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(54) **COMPOSITION FOR PRODUCTION OF  
PLANT BODY HAVING IMPROVED SUGAR  
CONTENT, AND USE THEREOF**

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(57) **ABSTRACT**

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The composition, in accordance with the present invention, for producing a plant body having an improved sugar content includes glutathione, a polynucleotide encoding  $\gamma$ -glutamyl-cysteine synthetase, or a polynucleotide encoding glutathione-binding plastid type fructose-1,6-bisphosphate aldolase. The composition preferably includes oxidized glutathione. This allows provision of a composition for easily producing a plant body having an improved sugar content.

FIG. 1

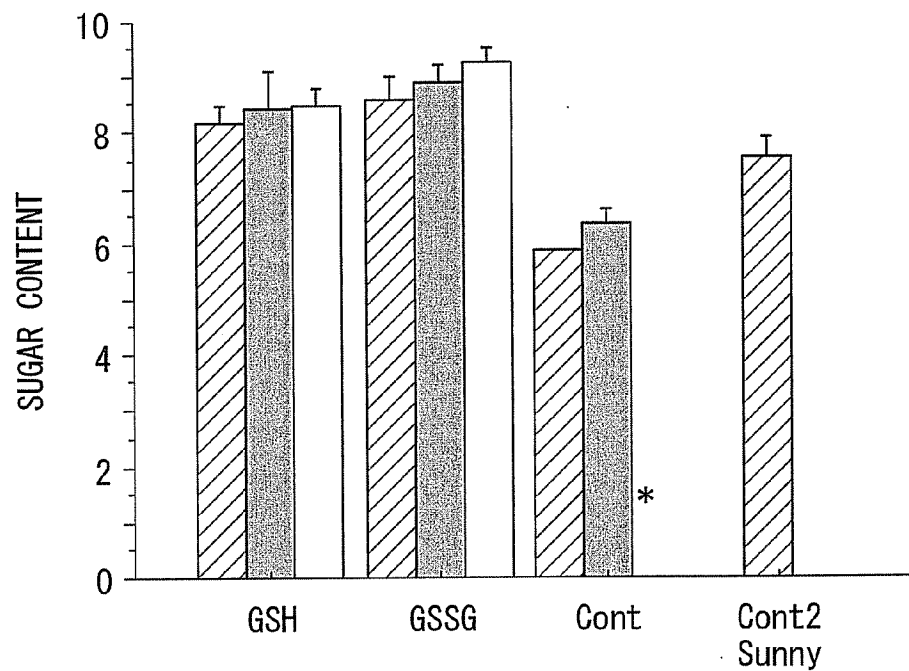


FIG. 2

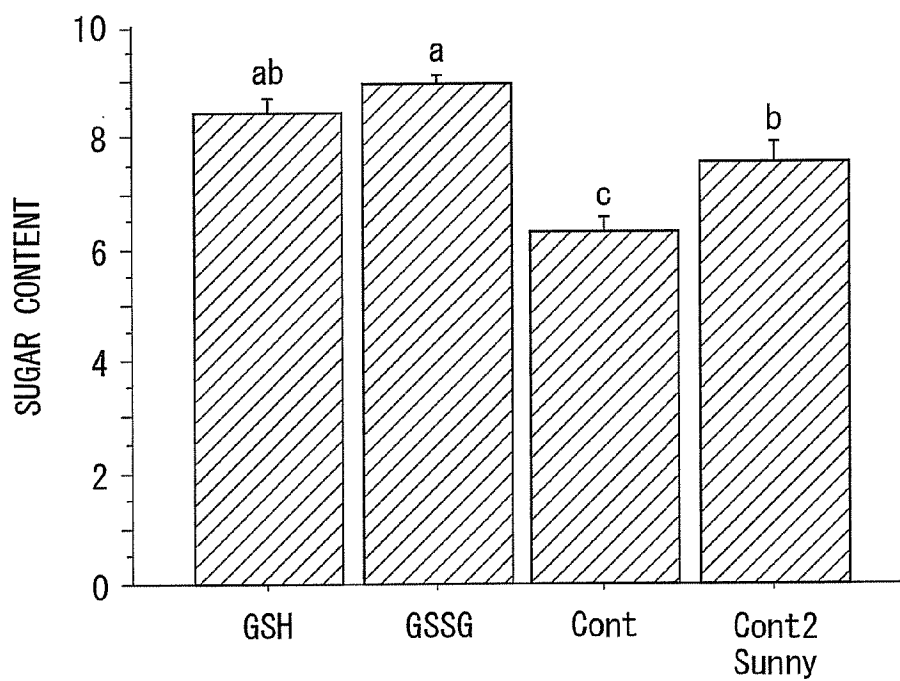


FIG. 3

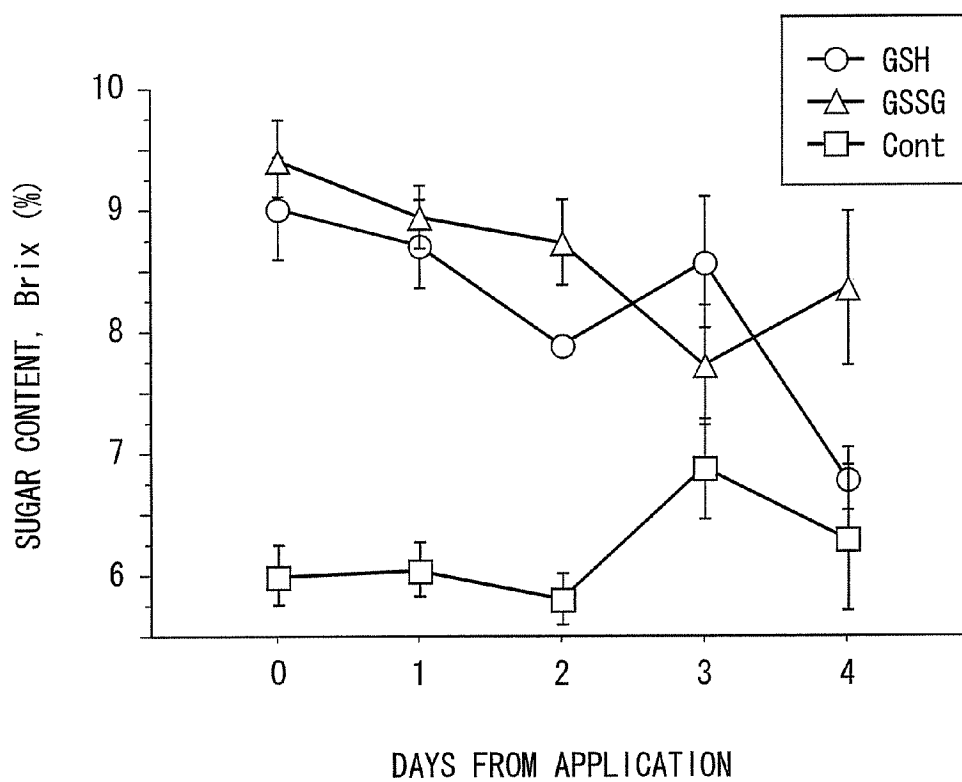


FIG. 4

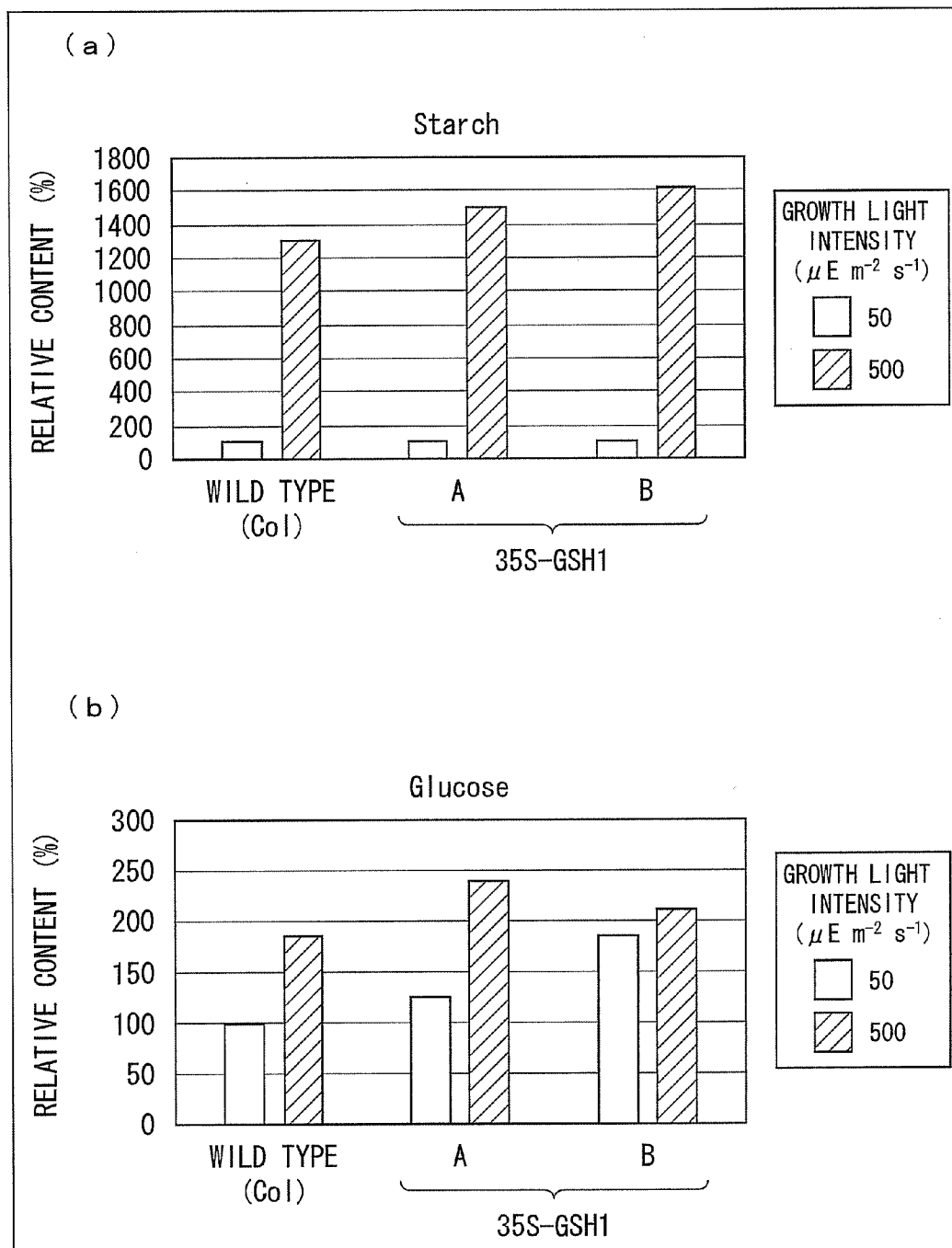


FIG. 5

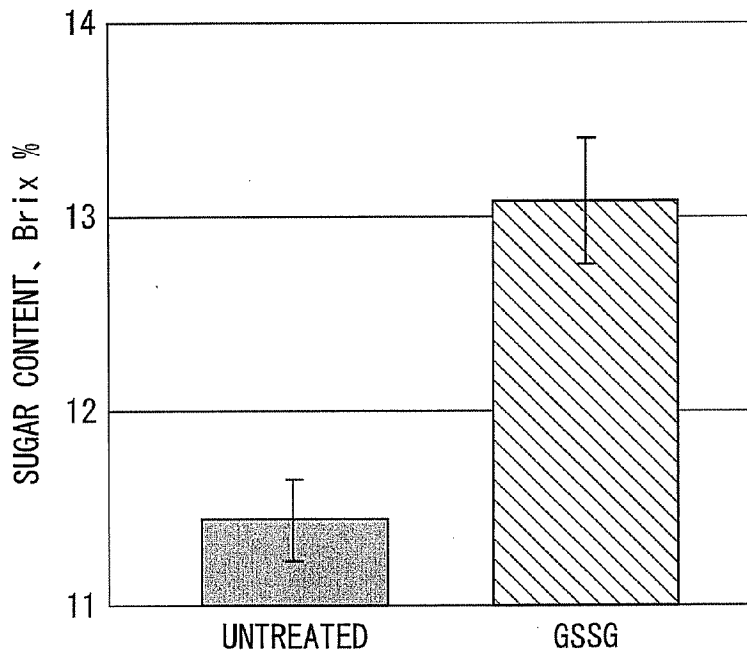


FIG. 6

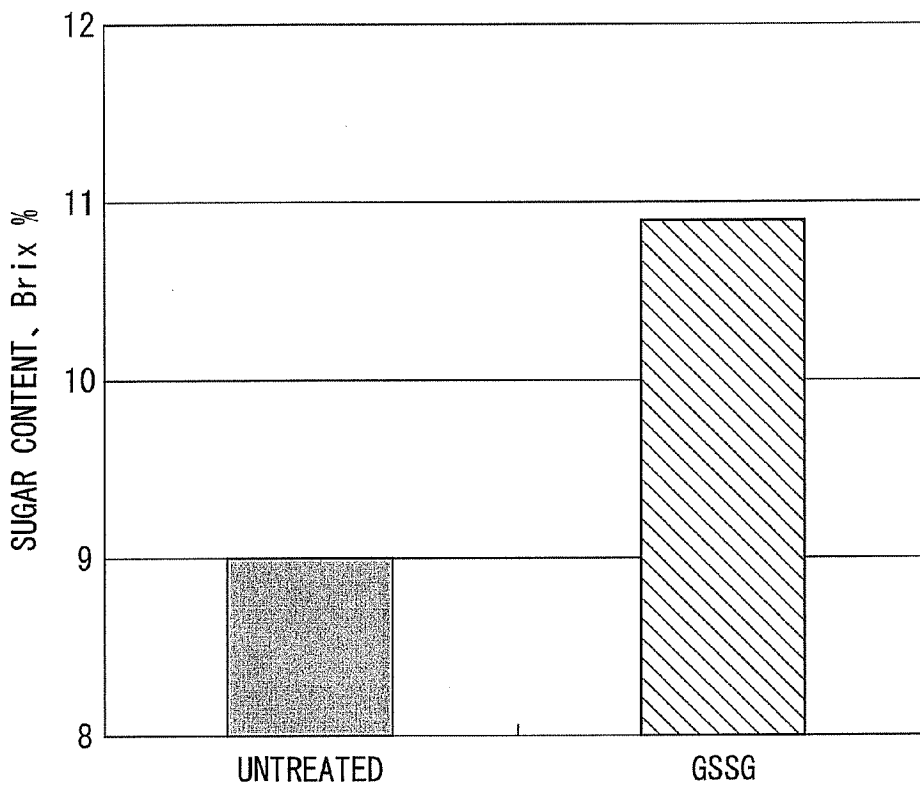


FIG. 7

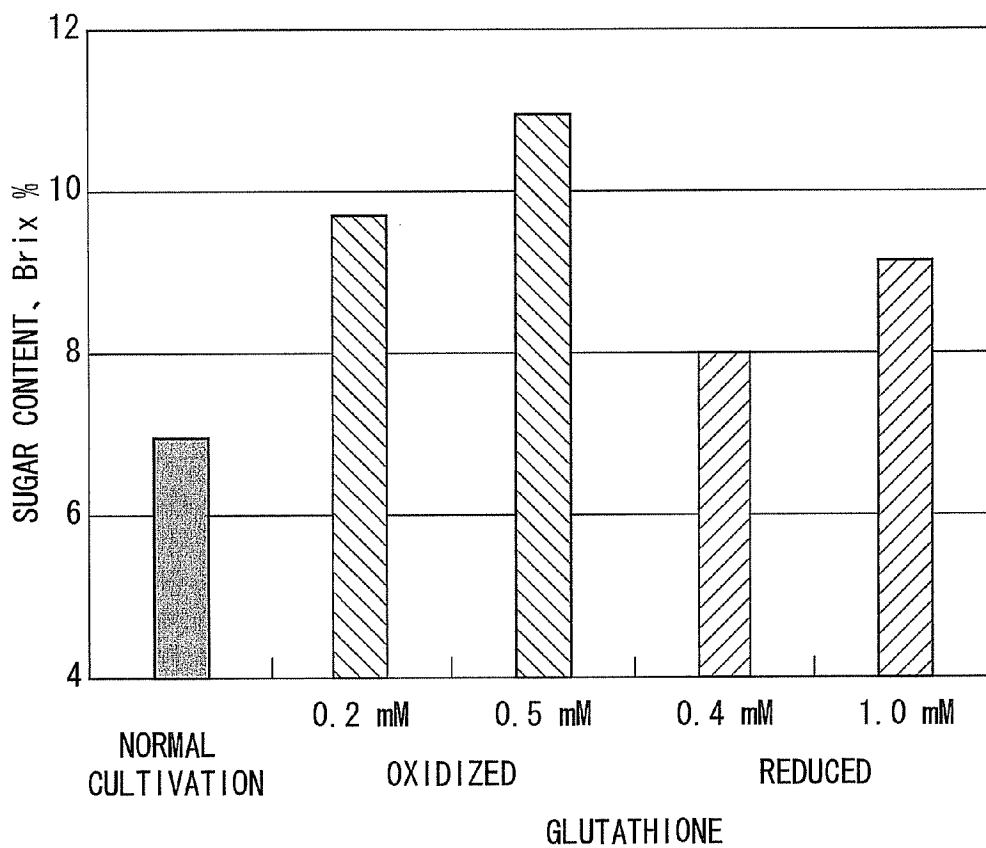


FIG. 8

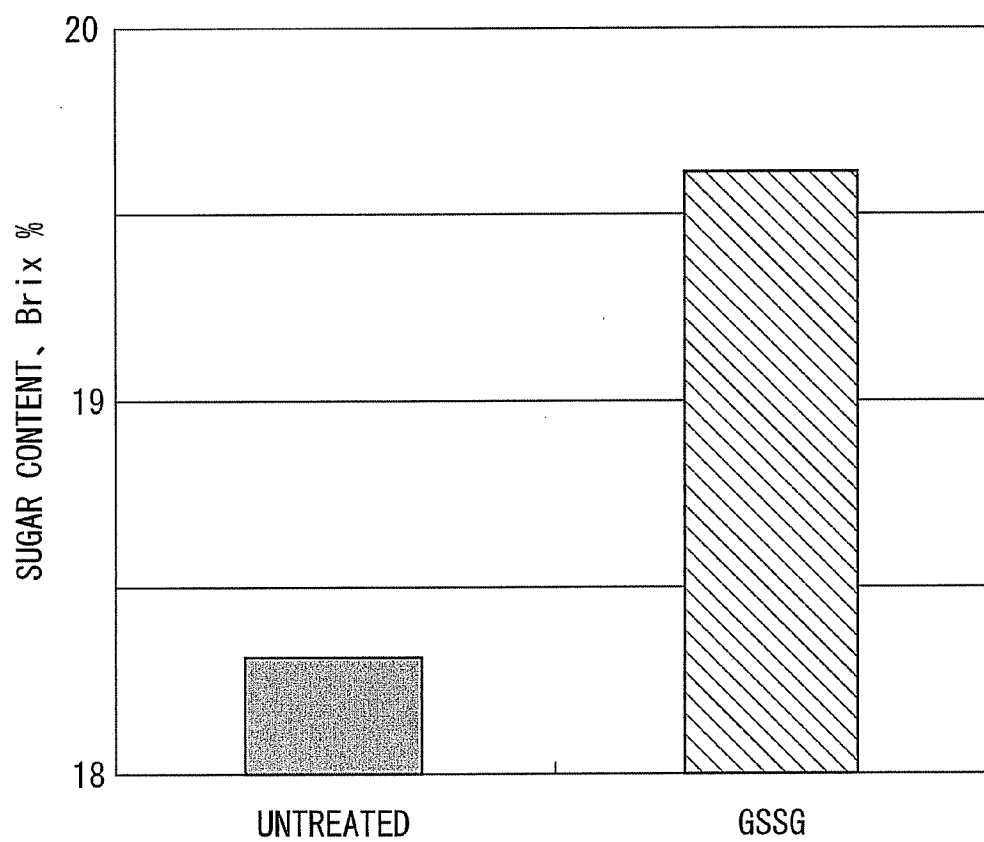
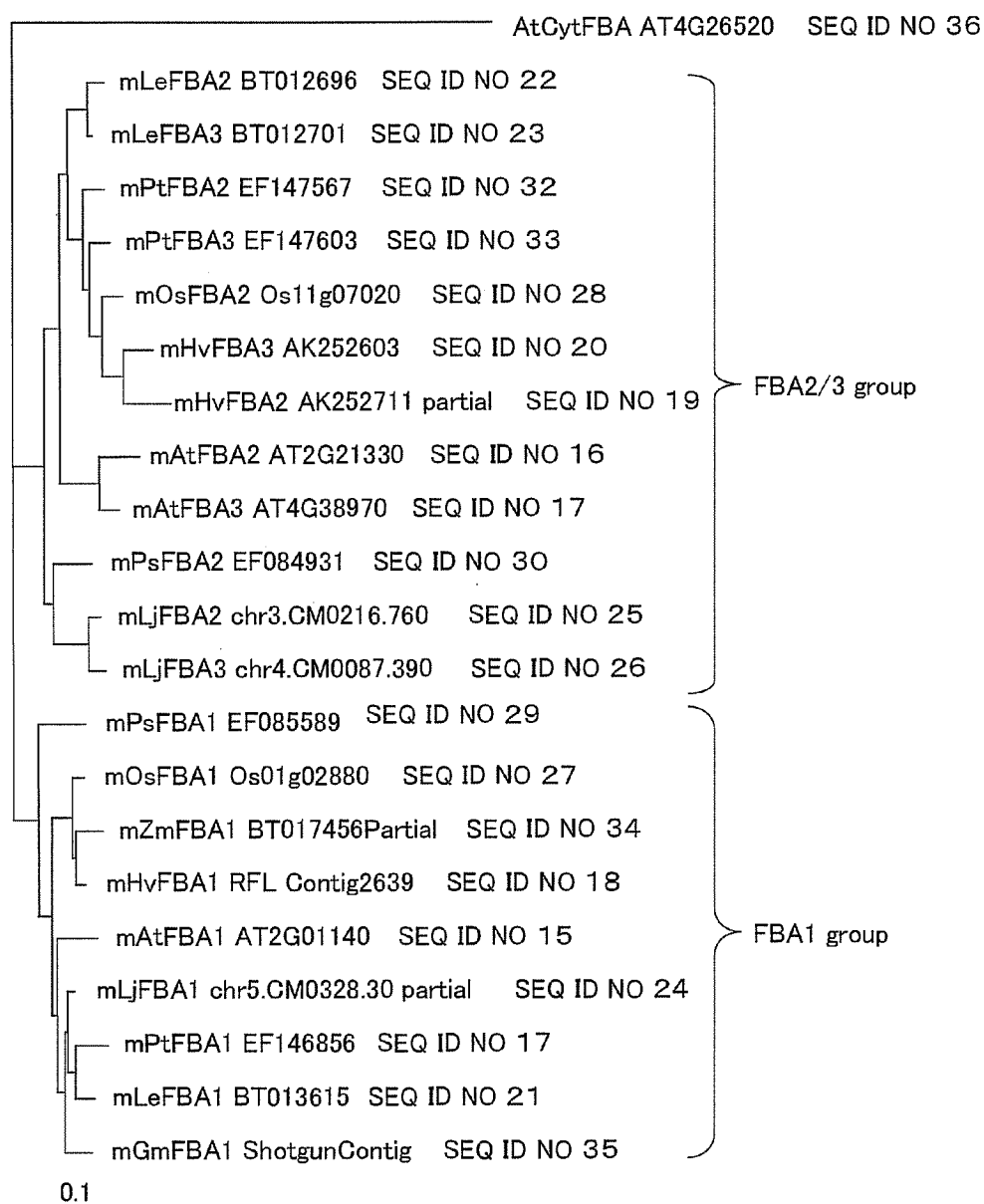


FIG. 9





## COMPOSITION FOR PRODUCTION OF PLANT BODY HAVING IMPROVED SUGAR CONTENT, AND USE THEREOF

### TECHNICAL FIELD

[0001] The present invention relates to a composition, including a substance for regulating an oxidation-reduction state of a cell, which is for producing a plant body having an improved sugar content. The present invention also relates to use of the composition.

### BACKGROUND ART

[0002] A plant such as fruit, vegetable, and cereal generally includes sugar. An amount of sugar in the plant is represented by a sugar content. The sugar content affects a commercial value of plant depending on a type of the plant. Therefore, in recent years, technical developments for increasing a sugar content of a plant have been carried out.

[0003] For example, tomatoes of high sugar content are produced mainly by soil culture. Further, a technique for producing tomatoes of high sugar content by nutrient solution culture has been suggested (Patent Literature 1).

[0004] It is known that a substance for regulating an oxidation-reduction state of a cell, such as glutathione, can function as a differentiation control agent for a cell or an organ (Patent Literature 2). Further, it is known that glutathione can function as a plant growth control auxiliary agent (Patent Literature 3).

### Citation List

- [0005] Patent Literature 1
- [0006] Japanese Patent Application Publication, Tokukaihei, No. 10-271924 (Publication Date: Oct. 13, 1998)
- [0007] Patent Literature 2
- [0008] International Publication WO 01/080638 (Publication Date: Nov. 1, 2001)
- [0009] Patent Literature 3
- [0010] Japanese Patent Application Publication, Tokukai No. 2004-352679 (Publication Date: Dec. 16, 2004)

### SUMMARY OF INVENTION

[0011] However, the conventional technique for improving a sugar content of a plant lacks in simplicity. Those who can produce tomatoes of high sugar content by soil culture are limited to few specialists. Further, production of tomatoes of high sugar content by nutrient solution culture requires a specialized technique and specialized production apparatus for cultivation management.

[0012] The present invention has been accomplished in view of such circumstances, and an object of the present invention is to provide a composition for easily producing a plant having an improved sugar content and to provide a technique using the composition.

[0013] In order to attain the object, the inventors of the present invention studied diligently. As a result, they found that a sugar content of a plant body was improved in a case where the plant body was grown in a culture medium (which includes soil and a soil improvement agent) to which a substance for regulating an oxidation-reduction state of a cell is added, or in a case where the plant body was sprayed or directly coated with the substance. The present invention was accomplished based on this totally new finding and includes the following inventions.

[0014] The composition in accordance with the present invention is a composition for producing a plant body having an improved sugar content, the composition including a substance (excluding hydrogen peroxide) for regulating an oxidation-reduction state of a cell.

