p>WA County/Province: Grant Proposed Release Start Date: 04/08/2016 Proposed Release End Date: 04/08/2017 No. of Releases: 2 Quantity: 10 Acres</p>	<p>1) (b)(6) Day Telephone: (b)(6) [REDACTED]</p>
Location Unique ID:	16-WA-Ta01	
Location GPS Coordinates:	[47.151634], [-119.560611]	
Release Site History:	this field has been planted to a potato, wheat, dry bean, corn, potato rotation with other minor crops like onions, sunflower, canola, peas, carrots, etc., mixed in as needed, for the past 20-plus years	
Critical Habitat Involved?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No	

13. DESIGN PROTOCOLS

Production Design

A detailed description of the purpose for the introduction of the regulated article including detailed description of the proposed experimental and/or production design:

[The purpose of the introduction is to evaluate the performance or produce seed for research purpose only. Plants will be grown under various environment with various level of fertilisation or various level of watering. The performance will be determined by collecting various phenotyping data as the grain yield. The release site will be spatially isolated by no less than 130 feet from sexually compatible species. The release site will be surrounded by border and/or buffer area. All equipment used in the release site will be thoroughly cleaned at the release site. After harvest, the remaining material will incorporate to the soil and left for devitalization by the elements.]

Destination or Release Description

A detailed description of the intended destination (including final and all intermediate destinations), uses, and/or distribution of the regulated article (e.g., greenhouses, laboratory, or growth chamber location; field trial location, pilot project location; production, propagation, and manufacture location; proposed sale and distribution location):

"While in storage, the wheat seeds will be kept in a locked storage facility with limited access. Storage containers are identified by labels. Storage areas are indicated by a label displaying ""Do Not Enter-Authorized Persons Only". Seeds are labelled with the USDA number and unique identifiers, and are stored in double containment. Equipment used in the facility and seed laboratory are thoroughly checked before use and cleaned after use. Equipment used in the field site release are thoroughly checked before use and cleaned after use, within the released field site. All regulated material movement between the facility and the field release must be packed at least in 2 closed containers."

Confinement Protocols

A detailed description of the proposed procedures, processes, and safeguards which will be used to prevent escape and dissemination of the regulated article at each of the intended destinations:

["Regulated wheat will be planted only at the field site specified in the permit. Field sites will be well-defined with stakes and GPS coordinates. A buffer area of no less than 13 feet will separate wheat regulated under this permit and any other planted agricultural material. The field site, border rows and buffer area will be monitored for volunteers for the four successive growing seasons after harvest. Volunteers will be removed prior to flowering and destroyed. A minimum of one monitoring every 4 weeks is performed at the field site. Any volunteer plants will be destroyed by any one of the following methods : mechanical grinding or other methods to incorporate the plant into the soil or chemical treatment. The monitoring area is left fallow or planted with a distinct and non-sexually compatible crop. The soil preparation and planting of the crop in the monitoring area is made independently from the rest of the field."]

Final Disposition Method: Destruction/Devitalization Other Storage in Contained Facility

Final Disposition Description:

[Seed or other material capable of propagation will be devitalized by autoclaving, burning or incineration, mechanical grinding or crushing, herbicide treatment, or returning to the field site and burying at the field site. Seed not used in the field trial will be returned to facility for storage or destruction.]

14. ATTACHMENTS

CBI	CBI-Deleted/Non-CBI
	Biogemma Revised Wheat Design Protocols (1/20/2016 @ 09:10 AM)

15. ADDITIONAL INFORMATION

16. COURTESY JUSTIFICATION

I, (b)(6), hereby certify that the information in this application and all attachments is complete and accurate to the best of my knowledge and belief.

I acknowledge this is not an application to move or import select agents, the genes expressing select agents, or the toxins made by the select agents, as described in 9 CFR 121.

I will not introduce the regulated articles described in this application until APHIS has deemed the application complete and has granted the permit. By signing this permit, I agree to comply with any and all state, local, and tribal laws and regulations that may apply to the introduction of the articles described in this applications.

If there are any changes to the information disclosed in this application, I will contact APHIS.

17. SIGNATURE OF RESPONSIBLE PERSON	18. DATE
(b)(6)	January 20, 2016