[0015] The composition in accordance with the present invention is preferably arranged so that the substance is glutathione, a polynucleotide encoding  $\gamma$ -glutamylcysteine synthetase, or a polynucleotide encoding glutathione-binding plastid type fructose-1,6-bisphosphate aldolase

[0016] The composition in accordance with the present invention is preferably arranged so that the substance is oxidized glutathione.

[0017] The kit in accordance with the present invention is a kit for producing a plant body having an improved sugar content, the kit including a substance (excluding hydrogen peroxide) for regulating an oxidation-reduction state of a cell.

[0018] The production method in accordance with the present invention is a method for producing a plant body having an improved sugar content, the method including the step of cultivating the plant body by using a substance (excluding hydrogen peroxide) for regulating an oxidation-reduction state of a cell.

[0019] The present invention also includes a plant body obtained by the production method in accordance with the present invention.

[0020] Additional objects, features, and strengths of the present invention will be made clear by the description below. Further, the advantages of the present invention will be evident from the following explanation in reference to the drawings.

### BRIEF DESCRIPTION OF DRAWINGS

[0021] FIG. 1 illustrates a determination result of sugar content of *Lycopersicon esculentum* fruit obtained in Example 2.

[0022] FIG. 2 illustrates a result of ANOVA analysis on the determination result of sugar content shown in FIG. 1.

[0023] FIG. 3 is a view illustrating a determination result of relation between sugar content and the number of days from a treatment day of GSSG or GSH.

[0024] FIG. 4 illustrates a determination result of starch and glucose of 35S-GSH1.

[0025] FIG. 5 illustrates a determination result of sugar content of *Prunus avium* fruit obtained in Example 8.

[0026] FIG. 6 illustrates a determination result of sugar content of *Citrus unshiu* fruit obtained in Example 9.

[0027] FIG. 7 illustrates a determination result of sugar content of *Fragaria ananassa* fruit obtained in Example 10.

[0028] FIG. 8 illustrates a determination result of sugar content of *Zea mays* L. var. *saccharata* Sturt fruit obtained in Example 11.

[0029] FIG. 9 is a view illustrating a genetic family tree of the genes of SEQ ID NO: 15 through 36.

### DESCRIPTION OF EMBODIMENTS

[0030] <1. Composition, in Accordance with the Present Invention, for Producing Plant Body Having Improved Sugar Content>

[0031] A composition, in accordance with the present invention, for producing a plant body having an improved sugar content (hereinafter referred to as "composition in

accordance with the present invention”) only has to include a substance for regulating an oxidation-reduction state of a cell.

**[0032]** By using the composition in accordance with the present invention, it becomes possible to easily produce a plant body having an improved sugar content. For example, the plant body can be produced in a culture medium that includes the composition in accordance with the present invention. Further, in a case where the substance for regulating an oxidation-reduction state of a cell is a polynucleotide as described later, what is necessary to do is only to introduce the polynucleotide into a plant by means of a conventional transformation technique and then grow the plant. This makes it possible to obtain the plant having an improved sugar content in an extremely simple way compared to the conventional technique such as the soil culture described above. This is because this case does not require skills, specialized techniques, specialized production apparatuses, or the like.

**[0033]** In the present invention, the substance for regulating an oxidation-reduction state of a cell is used for the purpose of production of a plant having an improved sugar content. This usage of the substance is new and totally differs from a conventional usage of the substance. Such an effect that the plant having an improved sugar content can be obtained could not have been expected from the conventional usage. Therefore, the present invention is accomplished based on a totally new finding by the inventors of the present invention.

**[0034]** In the present specification, the “plant body having an improved sugar content” is a plant body having a better sugar content than a wild strain of the plant body. In other words, the “plant body having an improved sugar content” has a higher sugar content than the wild strain. That is to say, the composition in accordance with the present invention is a composition used in production of a plant body having a higher sugar content than a wild strain. For example, by cultivating a plant body by using the composition in accordance with the present invention, it is possible to improve a sugar content of the plant body compared to a case of cultivating the plant body without the composition in accordance with the present invention. It is possible to determine a sugar content by a conventional method. It is also possible to determine a sugar content by using a conventional brix refractometer as described in Examples.

**[0035]** In the present specification, the “substance for regulating an oxidation-reduction state of a cell” is a substance that regulates oxidation/reduction of a substance that is responsible for oxidation-reduction of the cell. The substance for regulating an oxidation-reduction state of a cell includes substances that change values of, for example, an occurrence frequency of active oxygen, an absolute amount of glutathione, a ratio between reduced glutathione and oxidized glutathione, an absolute amount of reduced nicotinamide adenine dinucleotide phosphate (NAD(P)H), a ratio of NADPH/NADP<sup>+</sup>, a ratio of oxidized cytochrome c to reduced cytochrome c, and a ratio between oxidation and reduction of a component of electron transfer chain such as plastoquinone and ubiquinone. The substance responsible for oxidation-reduction of a cell is known in the art, but is not limited to those known in the art. The substances that change the values may be, for example, a substance that affects synthesis of glutathione or an amount of glutathione, a substance that promotes or inhibits synthesis of active oxygen, and a substance that promotes or inhibits change of a certain compound into either an oxidized form or a reduced form.

**[0036]** The substance, included in the composition in accordance with the present invention, for regulating an oxidation-reduction state of a cell is not limited as long as being included in the above-mentioned meaning. However, it is preferable that the substance affects synthesis of glutathione or an amount of glutathione. Such a substance makes it possible to obtain a plant having a higher sugar content.

**[0037]** In the present specification, the “substance that affects synthesis of glutathione or an amount of glutathione” is a substance that changes an amount of glutathione in a cell, and is preferably a substance that increases glutathione, such as glutathione itself, an enzyme for synthesis of glutathione, and a polynucleotide encoding the enzyme.

**[0038]** The substance for regulating an oxidation-reduction state of a cell can be classified into (i) a substance that can be absorbed into a plant by having contact with the plant and (ii) a substance that is introduced into genome of the plant. It will be understood that these substances can be used singularly or in combination.

**[0039]** The substance that affects synthesis of glutathione or an amount of glutathione and can be absorbed into a plant by having contact with the plant may be, for example, glutathione, glutathione conjugate, active oxygen (hydrogen peroxide, for example), active nitrogen, polyamine, oxidized titanium, jasmonic acid, salicylic acid, cysteine, cystine, heavy-metal cadmium, or iron ion. Polyamine can generate hydrogen peroxide. Oxidized titanium generates active oxygen in response to light. Cysteine and cystine are precursors of glutathione. In regard to heavy-metal cadmium and iron ion, excessive application is preferable. Among the substances exemplified above, glutathione is the most preferable to use. Glutathione includes reduced glutathione (hereinafter referred to as “GSH”) and oxidized glutathione (hereinafter referred to as “GSSG”). GSSG is preferable as glutathione to be included in the composition in accordance with the present invention. As described later in Examples, use of GSSG makes it possible to obtain a plant having a higher sugar content. Further, use of GSSG makes it possible to increase the number and size of fruit.

**[0040]** The substance that affects synthesis of glutathione or an amount of glutathione and is introduced into genome of a plant may preferably be, for example,  $\gamma$ -glutamylcysteine synthetase, a polynucleotide encoding the  $\gamma$ -glutamylcysteine synthetase (hereinafter referred to as “GSH1 gene”), glutathione-binding plastid type fructose-1,6-bisphosphate aldolase, or a polynucleotide encoding the glutathione-binding plastid type fructose-1,6-bisphosphate aldolase (hereinafter referred to as “FBA gene”).

**[0041]** Concrete examples of the GSH1 gene are not particularly limited, but include genes of, for example, *Zinnia elegans* (Genbank accession: AB158510), *Oryza sativa* (Genbank accession: AJ508915), and *Nicotiana tabacum* L. (Genbank accession: DQ444219). The genes of these plants can be suitably used in the present invention. Each translation product of these genes has a chloroplast transit signal peptide at its N-terminal region, like *Arabidopsis thaliana*.

**[0042]** In this regard, however, the following examples (a) through (d) are preferably used as the GSH1 gene in the present invention:

**[0043]** (a) a polynucleotide encoding a polypeptide which has the amino acid sequence of SEQ ID NO: 1 or 3;

**[0044]** (b) a polynucleotide encoding an polypeptide which has a  $\gamma$ -glutamylcysteine synthetase activity and

has an amino acid sequence with deletion, substitution, or addition of one or several amino acids in the amino acid sequence of SEQ ID NO: 1 or 3;

**[0045]** (c) a polynucleotide having the base sequence of SEQ ID NO: 2 or 4; and

**[0046]** (d) a polynucleotide which hybridizes under a stringent condition with a polynucleotide having a base sequence complementary to any one of the polynucleotides of the examples (a) through (c).

**[0047]** Note that the sequence of SEQ ID NO: 2 is an example of a base sequence encoding a polypeptide which has the amino acid sequence of SEQ ID NO: 1. Note also that the sequence of SEQ ID NO: 4 is an example of a base sequence encoding a polypeptide which has the amino acid sequence of SEQ ID NO: 3.

**[0048]** The FBA gene is not particularly limited, but may preferably be the following examples (e) through (h):

**[0049]** (e) a polynucleotide encoding a protein which has the amino acid sequence of any one of SEQ ID NO: 5, 6, and 15 through 36;

**[0050]** (f) a polynucleotide encoding a protein which has an activity of glutathione-binding plastid type fructose-1,6-bisphosphate aldolase and has an amino acid sequence with deletion, substitution, or addition of one or several amino acids in the amino acid sequence of any one of SEQ ID NO: 5, 6, and 15 through 36;

**[0051]** (g) a polynucleotide having the base sequences of SEQ ID NO: 7 and 37 through 56; and

**[0052]** (h) a polynucleotide which hybridizes under a stringent condition with a polynucleotide having a base sequence complementary to any one of the polynucleotides of the examples (e) through (g).

**[0053]** The sequence of SEQ ID NO: 8 shows a cDNA sequence of a protein having the amino acid sequence of SEQ ID NO: 5. In the base sequence of SEQ ID NO: 8, the sequence from position 145 to position 147 is a start codon, and the sequence from position 1318 to position 1320 is a stop codon. That is to say, an *Arabidopsis thaliana* FBA1 gene has the sequence from position 145 to position 1320 of the base sequence of SEQ ID NO: 8 as an open reading frame (ORF).

**[0054]** The sequence of SEQ ID NO: 9 shows an example of a base sequence encoding a protein which has the amino acid sequence of SEQ ID NO: 6. In the sequence of SEQ ID NO: 9, the sequence from position 104 to position 1300 is a region encoding the protein which has the amino acid sequence of SEQ ID NO: 6. Note that a peptide constituted by amino acids between methionine at position 1 and alanine at position 48 of the sequence of SEQ ID NO: 6 is a chloroplast transit peptide.

**[0055]** The base sequence of SEQ ID NO: 7 is a base sequence serving as an ORF in the *Arabidopsis thaliana* FBA1 gene. The base sequence of the *Arabidopsis thaliana* FBA1 gene is homologous with, for example, a gene (dbj|BAB55475.1) found on genome of *Oryza sativa*.

**[0056]** The sequences of SEQ ID NO: 37 through 56 are examples of DNA sequences encoding the amino acid sequences of SEQ ID NO: 15 through 34, respectively.

**[0057]** For reference, FIG. 9 shows a dendrogram of the amino acid sequences of SEQ ID NO: 15 through 36.

**[0058]** Persons skilled in the art can easily understand that, in a case where the above-mentioned amino acid sequences or DNA sequences include a region corresponding to a chloroplast transit signal, the region can be substituted by a chloroplast transit signal of another protein. The wording “deletion,

substitution, or addition of one or several amino acids” herein means deletion, substitution, or addition of such a number of amino acid(s) (preferably 10 or less, more preferably 7 or less, further preferably 5 or less) that can be deleted, substituted, or added by means of a known method for producing a mutant peptide, such as a site-specific mutation induction method. Such a mutant protein is not limited to a protein which is artificially mutated by means of a known method for producing a mutant polypeptide, but may be a naturally-existing protein being isolated and purified.

**[0059]** It is known in the art that some amino acids in an amino acid sequence of a protein can be easily altered without significantly affecting a structure or function of the protein. It is also known in the art that a protein has a naturally-existing mutant which does not significantly change a structure or function of the protein, apart from an artificially-altered protein.

**[0060]** It is preferable that a mutant includes conservative or non-conservative substitution, deletion, or addition of amino acid(s). In this regard, silent substitution, addition, and deletion are more preferable, and conservative substitution is particularly preferable. Such mutations do not change a polypeptide activity in accordance with the present invention.

**[0061]** It is considered that representative examples of the conservative substitution are: substitution of one amino acid with another among aliphatic amino acids Ala, Val, Leu, and Ile; replacement of hydroxyl residues Ser and Thr; replacement of acidic residues Asp and Glu; substitution between amide residues Asn and Gln; replacement of basic residues Lys and Arg; and substitution between aromatic residues Phe and Tyr.

**[0062]** The “stringent condition” in the present specification means such a condition that sequences hybridize with each other only when the sequences have at least 90% identity, preferably at least 95% identity, most preferably 97% identity. Specifically, the “stringent condition” includes, for example, incubation overnight at 42° C. in a hybridization solution (50% formamide, 5×SSC (15 mM trisodium citrate and 150 mM NaCl), 50 mM sodium phosphate (pH7.6), 5× Denhardt’s solution, 10% dextran sulfate, and 20 µg/ml denatured fragmented salmon sperm DNA) and washing of a filter in 0.1×SSC at approximately 65° C. The hybridization can be carried out by means of a known method such as one described in Sambrook et al., *Molecular cloning, A Laboratory Manual*, 3rd Ed., Cold Spring Harbor Laboratory (2001). Generally, the higher the temperature is and the lower the salt concentration is, the higher the stringency becomes (the hybridization becomes more difficult to occur). The higher stringency makes it possible to obtain a polynucleotide with a higher homology.

**[0063]** In a case where the composition in accordance with the present invention includes a polynucleotide among the above-mentioned polynucleotides, the composition in accordance with the present invention may include an expression vector including the polynucleotide. The expression vector may be constructed with a known method and is not particularly limited in construction method.

**[0064]** It is possible to use various known vectors as a base of the expression vector. For example, a plasmid, a phage, a cosmid, or the like can be used and selected as appropriate according to an introduction method or a plant cell into which the expression vector is introduced. Specifically, a pBR322 vector, a pBR325 vector, a pUC19 vector, a pUC119 vector, a pBluescript vector, a pBluescriptSK vector, a pBI vector, or

the like can be used, for example. In particular, it is preferable to use a pBI binary vector in a case where the composition in accordance with the present invention is used in introducing a vector that includes the polynucleotide into a plant body by means of the *Agrobacterium* method. Specifically, the pBI binary vector may be pBIG, pBIN19, pBI101, pBI121, pBI221, or the like, for example.

**[0065]** In the expression vector, a promoter is not particularly limited as long as being able to express a gene in the plant body, and a known promoter can be suitably used. The promoter may be, for example, a cauliflower mosaic virus 35S promoter (CaMV35S), an actin promoter, a nopaline synthetase promoter, a tobacco PR1a gene promoter, a tomato ribulose-1,5-bisphosphate carboxylase/oxydase small subunit promoter, or the like. Among these promoters, the cauliflower mosaic virus 35S promoter or the actin promoter can be preferably used. The expression vector with each of the promoters can strongly express a given gene when introduced into a plant cell.

**[0066]** The promoter only has to be introduced into the vector so as to be connected so that a gene encoding a transcription factor can be expressed. The promoter is not particularly limited in specific structure as the expression vector.

**[0067]** The expression vector may further include a DNA segment in addition to the promoter and the polynucleotide. The DNA segment is not particularly limited and may be a terminator, a selection marker, an enhancer, a base sequence for increasing translation efficiency, and the like. Further, the expression vector may include a T-DNA region. The T-DNA region can increase efficiency of gene introduction particularly in a case where the expression vector is introduced into a plant body by means of *Agrobacterium*.

**[0068]** The terminator is not particularly limited as long as having a function as a transcription termination site, and may be a known terminator. Specifically, it is possible to preferably use a transcription termination site of a nopaline synthetase gene (Nos terminator), a transcription termination site of a cauliflower mosaic virus 35S (CaMV35S terminator), or the like, for example. Among these, the Nos terminator can be more preferably used. By arranging the terminator at an appropriate site in the expression vector, it becomes possible to prevent, after introduction of the expression vector into a plant body, such phenomena that an unnecessarily-long transcript is synthesized and that a strong promoter decreases the number of plasmid copies.

**[0069]** The selection marker may be a drug resistance gene, for example. The drug resistance gene is, for example, one resistant to hygromycin, bleomycin, kanamycin, gentamycin, chloramphenicol, or the like. With the drug resistance gene, it is possible to easily select a transformed plant by cultivating plant bodies in a culture medium that includes the above-mentioned antibiotic and thereafter selecting a plant body that can grow in the culture medium.

**[0070]** The polynucleotide for increasing translation efficiency may be, for example, an omega sequence derived from a tobacco mosaic virus. By arranging the omega sequence in an untranslated region (5'UTR) of a promoter, it is possible to increase translation efficiency of the gene encoding a transcription factor. As described above, various DNA segments can be included in the expression vector according to purposes.

**[0071]** Specifically, the expression vector is constructed by, for example, a method which the promoter, the polynucleotide, and the DNA segment, if necessary, are introduced into

a base vector which is selected accordingly, so as to be arranged in a predetermined order. The polynucleotide and the promoter (and the terminator and the like, if necessary) can be connected so that an expression cassette is constructed, and the expression cassette can be introduced into the base vector. When constructing the expression cassette, it is possible to arrange so that, for example, each DNA segment includes a cleavage site as a protruding end that is complementary to a protruding end of other DNA segment, and these protruding ends are reacted via a ligation enzyme. This makes it possible to regulate an order of the DNA segments. In a case where the terminator is included in the expression cassette, the promoter, a polynucleotide encoding N-acetylglucosamine transferase, and the terminator are arranged in this order from the upstream. Reagents used in constructing the expression vector, i.e., restriction enzymes, ligation enzymes, and the like, are not particularly limited in type, and commercially available reagents can be accordingly selected and used.

**[0072]** The expression vector can be multiplied by a known method and a multiplication method (production method) of the expression vector is not particularly limited. In general, the expression vector is multiplied in *Escherichia coli* serving as a host. In this case, a type of *E. coli* can be selected as appropriate according to a type of the expression vector.

**[0073]** It is possible to singularly use the substances exemplified above and to use two or more kinds of the substances in combination.

**[0074]** In a case where the composition in accordance with the present invention includes, as a substance for regulating an oxidation-reduction state of a cell, a substance that can be absorbed into a plant by having contact with the plant, an amount of the substance is not particularly limited, but is preferably 0.01 mM to 20 mM, more preferably 0.1 mM to 2 mM. When the amount of the substance is within the range, it is possible to better improve a sugar content of the plant to be produced. It should be noted that the concentration of the substance may be changed as appropriate according to a desired sugar content, a type of the plant to which the substance is applied, and the like.

**[0075]** The composition in accordance with the present invention may include other component to such an extent that an effect of the composition in accordance with the present invention is not impaired. For example, in a case where the composition in accordance with the present invention includes, as a substance for regulating an oxidation-reduction state of a cell, a substance that can be absorbed into a plant by having contact with the plant, the composition may be dissolved in water, a known liquid carrier, or the like so as to be provided in the form of a liquid agent, an emulsion, a gel agent, or the like. Such a liquid carrier may be, for example, aromatic hydrocarbon such as xylene; alcohol such as ethanol and ethylene glycol; ketone such as acetone; ether such as dioxane and tetrahydrofuran; dimethylformamide, dimethylsulfoxide, acetonitrile, and the like, but is not limited to these. Alternatively, the substance for regulating an oxidation-reduction state of a cell may be supported by a solid carrier component so that the composition is provided as a solid agent, a powder agent, or the like. Such a solid carrier component may be, for example, an inorganic material such as talc, clay, vermiculite, diatomite, kaolin, calcium carbonate, calcium hydroxide, white clay, and silica gel; and an organic material such as flour and starch, but is not limited to these. Further, the composition in accordance with the present

invention may be combined with other auxiliary agent accordingly. Such an auxiliary agent may be, for example, an anion surface-active agent such as alkyl sulfate, alkyl sulfonate, alkyl aryl sulfonate, dialkyl sulfosuccinate; a cationic surface-active agent such as higher aliphatic amine salt; a nonionic surface-active agent such as polyoxyethylene glycol alkyl ether, polyoxyethylene glycol acyl ester, polyoxyethylene glycol polyalcohol acyl ester, and cellulose derivative; a thickening agent such as gelatin, casein, and gum arabic; a weighting agent; a binding agent; and the like.

**[0076]** Usage of the composition in accordance with the present invention is not particularly limited. For example, in a case where the composition in accordance with the present invention includes, as a substance for regulating an oxidation-reduction state of a cell, a substance that can be absorbed into a plant by having contact with the plant, and where the composition is a liquid agent or the like, the composition may be included in a culture medium or the like which is used in cultivation of the plant, or may be sprayed, dropped, or applied to entire plant body or a part of the plant body such as a vegetative point, a bud, a leaf, and a stem. Note that a "culture medium" used in cultivation of a plant in the present specification includes soil and a soil improvement agent.

**[0077]** In a case where the composition is a solid agent or the like, the composition may be included in a culture medium which is used in cultivation of a plant. Alternatively, in a case of hydroponic cultivation, the composition may be added to water and gradually dissolved therein. The composition may be applied as a solid agent or the like to be dissolved in water, and dissolved in water at the time of use. Further, the composition in accordance with the present invention may be applied to a plant as a mixture with a known fertilizer and an agent such as a plant hormone.

**[0078]** The composition in accordance with the present invention is not particularly limited in timing of application to a plant. For example, the composition may be applied to the plant from the time of sowing. Specifically, in a case where the composition is applied to a plant such as *Lycopersicon esculentum* which produces fruit approximately 2 months to half year after sowing, the composition may be applied on the day of sowing and preferably applied in regular intervals during 30 days after sowing, more preferably during 60 days after sowing, further preferably from the day of sowing to the day of harvest. In this case, an interval of application of the composition is not particularly limited, but is preferably one to four times a week, more preferably two or three times a week. The composition is not particularly limited in applied amount. The applied amount can be arranged as appropriate according to a type of plant. In a case of *Lycopersicon esculentum* or the like, for example, preferably 0.001 mmol or more and 0.1 mmol or less, more preferably 0.01 mmol or more and 0.05 mmol or less, of the substance for regulating an oxidation-reduction state of a cell is applied at a time per plant. In a case where the composition is included in a culture medium as described above, the composition is applied to a plant from the time when the plant is sowed in the culture medium or the time when a seedling or the like of the plant is transplanted to the culture medium.

**[0079]** The composition in accordance with the present invention may be applied to a plant after sowing and after the plant is grown to some extent, e.g., after a seedling of the plant is produced. For example, in a case where the composition is applied to a Gramineae plant such as *Zea mays* L. var. *saccharata* Sturt, the composition may be applied to the plant

after a seedling of the plant is grown. In this case, the composition in accordance with the present invention may be included in advance in a culture medium to which the seedling is to be transplanted, or may be periodically applied to the culture medium after the seedling is transplanted to the culture medium. In a case where the composition is applied after transplanting of the seedling, timing of the application is not particularly limited. However, it is preferable that, for example, the composition is applied one to four times a week, more preferably two or three times a week, from transplanting of the seedling until harvest. The composition in accordance with the present invention is not particularly limited in applied amount. The applied amount can be arranged as appropriate according to a type of plant. In a case of *Zea mays* L. var. *saccharata* Sturt or the like, for example, preferably 0.001 mmol or more and 0.1 mmol or less, more preferably 0.01 mmol or more and 0.05 mmol or less, of the substance for regulating an oxidation-reduction state of a cell is applied at a time per plant.

**[0080]** It is also possible to arrange timing of application of the composition in view of timing of flower production. For example, the composition may be applied while a flower bud is unbroken, after petals are fallen, from a period that the flower bud is unbroken until fruit bearing, from flowering time until fruit bearing, or from when the petals are fallen until fruit bearing. In a case where the composition is applied to *Vitis labrusca* as described later in Example, the composition may be applied to anthotaxy. In this Example, the composition is mixed with a plant hormone (gibberellin), which is for producing seedless fruit of *Vitis labrusca*, and applied when the plant hormone should be applied.

**[0081]** It is also possible to arrange timing of application of the composition based on back calculation of days from harvest time. For example, the composition may be applied 10 days or 20 days before harvest.

**[0082]** In a case where the composition in accordance with the present invention is applied to a plant during cultivation of the plant as described above, the composition may be mixed with a fertilizer and/or an agent such as a plant hormone as described above. In this case, timing of application of a mixture of the composition and the fertilizer or the like is not particularly limited, and the mixture may be applied at a time exemplified above or at a preferable time to apply the fertilizer or the like.

**[0083]** In a case where the composition in accordance with the present invention includes, as a substance for increasing glutathione in a cell, a substance to be introduced into genome of a plant, such as a polynucleotide described above, the composition may be used in such a way that the polynucleotide is introduced into the genome of the plant body by means of a known transformation method. For example, the composition may include a polynucleotide and may be introduced into a plant body by a known plant expression vector, or may include a vector that includes the polynucleotide.

**[0084]** The polynucleotide content of the composition in accordance with the present invention is not particularly limited. The polynucleotide may be dissolved in a buffer or the like which is generally used in polynucleotide preservation.

**[0085]** Introduction of a vector to a plant cell is carried out by a transformation method known in the art (for example, the *Agrobacterium* method, the particle gun, the polyethylene glycol method, and the electroporation method). In a case of the *Agrobacterium* method, for example, a constructed plant expression vector is introduced into suitable *Agrobacterium*

(e.g., *Agrobacterium tumefaciens*) and a aseptically-cultured leaf disc is infected with this strain by the leaf disc method (Hirofumi UCHIMIYA, Manuals for plant genetic manipulation, 1990, 27-31pp, Kodansha Scientific Ltd., Tokyo) or the like, so that a transformed plant can be obtained. In a case of the particle gun, it is possible to use (i) a plant body, plant organ, or plant tissue without any treatment, (ii) a cut piece of the plant body, plant organ, or plant tissue, or (iii) a protoplast of the plant body, plant organ, or plant tissue. Such a prepared sample can be processed using a gene introduction apparatus (e.g., PDS-1000, Bio-Rad Laboratories, Inc.). In this process, conditions differ according to a plant or a sample, however, are generally arranged so that a pressure is approximately 450 psi to 2000 psi and a distance is approximately 4 cm to 12 cm.

**[0086]** The cell or plant tissue into which a target gene is introduced is selected with a drug-resistance marker such as a kanamycin-resistance marker and a hygromycin-resistance marker, and then reproduced to be a plant body by a standard method. Reproduction of a plant body from a transformed cell can be carried out by a method known in the art according to a type of the plant cell.

**[0087]** In order to determine whether or not a target gene is introduced into a plant, it is possible to use PCR, southern hybridization, northern hybridization, or the like. For example, DNA is prepared from a transformed plant and then subjected to PCR with use of a primer specific to DNA having been introduced into the transformed plant. Then, an amplification product thus obtained is subjected to agarose gel electrophoresis, polyacrylamide gel electrophoresis, or capillary electrophoresis and thereafter stained with ethidium bromide. As a result, a target amplification product can be detected. In this way, it is possible to determine whether or not the plant is transformed.

**[0088]** Once a transformed plant body in which a target gene is introduced into genome is obtained, it is possible to obtain a progeny of the transformed plant body by sexual or asexual reproduction. Further, it is possible to mass-produce target plant bodies with a reproduction material (e.g., seed, protoplast) obtained from the plant body or the progeny or clone of the plant body.

**[0089]** In the present invention, a target plant for transformation is an entire plant body, a plant organ (for example, leaf, petal, stem, root, and seed), a plant tissue (for example, epidermis, phloem, parenchyma, xylem, vessel bundle, palisade parenchyma, sponge parenchyma), a plant culture cell, a plant cell in various forms (for example, suspension culture cell), protoplast, a cut piece of leaf, callus, or the like. The target plant for transformation is not particularly limited, and a plant capable of expressing a target gene may be selected accordingly.

**[0090]** The polynucleotide mentioned above is derived from *Arabidopsis thaliana*. It has been reported that, for example, transformed plants of *Nicotiana tabacum* L., *Populus*, *Citrus limon*, and the like can be produced with use of a gene of *Arabidopsis thaliana*. Such reports also can be used as references for how to use the composition in accordance with the present invention (Franke R, McMichael C M, Meyer K, Shirley A M, Cusumano J C, Chapple C. (2000) Modified lignin in tobacco and poplar plants over-expressing the *Arabidopsis* gene encoding ferulate 5-hydroxylase. Plant J. 22: 223-234; Pena L, Martin-Trillo M, Juarez J, Pina J A, Navarro L, Martinez-Zapater J M. (2001) Constitutive expression of *Arabidopsis* LEAFY or APETALA1 genes in citrus reduces their generation time. Nat Biotechnol. 19: 263-267).

**[0091]** Target plants for the composition in accordance with the present invention are not particularly limited. The composition can be applied to almost all plants such as various monocotyledonous plants, dicotyledonous plants, and trees. Examples of monocotyledonous plants include: Lemnaceae such as *Spirodela* (*Spirodela polyrrhiza* Schleid) and *Lemna* (*Lemna paucicostata* and *Lemna trisulca*); Orchidaceae such as *Cattleya*, *Cymbidium*, *Dendrobium*, *Phalaenopsis*, *Vanda*, *Paphlopedllum* and *Oncidium*; Typhaceae; Sparganiaceae; Potamogetonaceae; Najadaceae; Scheuchzeriaceae; Alismataceae; Hydrocharitaceae; Triuridaceae; Gramineae (e.g., *Zea mays* such as *Zea mays* L. var. *saccharata* Sturt), Cyperaceae; Palmae; Araceae; Eriocaulaceae; Commelinaceae; Pontederiaceae; Juncaceae; Stemonaceae; Liliaceae; Amaryllidaceae; Dioscoreaceae; Iridaceae; Musaceae; Zingiberaceae; Cannaceae; and Burmannia.

**[0092]** Examples of dicotyledonous plants include: Convolvulaceae such as *Pharbitis* (*Pharbitis nil* Choisy), *Calystegia* (*Calystegia japonica* Choisy, *Calystegia hederacea* and *Calystegia soldanella* Rohm. et Schult.), *Ipomoea* (*Ipomoea pes-caprae* and *Ipomoea batatas* Lam. var. *edulis* Maikno) and *Cuscuta* (*Cuscuta japonica* Choisy. and *Cuscuta australis*); Caryophyllaceae such as *Dianthus* (*Dianthus caryophyllus* L.), *Stellaria*, *Minuartia*, *Cerastium*, *Sagina*, *Arenaria*, *Moehringia*, *Pseudostellaria*, *Hankenya*, *Spergula*, *Spergularia*, *Silene*, *Lychnis*, *Melandryum* and *Cucubalus*; Casuarinaceae; Saururaceae; Piperaceae; Choranthaceae; Sailicaceae; Myricaceae; Juglandaceae; Betulaceae; Fagaceae; Ulmaceae; Moraceae; Urticaceae; Podostemaceae; Proteaceae; Olacaceae; Santalaceae; Loranthaceae; Aristolochiaceae; Rafflesiaceae; Balanophoraceae; Polygonaceae; Chenopodiaceae; Amaranthaceae; Nyctaginaceae; Cynocmbaceae; Phytolaccaceae; Aizoaceae; Portulacaceae; Magnoliaceae; Trochodendraceae; Cercidphyllaceae; Nymphaeaceae; Ceratophyllaceae; Ranunculaceae; Lardizabalaceae; Berberidaceae; Menispermaceae; Calycanthaceae; Lauraceae; Papaveraceae; Capparidaceae; Cruciferae; Droserraceae; Nepenthaceae; Crassulaceae; Saxifragaceae; Pittosporaceae; Hamamelidaceae; Platanaceae; Rosaceae; Leguminosae; Oxalidaceae; Geraniaceae; Linaceae; Zygophyllaceae; Rutaceae; Cimaroubaceae; Meliaceae; Polygalaceae; Euphorbiaceae; Callitrichaceae; Buxaceae; Empetraceae; Coriariaceae; Anacardiaceae; Aquifoliaceae; Celastraceae; Staphyleaceae; Icacinaceae; Aceraceae; Hippocastanaceae; Sapindaceae; Sabiaceae; Balsaminaceae; Rhamnaceae; Vitaceae; Elaeocarpaceae; Tiliaceae; Malvaceae; Stearculiaceae; Actinidiaceae; Theaceae; Guttiferae; Elatinaceae; Tamaricaceae; Violaceae; Flacourtiaceae; Stachyuraceae; Passifloraceae; Begoniaceae; Cactaceae; Thymelaeaceae; Elaegnaceae; Lythraceae; Punicaceae; Rhizophoraceae; Alangiaceae; Melastomataceae; Hydrocaryaceae; Oenotheraceae; Haloragaceae; Hippuridaceae; Araliaceae; Umbelliferae; Cornaceae; Diapensiaceae; Clethraceae; Pyrolaceae; Uricaceae; Myrsinaceae; Primulaceae; Plumbaginaceae; Ebenaceae; Symplocaceae; Styraceae; Oleaceae; Loganiaceae; Gentianaceae; Apocynaceae; Asclepiadaceae; Polemoniaceae; Boraginaceae; Verbenaceae; Labiatae; Solanaceae (e.g., *Lycopersicum esculentum*); Scrophulariaceae; Bignoniaceae; Pedaliaceae; Orobanchaceae; Gesneriaceae; Lentibulariaceae; Acanthaceae; Myoporaceae; Phrymaceae; Plantaginaceae; Rubiaceae; Caprifoliaceae; Adoxaceae; Valerianaceae; Dipsacaceae; Cucurbitaceae; Campanulaceae; and Compositae.

**[0093]** The present invention includes a kit for producing a plant body having an improved sugar content (hereinafter referred to as “kit in accordance with the present invention”). The kit in accordance with the present invention only has to include a substance for regulating an oxidation-reduction state of a cell (for example, glutathione, a polynucleotide encoding  $\gamma$ -glutamylcysteine synthetase, or a polynucleotide encoding glutathione-binding plastid type fructose-1,6-bisphosphate aldolase). Further, the kit in accordance with the present invention may include a component other than the substance above. The substance for regulating an oxidation-reduction state of a cell and the component may be provided together in a single container for containing the substance and the component of an appropriate amount and/or in an appropriate form, or may be separately provided in different containers. Further, the kit in accordance with the present invention may include an instrument for plant cultivation, a culture medium, and the like. In a case where a polynucleotide is included in the kit in accordance with the present invention, the kit may be such that a base vector of an expression vector for expressing the polynucleotide may be provided in a different container from the polynucleotide. Alternatively, the kit may include the base vector into which the polynucleotide is introduced in advance. Further, the kit in accordance with the present invention may include a reagent and the like which is used in a known plant transformation method.

**[0094]** <2. Method, in Accordance with the Present Invention, for Producing Plant Body Having Improved Sugar Content>

**[0095]** A method, in accordance with the present invention, for producing a plant body having an improved sugar content (hereinafter referred to as “method in accordance with the present invention”) only has to include a step for cultivating a plant body with use of a substance for regulating an oxidation-reduction state of a cell (for example, glutathione, a polynucleotide encoding  $\gamma$ -glutamylcysteine synthetase, or a polynucleotide encoding glutathione-binding plastid type fructose-1,6-bisphosphate aldolase).

**[0096]** In a case where a substance that can be absorbed into a plant by having contact with the plant is used in regulation of an oxidation-reduction state of a cell, the step may include, for example, causing the plant to absorb the substance. How to cause the plant to absorb the substance for regulating an oxidation-reduction state of a cell is not particularly limited. For example, it is possible to cause the plant to absorb the substance by cultivating the plant on a culture medium (including soil and an soil improvement agent) that includes the substance, or by spraying or coating the plant with the substance during cultivation of the plant. Alternatively, it is also possible to cultivate the plant on a culture medium that includes absorbent such as an ion-exchange resin into which the substance is absorbed, where the absorbent is buried in soil of the culture medium, for example.

**[0097]** In a case where a substance such as a polynucleotide which is to be introduced into genome of a plant is used in regulation of an oxidation-reduction state of a cell, the method does not include causing the plant to absorb the substance, but may include introducing the substance to the plant in advance so as to produce a transformed plant and then cultivating the transformed plant. How to introduce a polynucleotide into the plant is described above in the explanation of the composition in accordance with the present invention.

**[0098]** The present invention includes a plant body obtained by the method in accordance with the present inven-

tion. It is possible to easily identify the plant body by measuring at least either a content or ratio, in the plant body, of the substance for regulating an oxidation-reduction state of a cell. Therefore, it is possible to clearly distinguish the plant body from one obtained by other method. The plant body can be identified also by, for example, comparing gene expression patterns by means of DNA microarray or the like, other than by measuring the content and concentration of the substance. In a case where GSSG is used as the substance, it is possible to take the following procedures, for example: (i) a gene expression pattern of a plant cultivated after being applied with GSSG is analyzed in advance; (ii) an expression pattern unique to the plant body applied with GSSG (GSSG expression pattern) is determined by comparison of gene expression pattern between the plant body applied with GSSG and a plant body cultivated by other method; (iii) an expression pattern of a target plant body is analyzed; and then (iv) the expression pattern of the target plant body is compared with the GSSG expression pattern. This allows an easy identification of the plant body applied with GSSG. Further, as another example of the identification, comparison of a two-dimensional electrophoretic profile of a glutathione-binding protein to a pattern change analyzed in advance makes it possible to determine whether or not GSSG is applied. In a case where a polynucleotide is used, it is possible to distinguish the plant body in accordance with the present invention from other plant body by identifying the polynucleotide in the plant body by means of PCR, southern hybridization, northern hybridization, or the like.

**[0099]** Details of the embodiments of the present invention are described below in Examples. It will be obvious that the present invention is not limited to the descriptions of the examples below and details of the present invention may be varied in many ways. The present invention is not limited to the description of the embodiments above, but may be altered by a skilled person within the scope of the claims. An embodiment based on a proper combination of technical means disclosed in different embodiments is encompassed in the technical scope of the present invention. All documents cited is incorporated herein by reference.

#### Examples

##### Example 1

##### Production of *Lycopersicon esculentum*

**[0100]** In the present example, *Lycopersicon esculentum* was cultivated with use of GSSG or GSH. Details of cultivation are described below.

**[0101]** First, *Lycopersicon esculentum* seedlings (TAKII & CO. Ltd., product name: Osama tomato reika) were transplanted into a hydroponic culture pot ( $1/2000$  a). In the hydroponic culture pot, 6 L of vermiculite (ASAHI INDUSTRIES Co., LTD.), 3 L of KUREHA horticultural soil (KUREHA CORPORATION), and 3 L of vermiculite were layered as a lower, middle, and upper layers, respectively.

**[0102]** During the cultivation of *Lycopersicon esculentum*, 50 mL of 0.5 mM GSSG or 0.5 mM GSH (adjusted with 0.1N NaOH to be at pH 7) was applied twice a week at a root per plant. The *Lycopersicon esculentum* plants were grown for 60 days without being subjected to bud removal. Last 10 days was used as a harvest period for harvesting fruit of the plants. For comparison, a *Lycopersicon esculentum* plant was grown under the same condition, except that GSSG and GSH were not applied. To the plants of any condition, 3 g of Kumiai

phosphate ammonium nitrate potassium S-604 (Chisso Asahi Fertilizer Co., Ltd.) was applied as an additional fertilizer once in 2 weeks.

[0103] Next, the fruit harvested was subjected to sensory tests of sugar content and the like. As a result, it was determined that fruit of the plant applied with GSSG increased in sugar content compared to that of the plant not applied with GSSG or GSH. Further, it was determined that the plant applied with GSSG increased in number of fruit. It was determined that fruit of the plant applied with GSH increased in sugar content and acidity.

[0104] These results indicated that *Lycopersicon esculentum* having an increased sugar content could be produced by cultivation using a culture medium that contains

[0105] GSSG or GSH.

#### Example 2

##### Sugar Content Determination

[0106] Cultivated were *Lycopersicon esculentum* plants to which GSSG or GSH was applied by the method described in Example 1. Then, obtained fruit of the plants was subjected to sugar content determination using "Pocket" Refractometer APAL-1 (ATAGO CO., LTD.).

[0107] For comparison, *Lycopersicon esculentum* plants were cultivated under two types of conditions (referred to as "Cont" and "Cont2 Sunny"). In the Cont condition, *Lycopersicon esculentum* plants were cultivated by the same method as in Example 1, except that GSSG and GSH were not applied. In the Cont2 Sunny condition, a *Lycopersicon esculentum* plant was not applied with GSSG or GSH and was independently cultivated at a site sufficiently irradiated with sunlight so that illuminance on the *Lycopersicon esculentum* plant becomes 100%. In the Cont condition and a condition in which GSSG or GSH was applied, the plants were planted at intervals of 40 cm to 50 cm. In this case, a plant may intercept light irradiating another plant. Therefore, illuminance on such plants becomes less than 100%.

[0108] In the condition in which GSSG was applied, the condition in which GSH is applied, and the Cont condition, three *Lycopersicon esculentum* plants were cultivated, respectively. In the Cont2 Sunny condition, one *Lycopersicon esculentum* plant was cultivated.

[0109] FIGS. 1 and 2 show results of the sugar content determination. FIG. 1 shows a result of sugar content determination of *Lycopersicon esculentum* plants obtained in the present example. In FIG. 1, the vertical scale indicates sugar content (Brix, unit: %) and the horizontal scale indicates cultivation conditions. In FIG. 1, the reference sign \* indicates that fruit could not be obtained during the harvest period. FIG. 2 shows a result of ANOVA analysis on the result of sugar content determination shown in FIG. 1. In FIG. 2, the vertical scale indicates sugar content and the horizontal scale indicates cultivation conditions. In FIG. 2, alphabetic characters above each bar are for indicating that bars indicated by a same character belong to a same group when being grouped based on ANOVA analysis. The ANOVA analysis was carried out by means of StatView 5.0 (SAS Institute Inc.) with a significant difference level of 5%.

[0110] As shown in FIGS. 1 and 2, application of GSSG or GSH made it possible to obtain *Lycopersicon esculentum* fruit which was significantly increased in sugar content compared to *Lycopersicon esculentum* fruit cultivated under the Cont condition and also to *Lycopersicon esculentum* fruit

sufficiently irradiated with sunlight. Especially, application of GSSG made it possible to obtain *Lycopersicon esculentum* having an extremely high sugar content.

#### Example 3

##### Production of *Zea mays* L. var. *saccharata* Sturt

[0111] In the present example, *Zea mays* L. var. *saccharata* Sturt was cultivated. First, a *Zea mays* L. var. *saccharata* Sturt seed (TAKII & CO. Ltd., product number: Canberra 90) was sown in vermiculite (ASAHI INDUSTRIES Co., LTD.). Two weeks after sowing, a *Zea mays* L. var. *saccharata* Sturt plant was transplanted to a hydroponic culture pot described in Example 1. To the plant, 3 g of Kumiai phosphate ammonium nitrate potassium S-604 (Chisso Asahi Fertilizer Co., Ltd.) was applied as an additional fertilizer 4 weeks and 6 weeks after the sowing.

[0112] Within 2 weeks from the 5th week after the sowing, 50 mL of 0.2 mM GSSG was applied 4 times at a root of the plant. Within 2 weeks from the 7th week after the sowing, 50 mL of 0.2 mM GSSG was sprayed 4 times to leaves of the plant. For comparison, a *Zea mays* L. var. *saccharata* Sturt plant was cultivated by the same method as in the present example, except that GSSG was not applied, and fruit thereof was harvested.

[0113] Fruit was harvested 90 days after the sowing and subjected to a sensory test of sugar content. As a result, it was determined that fruit of the plant applied with GSSG increased in sugar content compared to that of the plant applied with no GSSG. Further, it was determined that the plant applied with GSSG increased in size and number of fruit.

#### Example 4

##### Production of *Zea mays* L. var. *saccharata* Sturt (2)

[0114] In the present example, *Zea mays* L. var. *saccharata* Sturt was cultivated under a condition different from Example 3 in how to apply GSSG. First, a *Zea mays* L. var. *saccharata* Sturt seed (TAKII & CO. Ltd., product number: Canberra 90) was sown in vermiculite (ASAHI INDUSTRIES Co., LTD.). One week after sowing, a *Zea mays* L. var. *saccharata* Sturt plant was transplanted to a hydroponic culture pot described in Example 1. To the plant, 3 g of Kumiai phosphate ammonium nitrate potassium S-604 (Chisso Asahi Fertilizer Co., Ltd.) was applied as an additional fertilizer 4 weeks and 6 weeks after the sowing.

[0115] During 12 weeks after germination, 200 mL of 0.5 mM GSSG was applied at a root of the plant twice a week. For comparison, a *Zea mays* L. var. *saccharata* Sturt plant was cultivated by the same method as in the present example, except that GSSG was not applied, and fruit thereof was harvested.

[0116] Fruit was harvested 12 weeks after the sowing and subjected to a sensory test of sugar content. As a result, it was determined that fruit of the plant applied with GSSG increased in sugar content compared to that of the plant applied with no GSSG. Further, it was determined that the plant applied with GSSG increased in size and number of fruit.

#### Example 5

##### Production of *Vitis labrusca*

[0117] In the present invention, *Vitis labrusca* was cultivated. Specifically, immediately after flowering of a *Vitis*



*labrusca* (Delaware) plant, a mixed solution of 1 mM gibberellin (GA3) and 1 mM of an agent was applied to anthotaxy of the plant. The agent was GSSG or GSH. Then, the plant was coated with the agent and thereafter produced fruit was harvested. For comparison, a *Vitis labrusca* plant was cultivated in the same way, except that GA3, but not GSSG or GSH, was applied, and fruit thereof was harvested and subjected to a sensory test described below.

[0118] The fruit harvested was subjected to a sensory test of sugar content. As a result, it was determined that fruit of the plant applied with GA3 and GSSG or GSH increased in sugar content compared to that of the plant applied with only GA3. Further, it was determined that the plant applied with GSSG and GA3 increased in size of fruit.

[0119] In addition, it was determined that a *Vitis labrusca* plant applied with GSSG or GSH but not GA3 increased in sugar content. In this case, effect of producing seedless grape was suppressed without GA3.

#### Example 6

##### Change Over Time After Application of Substance for Regulating Oxidation-Reduction State of Cell

[0120] In the present example, a sugar content of a plant was determined after a substance for regulating an oxidation-reduction state of a cell was applied to the plant. The substance for regulating an oxidation-reduction state of a cell was GSH or GSSG. As in the case of Example 1, *Lycopersicum esculentum* was used as the plant. Specifically, the following operations were carried out.

[0121] Ninety days after sowing of *Lycopersicum esculentum* seeds, *Lycopersicum esculentum* plants were subjected to a GSH or GSSG treatment. The *Lycopersicum esculentum* plants were cultivated by the same method as in Example 1 except for the GSH or GSSG treatment. The GSH or GSSG treatment was such that 50 mL of 0.5 mM GSSH or 0.5 mM GSH (adjusted with 0.1N NaOH to be at pH 7) was applied once at a root per plant. Then, fruit of the plants was harvested every day from the 0th day until the 4th day after application of GSH or GSSG, and subjected to sugar content determination. FIG. 3 shows a result of the sugar content determination. FIG. 3 is a graph showing a determination result of relation between sugar content and the number of days from an application day of GSH or GSSG. In FIG. 3, the vertical scale indicates sugar content (Brix, unit: %) and the horizontal scale indicates days from the application day. In FIG. 3, lines labeled with circles, triangles, and squares show results of the plants applied with GSH, GSSG, and no GSH and no GSSG, respectively. Note that GSSG or GSH was applied in the morning of the 0th day, and a result of the 0th day in FIG. 3 was obtained by harvesting fruit and determining a sugar content of the fruit in the evening of the 0th day.

[0122] As shown in FIG. 3, it was shown that application of GSSG or GSH made it possible to rapidly improve a sugar content of fruit.

#### Example 7

##### Production of Plant into which GSH1 Gene is Introduced

[0123] In the present example, a clone of a  $\gamma$ -glutamylcysteine synthetase gene was used as a substance for regulating an oxidation-reduction state of a cell. The clone is a polynu-

clootide having a sequence of SEQ ID NO:3, is one of GSH1 genes, and is referred to merely as "GSH1 gene" in the present example.

#### (1) Plant to be Used

[0124] In order to produce a transformed plant, a wild type *Arabidopsis thaliana* Columbia (Col-0) was used as a parent plant. The Columbia (Col-0) was sown in soil in a square plastic pot (6.5×6.5×5 cm), which soil is constituted by three layers of vermiculite (ASAHI INDUSTRIES Co., LTD., Okayama), KUREHA culture soil (KUREHA horticultural soil, KUREHA CORPORATION, Tokyo), and vermiculite being layered in this order from the bottom at a ratio of 2:1:1. Then, the Columbia (Col-0) was cultivated at a growth temperature of 22° C. under a long-day condition (16-hour light period/8-hour dark period).

#### (2) Cloning of GSH1 Gene, Alteration of GSH1 Gene, and Production of GSH1-Transformed Plant

[0125] Entire RNA of a 3-week-old wild type *Arabidopsis thaliana* Columbia (Col-0) was isolated, and cDNA was synthesized based on the RNA by using a Prostar first strand RT-PCR kit (Stratagene, La Jolla, Calif., USA).

[0126] With use of the following specific primers designed based on a cDNA sequence of a GSH1 gene, a full-length cDNA was amplified as two fragments by PCR:

GSH1\_5'-3':  
5'-GCTTCTCTCTAGATTTTCGACGG-3' (SEQ ID NO: 10)

GSH1\_3'-3':  
5'-CCTGATCATATCAGCTTCTGAGC-3' (SEQ ID NO: 11)

GSH1\_5'-2':  
5'-ATGCCAAAGGGGAGATACGA-3' (SEQ ID NO: 12)

GSH1\_3'-2':  
5'-GGAGACTCGAGCTTTCAGATAG-3' (SEQ ID NO: 13)

[0127] Then, subcloning was carried out so that each of the fragments was inserted into a pGEM-T Easy vector (Promega, Madison, Wis., USA). The primers GSH1\_5'-3 and GSH1\_3'-2 respectively includes XbaI and SacI cleavage sites required for introduction of the fragments to a binary vector pBI121 used in plant transformation.

[0128] The two fragments were fused with each other at a KpnI cleavage site, so that a vector (Ch1.GSH1-pGEM) including the full-length cDNA was constructed. The Ch1.GSH1-pGEM was treated with restriction enzymes XbaI and SacI and a fragment thus obtained was substituted with a region of a binary vector pBI121, which region encodes  $\beta$ -glucuronidase (GUS) and is located downstream of a cauliflower mosaic virus 35S promoter. As a result, a construct (35S-Ch1.GSH1-pBI121) for producing the transformed plant was produced. There is only one copy of the GSH1 gene in genome of *Arabidopsis thaliana*, and the GSH1 gene includes a chloroplast transit signal. For the purpose of accumulating GSH1 gene products ( $\gamma$ -glutamylcysteine synthetase) in cytoplasm, produced was a construct (35S-cyt.GSH1-pBI121) for expressing a protein in which the 73rd amino acid from an N-terminal, which amino acid was presumed to be the chloroplast transit signal, was deleted and an alanine residue at the 74th position from the N-terminal was substituted with a methionine residue. First, PCR was performed with the primer GSH1\_3'-3 and the following primer

GSH1(cyt.)\_5' (a base substitution site is underlined) in which the alanine residue at the 74th position from the N-terminal was substituted with the methionine residue and an XbaI cleavage site was inserted upstream of the 74th position:

GSH1 (cyt.)\_5':  
5'-AGGGCATCTAGAGACCATGGCAAGTCC-3'. (SEQ ID NO: 14)

[0129] Then, a fragment thus obtained was treated with restriction enzymes XbaI and KpnI. Thereafter, subcloning was carried out so that the fragment was inserted into a pBluescript vector (Stratagene, La Jolla, Calif. USA) (cyt. GSH-1pBS). The cyt.GSH1-pBS was treated with the restriction enzymes XbaI and KpnI, and a fragment thus obtained was substituted with a XbaI-KpnI fragment of the 35S-Ch1. GSH1-pBI121. As a result, the 35S-cyt.GSH1-pBI121 was produced.

[0130] The two types of expression vectors produced as above, i.e., the 35S-Ch1.GSH1-pBI121 and the 35S-cyt.GSH1-pBI121, were introduced into the Col-0 by the *Agrobacterium* method (Clough, S. J. and SH1-pB Bent, A. F. (1998) Floral dip: A simplified method for *Arabidopsis thaliana*. Plant J. 16: 735-743). As a result, a transformed plant was produced.

[0131] Specifically, selection of the transformed plant was repeated on an agar medium (Murashige-Skoog medium of a half concentration) which contains kanamycin serving as a selection marker, until such a generation occurred that all seeds exhibit kanamycin resistance (a generation does not exhibit divergence). In process of the selection, it was determined that characters of the kanamycin resistance were diverged at a ratio of 3:1 and that the expression vectors were introduced into at least single chromosome.

[0132] The plant obtained as above is hereinafter referred to as "35S-GSH1".

### (3) Sugar Content Determination

[0133] A 35S-GSH1 and a wild type *Arabidopsis thaliana* (Col-0) for comparison were cultivated at a growth light intensity of  $50 \mu\text{Em}^{-2}\text{s}^{-1}$  or  $500 \mu\text{Em}^{-2}\text{s}^{-1}$ . After one-week cultivation, each plant body was collected. Then, each plant body was frozen with liquid nitrogen, ground into powder, and thereafter subjected to extraction using 100  $\mu\text{l}$  of 50 mM sodium acetate buffer per 50 mg of plant body.

[0134] Next, a glucose content and a starch content of each extract thus obtained were determined. The glucose content was determined using Glucose CII-Test Wako (Wako Pure Chemical Industries, Ltd.). The starch content was determined by mixing the extract with 35 Units/ml amyloglucanase and a sodium acetate buffer (50 mM, pH4.5), leaving at rest the resulting mixture for 1 hour, and then determining an amount of glucose. Results of determination are shown in FIG. 4. FIG. 4 shows determination results of starch and glucose contents of 35S-GSH1. In FIG. 4, (a) shows starch contents, and (b) shows glucose contents. In (a) and (b) of FIG. 4, the vertical scales indicate relative contents of starch and glucose, respectively, and the horizontal scales indicate types of plants. A and B shown in FIG. 4 are results of the 35S-GSH1. In the present example, two 35S-GSH1 plants were used in an experiment as A and B shown in FIG. 4. The term "relative content" above means a relative amount where an amount in the Col-0 cultivated at a growth light intensity of  $50 \mu\text{Em}^{-2}\text{s}^{-1}$  is 100.

[0135] As shown in FIG. 4, the 35S-GSH1 had a higher starch content and a higher sugar content than the Col-0.

### Example 8

#### Production of *Prunus avium*

[0136] In the present example, *Prunus avium* was cultivated. Specifically, 4 weeks and 3 weeks before an expected date of harvesting *Prunus avium* (Napoleon) fruit, a surface of a leaf on a branch having the fruit to be harvested was coated with 0.5 mM GSSG. The fruit was harvested on the expected date.

[0137] Next, the fruit harvested was subjected to a sensory test of sugar content. As a result, it was determined that the fruit applied with GSSG increased in sugar content and decreased in acidity. Further, it was determined that the fruit applied with GSSG increased in weight. Furthermore, the fruit obtained was subjected to sugar content determination using "Pocket" Refractometer APAL-1 (ATAGO CO., LTD.). For comparison, fruit applied with no GSSG was also subjected to the sugar content determination. FIG. 5 shows a result of determination of sugar content of *Prunus avium* fruit obtained in the present example. In FIG. 5, the vertical scale indicates sugar content (Brix, unit: %). Further, an ANOVA analysis was carried out by using StatView5.0 (SAS Institute Inc.) with a significant difference level of 5%. As a result, a significant difference was shown.

[0138] As described above, application of GSSG made it possible to obtain *Prunus avium* fruit having a significantly improved sugar content.

### Example 9

#### Production of *Citrus unshiu*

[0139] In the present example, *Citrus unshiu* was cultivated. Specifically, one week before an expected date of harvesting *Citrus unshiu* fruit, a surface of a leaf on a branch having the fruit to be harvested was coated with 0.5 mM GSSG. The fruit was harvested on the expected date.

[0140] Next, the fruit harvested was subjected to a sensory test of sugar content. As a result, it was determined that the fruit applied with GSSG increased in sugar content and decreased in acidity. Further, it was determined that the fruit applied with GSSG increased in weight. Furthermore, the fruit obtained was subjected to sugar content determination using "Pocket" Refractometer APAL-1 (ATAGO CO., LTD.). For comparison, fruit applied with no GSSG was also subjected to the sugar content determination. FIG. 6 shows a result of determination of sugar content of *Citrus unshiu* fruit obtained in the present example. In FIG. 6, the vertical scale indicates sugar content (Brix, unit: %). Further, an ANOVA analysis was carried out by using StatView5.0 (SAS Institute Inc.) with a significant difference level of 5%. As a result, a significant difference was shown.

[0141] As described above, application of GSSG made it possible to obtain *Citrus unshiu* fruit having a significantly improved sugar content.

### Example 10

#### Production of *Fragaria ananassa*

[0142] In the present example, *Fragaria ananassa* was cultivated with use of GSSG or GSH. Details of cultivation are described below.

[0143] First, *Fragaria ananassa* seedlings were transplanted to a planter. In the planter, 6 L of vermiculite (ASAHI INDUSTRIES Co., LTD.), 3 L of KUREHA horticultural soil (KUREHA CORPORATION), and 3 L of vermiculite were layered as a lower, middle, and upper layers, respectively.

[0144] During cultivation of *Fragaria ananassa* plants, 50 mL of 0.2 mM or 0.5 mM GSSG or 50 mL of 0.4 mM or 0.5 mM GSH (adjusted with 0.1N NaOH to be at pH7) was applied once a week at a root per plant. The plants were grown for 63 days without being subjected to bud removal. For comparison, a *Fragaria ananassa* plant was grown under the same condition, except that GSSG and GSH were not applied. To the plants of any condition, 3 g of Kumiai phosphate ammonium nitrate potassium S-604 (Chisso Asahi Fertilizer Co., Ltd.) was applied as an additional fertilizer once in 2 weeks.

[0145] Next, the fruit harvested was subjected to sensory tests of sugar content and the like. As a result, it was determined that fruit of the plant applied with GSSG increased in sugar content and decreased in acidity compared to that of the plant not applied with GSSG or GSH. Further, it was determined that the plant applied with GSSG increased in number of fruit. It was also determined that fruit of the plant applied with GSH increased in sugar content and acidity.

[0146] Further, the fruit obtained was subjected to sugar content determination using "Pocket" Refractometer APAL-1 (ATAGO CO., LTD.). For comparison, fruit not applied with GSSG or GSH was also subjected to the sugar content determination. FIG. 7 shows a result of determination of sugar content of *Fragaria ananassa* fruit obtained in the present example. In FIG. 7, the vertical scale indicates sugar content (Brix, unit: %). Further, an ANOVA analysis was carried out by using StatView5.0 (SAS Institute Inc.) with a significant difference level of 5%. As a result, a significant difference was shown.

[0147] These results indicated that *Fragaria ananassa* fruit having an increased sugar content could be produced by cultivation using a culture medium that contains GSSG or GSH.

#### Example 11

##### Production of *Zea mays* L. var. *saccharata* Sturt

[0148] In the present example, *Zea mays* L. var. *saccharata* Sturt was cultivated. First, a *Zea mays* L. var. *saccharata* Sturt seed (TAKII & CO. Ltd., product number: Canberra 86) was sown in vermiculite (ASAHI INDUSTRIES Co., LTD.). Two weeks after sowing, a *Zea mays* L. var. *saccharata* Sturt plant was transplanted to a hydroponic culture pot described in Example 1. To the plant, 3 g of Kumiai phosphate ammonium nitrate potassium S-604 (Chisso Asahi Fertilizer Co., Ltd.) was applied as an additional fertilizer 4 weeks and 6 weeks after the sowing.

[0149] In the 5th, 6th, 7th, and 8th week after the sowing, 0.5 mM GSSG (dissolved in 0.1% Tween80 serving as a

spreading agent) was sprayed onto a leaf surface. For comparison, a *Zea mays* L. var. *saccharata* Sturt plant was cultivated by the same method as in the present example, except that Tween80, but not GSSG, was applied, and fruit thereof was harvested.

[0150] Fruit was harvested 86 days after the sowing and subjected to a sensory test of sugar content. As a result, it was determined that fruit of the plant applied with GSSG increased in sugar content compared to that of the plant applied with no GSSG. Further, the fruit obtained was subjected to sugar content determination using "Pocket" Refractometer APAL-1 (ATAGO CO., LTD.). For comparison, the fruit of the plant applied with no GSSG was also subjected to the sugar content determination. FIG. 8 shows a result of determination of sugar content of *Zea mays* L. var. *saccharata* Sturt fruit obtained in the present example. In FIG. 8, the vertical scale indicates sugar content (Brix, unit: %). Further, an ANOVA analysis was carried out by using StatView5.0 (SAS Institute Inc.) with a significant difference level of 5%. As a result, a significant difference was shown.

[0151] It was also determined that the plant applied with GSSG increased in size and number of fruit. Further, it was determined that the fruit of the plant applied with GSSG was already able to be harvested 70 days after the sowing.

[0152] The results above indicated that *Zea mays* L. var. *saccharata* Sturt fruit having an increased sugar content could be produced by cultivation using a culture medium that includes GSSG.

[0153] The composition, in accordance with the present invention, for producing a plant body having an improved sugar content includes a substance for regulating an oxidation-reduction state of a cell. Therefore, with the composition in accordance with the present invention, it is possible to easily produce the plant body having an improved sugar content.

[0154] The embodiments and concrete examples of implementation discussed in the foregoing detailed explanation serve solely to illustrate the technical details of the present invention, which should not be narrowly interpreted within the limits of such embodiments and concrete examples, but rather may be applied in many variations within the spirit of the present invention, provided such variations do not exceed the scope of the patent claims set forth below.

#### INDUSTRIAL APPLICABILITY

[0155] The composition in accordance with the present invention, with which a plant having an improved sugar content can be easily produced, is industrially applicable in agriculture, food industry, and the like. Further, because ethanol can be produced with high efficiency from a plant having a high sugar content, the composition in accordance with the present invention is applicable to a wide range of industries such as energy industry.

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 35          40          45
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 50          55          60
Ser Lys Arg Gly His Gln Leu Ile Val Ala Ala Ser Pro Pro Thr Glu
 65          70          75          80
Glu Ala Val Val Ala Thr Glu Pro Leu Thr Arg Glu Asp Leu Ile Ala
 85          90          95
Tyr Leu Ala Ser Gly Cys Lys Thr Lys Asp Lys Tyr Arg Ile Gly Thr
 100         105         110
Glu His Glu Lys Phe Gly Phe Glu Val Asn Thr Leu Arg Pro Met Lys
 115         120         125
Tyr Asp Gln Ile Ala Glu Leu Leu Asn Gly Ile Ala Glu Arg Phe Glu
 130         135         140
Trp Glu Lys Val Met Glu Gly Asp Lys Ile Ile Gly Leu Lys Gln Gly
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Ala Pro Leu Glu Thr Leu His Gln Thr Cys Ala Glu Val Asn Ser His
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Leu Tyr Gln Val Lys Ala Val Ala Glu Glu Met Gly Ile Gly Phe Leu
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Gly Ile Gly Phe Gln Pro Lys Trp Arg Arg Glu Asp Ile Pro Ile Met
 210         215         220
Pro Lys Gly Arg Tyr Asp Ile Met Arg Asn Tyr Met Pro Lys Val Gly
 225         230         235         240
Thr Leu Gly Leu Asp Met Met Leu Arg Thr Cys Thr Val Gln Val Asn
 245         250         255
Leu Asp Phe Ser Ser Glu Ala Asp Met Ile Arg Lys Phe Arg Ala Gly
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Leu Ala Leu Gln Pro Ile Ala Thr Ala Leu Phe Ala Asn Ser Pro Phe
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195          200          205

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&lt;210&gt; SEQ ID NO 6

&lt;211&gt; LENGTH: 398

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 6

Met Ala Ser Thr Ser Leu Leu Lys Ala Ser Pro Val Leu Asp Lys Ser  
 1 5 10 15

Glu Trp Val Lys Gly Gln Ser Val Leu Phe Arg Gln Pro Ser Ser Ala  
 20 25 30

Ser Val Val Leu Arg Asn Arg Ala Thr Ser Leu Thr Val Arg Ala Ala  
 35 40 45

Ser Ser Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Ile Ala Ser  
 50 55 60

Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys Gly  
 65 70 75 80

Lys Arg Leu Asp Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn Arg Gln  
 85 90 95

Ala Phe Arg Thr Leu Leu Val Ser Ala Pro Gly Leu Gly Gln Tyr Val  
 100 105 110

Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Thr Glu  
 115 120 125

Gly Lys Lys Met Val Asp Val Leu Val Glu Gln Asn Ile Val Pro Gly  
 130 135 140

Ile Lys Val Asp Lys Gly Leu Val Pro Leu Val Gly Ser Asn Asn Glu  
 145 150 155 160

Ser Trp Cys Gln Gly Leu Asp Gly Leu Ser Ser Arg Thr Ala Ala Tyr  
 165 170 175

Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser Ile  
 180 185 190

Pro Asn Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp Gly Leu  
 195 200 205

Ala Arg Tyr Ala Ala Ile Ser Gln Asp Ser Gly Leu Val Pro Ile Val  
 210 215 220

Glu Pro Glu Ile Leu Leu Asp Gly Glu His Asp Ile Asp Arg Thr Tyr  
 225 230 235 240

Asp Val Ala Glu Lys Val Trp Ala Glu Val Phe Phe Tyr Leu Ala Gln  
 245 250 255

Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val Thr  
 260 265 270

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Pro Gly Ala Glu Ser Lys Asp Arg Ala Thr Pro Glu Gln Val Ala Ala  
 275 280 285

Tyr Thr Leu Lys Leu Leu Arg Asn Arg Val Pro Pro Ala Val Pro Gly  
 290 295 300

Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu Asn  
 305 310 315 320

Leu Asn Ala Met Asn Gln Ala Pro Asn Pro Trp His Val Ser Phe Ser  
 325 330 335

Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Gly Gly Arg  
 340 345 350

Pro Glu Asn Val Asn Ala Ala Gln Thr Thr Leu Leu Ala Arg Ala Lys  
 355 360 365

Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Gly Glu Gly Glu Ser  
 370 375 380

Glu Glu Ala Lys Glu Gly Met Phe Val Lys Gly Tyr Thr Tyr  
 385 390 395

&lt;210&gt; SEQ ID NO 7

&lt;211&gt; LENGTH: 1176

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 7

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atggcgtctg ctagcttctg taagcctaac accctctctt ctccatggat cggccaacgc      60
tcctttgtgc acacctctgc ttcttcttct cctcctcctc gagtctcctt cgegatccgc      120
gccggtgctt actccgacga gcttggttaa accgcaaaa gcattgcatc cctggggaga      180
ggtatcttgg cgatcgatga gtccaatgca acctgtggga agaggcttgc ttctatcggc      240
ttggataaca ccgaggacaa ccgtcaggcc tacaggcaac ttctgcttac cactcctggc      300
ctggcgatt acatctctgg ttccattctc ttcgaggaga ctctttacca gtccaccaag      360
gacggtaaga cttttgtcga ttgcttgcgc gatgccaaca tcgtccctgg catcaaagtt      420
gacaagggct tgtctccctc agccggttcc aacgaagagt cttggtgcca aggcttggat      480
ggattggcct cacgctctgc tgagtactac aagcaaggcg ctcgttttgc caagtggagg      540
acagtgggta gtgttccctg cggtccttca gcaactggctg tgaaggaagc tgcgtggggg      600
ctggctcgct atgcagccat ctctcaggat aatggtcttg tccccattgt ggagccagag      660
atccttctgg acggggacca cccaatagag aggactctgg aggtggcaga gaaagtgtgg      720
tcagaggtgt tcttctactt ggcacagAAC aacgtcatgt ttgagggcat tctgttgaag      780
ccgagcatgg tcaccccagg cgctgagcac aagaacaagg cctctcccga gaccgttgca      840
gatttcacgc tcaccatgct gaaaaggagg gttcctccgg ctgtcccagg gatcatgttt      900
ctgtcaggag gacaatcaga ggcagaggcc acaactgaacc tgaacgccat gaaccagagc      960
ccaaacccat ggcattgtgc cttctcatac gcacgtgccc tgcagaactc cgtgctcaga     1020
acatggcaag gcaagccgga gaagattgag gctcgcaga aggcactggt ggtgagggca     1080
aaggccaact cactggccca gctcggcaaa tactcagccg agggagagaa cgaggatgcc     1140
aagaaaggaa tgtttgcTca gggttacacc tactga                                  1176

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&lt;210&gt; SEQ ID NO 8

&lt;211&gt; LENGTH: 1515

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
        Synthesized Primer Sequence

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<400> SEQUENCE: 8

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ccaaagtaga cgactactaa tagtagtaaa caaaaccttt ggctttaaca ctctcctcca      60
aatcccagat ctctctctgt ctctgtcccg eggagtcgcc gagagattga tcaccatcac      120
ttttgtacct tccttgact acctatggcg tctgctagct tcgttaagcc taacaccctc      180
tcttctccat ggatcggcca acgctccttt gctcacacct ctgcttcttc ttctcctcct      240
cctcgagtct ccttcgcat ccgcgcgggt gcttactccg acgagcttgt taaaaccgcc      300
aaaagcattg catcccctgg gagaggtatc ttggcgatcg atgagtccaa tgcaacctgt      360
gggaagaggc ttgcttctat cgcttgatg aacaccgagg acaaccgtca ggctacaggg      420
caacttctgc ttaccactcc tggcctcggc gattacatct ctggttccat tctcttcgag      480
gagactcttt accagtccac caaggacggg aagaccttg tcgattgctt gcgcgatgcc      540
aacatcgtcc ctggcatcaa agttgacaag ggcttgtctc ccctagccgg ttccaacgaa      600
gagtcctggg gccaaaggct ggatggattg gcctcacgct ctgctgagta ctacaagcaa      660
ggcgcctggt ttgccaaagt gaggacagtg gtgagtgttc cctgcgggtc ttcagcactg      720
gctgtgaagg aagctgcgtg ggggctggct cgctatgcag ccatctctca ggataatggt      780
cttgtcccca ttgtggagcc agagatcctt ctggacgggg accaccaat agagaggact      840
ctggaggtgg cagagaaagt gtggtcagag gtgttcttct acttggcaca gaacaacgtc      900
atgtttgagg gcattctggt gaagccgagc atggtcaccc caggcgtga gcacaagaac      960
aaggcctctc ccgagaccgt tgcagatttc acgctcacca tgcctgaaaag gagggttcct     1020
ccggctgtcc cagggatcat gtttctgtca ggaggacaat cagaggcaga ggccacactg     1080
aacctgaacg ccatgaacca gagcccaaac ccatggcatg tgccttctc atacgcacgt     1140
gcctgcaga actccgtgct cagaacatgg caaggcaagc cggagaagat tgaggcctcg     1200
cagaaggcac tgttggtgag ggcaaaggcc aactcactgg ccagctcgg caaataactca     1260
gccgagggag agaacgagga tgccaagaaa ggaatgttg tcaagggtta cacctactga     1320
tttgtaatt tcagagatcg taataaggat taaggacat tgttgtcttt tgtttttttt     1380
tcctttttt gttttgtctc tgagaaagaa agacagtcac gagtcacgat catatcatat     1440
atgtatgtga gcaacgtgaa aacatcctct taaatctata tttcctctca gaaagactga     1500
ttactgttg actgc      1515

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<210> SEQ ID NO 9
<211> LENGTH: 1518
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 9

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aaaagagggg ggagtgagag ataaggggtg tgcataagc gtttactgtg agtctctcaa      60
agaaacccaaa ggcagagaaa agagataaca cacacaaaaa aaaatggcat caacctcact     120
cctcaaggct tctccggtgt tggacaatc cgaatgggtc aagggacaaa gcgttctctt     180
cgcgcagcct tcttcgctt ctgtcgtcct ccgcaaccgt gccacctccc tcaccgtccg     240

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tgccgcttcc tccctacgccg atgagcttgt taagacagcg aaaactattg cgtctcccgg	300
acgtggaatc ttggcgatgg acgagtcaaa cgcgacttgc gggaaacgtt tggattcgat	360
agggctagag aacctgagg caaatcgta agctttccgg actttgctgg tctctgcacc	420
gggactcgga cagtacgtct ccggcgcaat tctatttgag gagactctgt accagtctac	480
caccgaaggc aagaaaatgg tcgacgtcct cgtcgagcag aacattgtcc ctggatcaa	540
agtcgacaag ggtttggtgc cacttggttg atccaacaat gagtcaggt gccaaaggact	600
agatggctta tcctctcgaa ctgctgctta ctatcaacag ggtgocggt tcgccaatg	660
gcgtactgtc gtgagcattc ctaacggtcc gtctgccctc gccgtcaaag aagctgcttg	720
gggtcttctc cgataccgtc ccatttcaca ggacagcggg ttggttccga ttggtgagcc	780
agagatcttg ttggatggag aacacgacat tgacagaaca tacgacgtag cagagaaggt	840
ttgggctgag gttttctttt accttgctca gaacaatgtc atgtttgaag gtatcctcct	900
aaaaccgagc atgggtgactc ccggagctga gtctaaagac agagctactc ctgaacaagt	960
tgccgcctac acctcaagc tctccgcaa cagagtcctc cccgcagtcc ccggaatcat	1020
gtttttgtcc ggaggacagt cggagggtga ggcaacactc aacttgaacg caatgaacca	1080
ggcaccaaaac ccattggcacg tgtccttctc ctacgcacgt gcgttgacaga acacttctct	1140
gaaaacatgg ggcggcagac ccgagaacgt gaacgcagct cagaccactc tcttgccccg	1200
tgccaaggcc aattcgttgg ctacagctcg aaaatacacc ggtgagggtg agtccgaaga	1260
ggctaaggag ggcattgttc tcaaagggtg cacctattga agagatgatg ctgtgaaaaa	1320
agagatgaag cagatgtttt aatcacattt gtttttgagt ttgcttgta ttaatcatgt	1380
caaatcatta tttctctgc ttactttgct ttagctactc cttttaataa gttctattat	1440
attgaagtta tctatctctc ttgatctatt taaacttgaa actacaacta ttccataatc	1500
aaccaatttt aaattttg	1518

<210> SEQ ID NO 10  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 10

gctttcttct agatttcgac gg	22
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<210> SEQ ID NO 11  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 11

cctgatcata tcagcttctg agc	23
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<210> SEQ ID NO 12  
 <211> LENGTH: 20  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 12  
atgccaaagg ggagatacga 20

<210> SEQ ID NO 13  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 13  
ggagactcga gctcttcaga tag 23

<210> SEQ ID NO 14  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 14  
agggcatcta gagacatgg caagtcc 27

<210> SEQ ID NO 15  
<211> LENGTH: 351  
<212> TYPE: PRT  
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 15

Ala Gly Ala Tyr Ser Asp Glu Leu Val Lys Thr Ala Lys Ser Ile Ala  
1 5 10 15

Ser Pro Gly Arg Gly Ile Leu Ala Ile Asp Glu Ser Asn Ala Thr Cys  
20 25 30

Gly Lys Arg Leu Ala Ser Ile Gly Leu Asp Asn Thr Glu Asp Asn Arg  
35 40 45

Gln Ala Tyr Arg Gln Leu Leu Leu Thr Thr Pro Gly Leu Gly Asp Tyr  
50 55 60

Ile Ser Gly Ser Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Lys  
65 70 75 80

Asp Gly Lys Thr Phe Val Asp Cys Leu Arg Asp Ala Asn Ile Val Pro  
85 90 95

Gly Ile Lys Val Asp Lys Gly Leu Ser Pro Leu Ala Gly Ser Asn Glu  
100 105 110

Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Glu  
115 120 125

Tyr Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser  
130 135 140

Val Pro Cys Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp Gly  
145 150 155 160

Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile  
165 170 175

Val Glu Pro Glu Ile Leu Leu Asp Gly Asp His Pro Ile Glu Arg Thr  
180 185 190

Leu Glu Val Ala Glu Lys Val Trp Ser Glu Val Phe Phe Tyr Leu Ala  
195 200 205

Gln Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val

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210	215	220
Thr Pro Gly Ala Glu His Lys Asn Lys Ala Ser Pro Glu Thr Val Ala		
225	230	235 240
Asp Phe Thr Leu Thr Met Leu Lys Arg Arg Val Pro Pro Ala Val Pro		
	245	250 255
Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Ala Glu Ala Thr Leu		
	260	265 270
Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe		
	275	280 285
Ser Tyr Ala Arg Ala Leu Gln Asn Ser Val Leu Arg Thr Trp Gln Gly		
	290	295 300
Lys Pro Glu Lys Ile Glu Ala Ser Gln Lys Ala Leu Leu Val Arg Ala		
305	310	315 320
Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Ser Ala Glu Gly Glu		
	325	330 335
Asn Glu Asp Ala Lys Lys Gly Met Phe Val Lys Gly Tyr Thr Tyr		
	340	345 350

&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 352

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 16

Ala Ala Ser Ala Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Ile		
1	5	10 15
Ala Ser Pro Gly His Gly Ile Met Ala Met Asp Glu Ser Asn Ala Thr		
	20	25 30
Cys Gly Lys Arg Leu Ala Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn		
	35	40 45
Arg Gln Ala Tyr Arg Thr Leu Leu Val Ser Ala Pro Gly Leu Gly Gln		
	50	55 60
Tyr Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr		
	65	70 75 80
Thr Asp Gly Lys Lys Met Val Asp Val Leu Val Glu Gln Asn Ile Val		
	85	90 95
Pro Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Val Gly Ser Tyr		
	100	105 110
Asp Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Thr Ala		
	115	120 125
Ala Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val		
	130	135 140
Ser Ile Pro Asn Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp		
	145	150 155 160
Gly Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Ser Gly Leu Val Pro		
	165	170 175
Ile Val Glu Pro Glu Ile Met Leu Asp Gly Glu His Gly Ile Asp Arg		
	180	185 190
Thr Tyr Asp Val Ala Glu Lys Val Trp Ala Glu Val Phe Phe Tyr Leu		
	195	200 205
Ala Gln Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met		
	210	215 220

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Val Thr Pro Gly Ala Glu Ala Thr Asp Arg Ala Thr Pro Glu Gln Val
225                230                235                240

Ala Ser Tyr Thr Leu Lys Leu Leu Arg Asn Arg Ile Pro Pro Ala Val
                245                250                255

Pro Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Leu Glu Ala Thr
                260                265                270

Leu Asn Leu Asn Ala Met Asn Gln Ala Pro Asn Pro Trp His Val Ser
                275                280                285

Phe Ser Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Gly
                290                295                300

Gly Lys Glu Glu Asn Val Lys Ala Ala Gln Asp Ile Leu Leu Ala Arg
305                310                315                320

Ala Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Gly Glu Gly
                325                330                335

Glu Ser Glu Glu Ala Lys Glu Gly Met Phe Val Lys Gly Tyr Thr Tyr
                340                345                350

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&lt;210&gt; SEQ ID NO 17

&lt;211&gt; LENGTH: 352

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 17

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Ala Ala Ser Ser Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Ile
1                5                10                15

Ala Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr
                20                25                30

Cys Gly Lys Arg Leu Asp Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn
                35                40                45

Arg Gln Ala Phe Arg Thr Leu Leu Val Ser Ala Pro Gly Leu Gly Gln
50                55                60

Tyr Val Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr
65                70                75                80

Thr Glu Gly Lys Lys Met Val Asp Val Leu Val Glu Gln Asn Ile Val
                85                90                95

Pro Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Val Gly Ser Asn
                100                105                110

Asn Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ser Ser Arg Thr Ala
                115                120                125

Ala Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val
130                135                140

Ser Ile Pro Asn Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp
145                150                155                160

Gly Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Ser Gly Leu Val Pro
                165                170                175

Ile Val Glu Pro Glu Ile Leu Leu Asp Gly Glu His Asp Ile Asp Arg
                180                185                190

Thr Tyr Asp Val Ala Glu Lys Val Trp Ala Glu Val Phe Phe Tyr Leu
195                200                205

Ala Gln Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met
210                215                220

Val Thr Pro Gly Ala Glu Ser Lys Asp Arg Ala Thr Pro Glu Gln Val
225                230                235                240

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Ala Ala Tyr Thr Leu Lys Leu Leu Arg Asn Arg Val Pro Pro Ala Val  
245 250 255

Pro Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr  
260 265 270

Leu Asn Leu Asn Ala Met Asn Gln Ala Pro Asn Pro Trp His Val Ser  
275 280 285

Phe Ser Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Gly  
290 295 300

Gly Arg Pro Glu Asn Val Asn Ala Ala Gln Thr Thr Leu Leu Ala Arg  
305 310 315 320

Ala Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Gly Glu Gly  
325 330 335

Glu Ser Glu Glu Ala Lys Glu Gly Met Phe Val Lys Gly Tyr Thr Tyr  
340 345 350

&lt;210&gt; SEQ ID NO 18

&lt;211&gt; LENGTH: 353

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Hordeum Vulgare

&lt;400&gt; SEQUENCE: 18

Ala Ser Gly Gly Ser Tyr Ala Asp Glu Leu Val Ser Thr Ala Lys Thr  
1 5 10 15

Val Ala Ser Pro Gly Arg Gly Ile Leu Ala Ile Asp Glu Ser Ser Ala  
20 25 30

Thr Cys Gly Lys Arg Leu Ala Ser Ile Gly Leu Asp Asn Thr Glu Val  
35 40 45

Asn Arg Gln Ala Tyr Arg Gln Leu Leu Leu Thr Thr Ala Gly Leu Gly  
50 55 60

Glu Tyr Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser  
65 70 75 80

Thr Thr Asp Gly Lys Thr Phe Val Asp Val Leu Lys Asp Gln Asn Ile  
85 90 95

Met Pro Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Pro Gly Ser  
100 105 110

Asn Asn Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Cys  
115 120 125

Ala Glu Tyr Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val  
130 135 140

Val Ser Ile Pro Cys Gly Pro Thr Ala Leu Ala Val Lys Glu Ala Ala  
145 150 155 160

Trp Gly Leu Ala Arg Tyr Ala Ala Ile Ala Gln Asp Asn Gly Leu Val  
165 170 175

Pro Ile Val Glu Pro Glu Ile Leu Leu Asp Gly Asp His Gly Ile Glu  
180 185 190

Arg Thr Leu Glu Val Ala Glu Lys Val Trp Ser Glu Val Phe Phe Tyr  
195 200 205

Leu Ala Glu Asn Asn Val Leu Phe Glu Gly Ile Leu Leu Lys Pro Ser  
210 215 220

Met Val Thr Pro Gly Ala Glu His Lys Glu Lys Ala Ser Pro Glu Ala  
225 230 235 240

Ile Ala Lys Asn Thr Leu Thr Met Leu Arg Arg Arg Val Pro Pro Ala





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<210> SEQ ID NO 20
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 20

Ala Gly Ala Tyr Asp Asp Glu Leu Val Lys Thr Ala Lys Thr Ile Ala
1          5          10          15
Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys
          20          25          30
Gly Lys Arg Leu Asp Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn Arg
          35          40          45
Gln Ala Phe Arg Thr Leu Leu Val Ser Val Pro Gly Leu Gly Asn His
          50          55          60
Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Val
65          70          75          80
Asp Gly Lys Lys Ile Val Asp Ile Leu Ala Glu Gln Gly Ile Val Pro
          85          90          95
Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Thr Gly Ser Asn Asp
          100         105         110
Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Glu Ala Ala
          115         120         125
Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser
          130         135         140
Ile Pro Asn Gly Pro Ser Glu Leu Ala Val Lys Glu Ala Ala Trp Gly
145         150         155         160
Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile
          165         170         175
Val Glu Pro Glu Ile Leu Leu Asp Gly Glu His Gly Ile Gly Arg Thr
          180         185         190
Phe Glu Val Ala Gln Lys Val Trp Ala Glu Thr Phe Tyr Gln Met Ser
          195         200         205
Gln Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val
          210         215         220
Thr Pro Gly Ala Glu Cys Lys Asp Arg Ala Thr Pro Glu Gln Val Ala
225         230         235         240
Gly Tyr Thr Leu Lys Leu Leu Ser Arg Arg Val Pro Pro Ala Val Pro
          245         250         255
Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu
          260         265         270
Asn Leu Asn Ala Met Asn Gln Gly Pro Asn Pro Trp His Val Ser Phe
          275         280         285
Ser Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Gly Gly
          290         295         300
Arg Pro Glu Asn Val Lys Ala Ala Gln Glu Ala Leu Leu Leu Arg Ala
305         310         315         320
Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Ser Asp Gly Glu
          325         330         335
Ala Ala Glu Ala Lys Glu Gly Met Phe Val Lys Asn Tyr Ser Tyr
          340         345         350

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<210> SEQ ID NO 21
<211> LENGTH: 352
<212> TYPE: PRT
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 21
Ala Ala Gly Ser Tyr Thr Asp Glu Leu Ile Lys Thr Ala Lys Thr Ile
1          5          10          15
Ala Ser Pro Gly Arg Gly Ile Leu Ala Ile Asp Glu Ser Asn Ala Thr
20          25          30
Ala Gly Lys Arg Leu Ala Ser Ile Gly Leu Asp Asn Thr Glu Ala Asn
35          40          45
Arg Gln Ala Tyr Arg Gln Leu Leu Thr Thr Pro Gly Leu Gly Asp
50          55          60
Tyr Ile Ser Gly Ser Ile Leu Phe Glu Glu Thr Leu Phe Gln Ser Thr
65          70          75          80
Thr Asp Gly Lys Lys Phe Val Asp Val Leu Arg Asp Gln Lys Ile Val
85          90          95
Pro Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Pro Gly Ser Asn
100         105         110
Asn Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala
115         120         125
Glu Tyr Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val
130         135         140
Ser Ile Pro Cys Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp
145         150         155         160
Gly Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro
165         170         175
Ile Val Glu Pro Glu Ile Leu Leu Asp Gly Asp His Pro Ile Glu Arg
180         185         190
Thr Leu Glu Val Ala Glu Arg Val Trp Ala Glu Val Phe Tyr Tyr Leu
195         200         205
Ala Glu Asn Asn Val Val Phe Glu Gly Ile Leu Leu Lys Pro Ser Met
210         215         220
Val Thr Pro Gly Ala Glu His Lys Glu Lys Ala Thr Pro Glu Thr Ile
225         230         235         240
Ala Lys Tyr Thr Leu Thr Met Leu Arg Arg Arg Val Pro Pro Ala Val
245         250         255
Pro Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr
260         265         270
Leu Asn Leu His Glu Met Asn Gln Ser Pro Asn Pro Trp His Val Ser
275         280         285
Phe Ser Tyr Ala Arg Ala Leu Gln Asn Thr Val Leu Lys Thr Trp Gln
290         295         300
Gly Arg Pro Glu Asn Val Asp Ala Ala Gln Arg Ala Leu Leu Ile Arg
305         310         315         320
Ala Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Ser Ala Glu Gly
325         330         335
Glu Ser Glu Glu Ala Lys Lys Gly Met Phe Val Lys Gly Tyr Thr Tyr
340         345         350

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<210> SEQ ID NO 22
<211> LENGTH: 351

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<212> TYPE: PRT
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 22

Ala Ser Ser Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Ile Ala
1          5          10          15
Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys
20          25          30
Gly Lys Arg Leu Ala Ser Ile Gly Met Glu Asn Thr Glu Ala Asn Arg
35          40          45
Gln Ala Phe Arg Thr Leu Leu Val Ser Val Pro Gly Leu Gly Glu Tyr
50          55          60
Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Val
65          70          75          80
Glu Gly Lys Lys Met Val Asp Val Leu Val Glu Gln Asn Ile Val Pro
85          90          95
Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Ala Gly Ser Asn Asn
100         105         110
Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Ala
115         120         125
Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser
130         135         140
Ile Pro Asn Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp Gly
145         150         155         160
Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile
165         170         175
Val Glu Pro Glu Ile Leu Leu Asp Gly Glu His Asn Ile Asp Arg Thr
180         185         190
Phe Glu Val Ala Lys Gln Val Trp Ala Glu Val Phe Phe Tyr Leu Ala
195         200         205
Gln Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val
210         215         220
Thr Pro Gly Ala Glu Cys Lys Asp Arg Ala Thr Pro Gln Gln Val Ala
225         230         235         240
Asp Tyr Thr Leu Ser Leu Leu Arg Gln Arg Ile Pro Pro Ala Val Pro
245         250         255
Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu
260         265         270
Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe
275         280         285
Ser Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Ser Gly
290         295         300
Arg Pro Glu Asn Val Lys Ala Ala Gln Asp Ala Leu Leu Val Arg Ala
305         310         315         320
Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Gly Glu Gly Glu
325         330         335
Ser Asp Glu Ala Lys Lys Gly Met Phe Val Lys Gly Tyr Val Tyr
340         345         350

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<210> SEQ ID NO 23
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Lycopersicon esculentum

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-continued

&lt;400&gt; SEQUENCE: 23

Ala Ser Ser Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Val Ala  
 1 5 10 15  
 Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys  
 20 25 30  
 Gly Lys Arg Leu Asp Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn Arg  
 35 40 45  
 Gln Ala Tyr Arg Thr Leu Leu Val Ser Ala Pro Gly Leu Gly Asn Tyr  
 50 55 60  
 Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Val  
 65 70 75 80  
 Asp Gly Lys Lys Ile Val Asp Val Leu Leu Glu Gln Asn Ile Val Pro  
 85 90 95  
 Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Ala Gly Ser Asn Asn  
 100 105 110  
 Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Ala  
 115 120 125  
 Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser  
 130 135 140  
 Ile Pro Asn Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp Gly  
 145 150 155 160  
 Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile  
 165 170 175  
 Val Glu Pro Glu Ile Leu Leu Asp Gly Glu His Asn Ile Asp Arg Thr  
 180 185 190  
 Phe Glu Val Ala Gln Gln Val Trp Ala Glu Val Phe Phe Tyr Leu Ala  
 195 200 205  
 Glu Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val  
 210 215 220  
 Thr Pro Gly Ala Glu Cys Lys Glu Arg Ala Thr Pro Glu Gln Val Ala  
 225 230 235 240  
 Asp Tyr Thr Leu Lys Leu Leu Gln Arg Arg Ile Pro Pro Ala Val Pro  
 245 250 255  
 Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu  
 260 265 270  
 Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe  
 275 280 285  
 Ser Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Gly Gly  
 290 295 300  
 Arg Pro Glu Asn Val Glu Ala Ala Gln Lys Ala Leu Leu Thr Arg Ala  
 305 310 315 320  
 Ser Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Gly Glu Gly Glu  
 325 330 335  
 Ser Glu Glu Ala Lys Glu Gly Met Phe Val Lys Gly Tyr Val Tyr  
 340 345 350

&lt;210&gt; SEQ ID NO 24

&lt;211&gt; LENGTH: 339

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Lotus japonicus

&lt;400&gt; SEQUENCE: 24

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Lys Thr Ile Ala Ser Pro Gly Arg Gly Ile Leu Ala Ile Asp Glu Ser  
 1 5 10 15  
 Asn Ala Thr Ala Gly Lys Arg Leu Ala Ser Ile Gly Leu Asp Asn Thr  
 20 25 30  
 Glu Thr Asn Arg Gln Ala Tyr Arg Gln Leu Leu Thr Thr Pro Gly  
 35 40 45  
 Leu Gly Glu Tyr Ile Ser Gly Ala Ile Phe Phe Glu Glu Thr Leu Tyr  
 50 55 60  
 Gln Ser Thr Thr Asp Gly Lys Lys Phe Val Asp Cys Leu Arg Glu Glu  
 65 70 75 80  
 Asn Ile Val Pro Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Pro  
 85 90 95  
 Gly Ser Asn Asn Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser  
 100 105 110  
 Arg Ser Ala Glu Tyr Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg  
 115 120 125  
 Thr Val Val Ser Ile Pro Cys Gly Pro Ser Ala Leu Ala Val Lys Glu  
 130 135 140  
 Ala Ala Trp Gly Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly  
 145 150 155 160  
 Leu Val Pro Ile Val Glu Pro Glu Ile Leu Leu Asp Gly Asp His Pro  
 165 170 175  
 Ile Glu Arg Thr Leu Glu Val Ala Glu Lys Val Trp Ser Glu Val Phe  
 180 185 190  
 Phe Tyr Leu Ala Glu Asn Asn Val Val Phe Glu Gly Ile Leu Leu Lys  
 195 200 205  
 Pro Ser Met Val Thr Pro Gly Ala Glu His Lys Gln Lys Ala Ser Pro  
 210 215 220  
 Glu Thr Ile Ala Asn Asn Thr Leu Thr Met Leu Arg Arg Arg Val Pro  
 225 230 235 240  
 Pro Ala Val Pro Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val  
 245 250 255  
 Glu Ala Thr Leu Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp  
 260 265 270  
 His Val Ser Phe Ser Tyr Ala Arg Ala Leu Gln Asn Thr Val Leu Lys  
 275 280 285  
 Thr Trp Gln Gly Arg Pro Glu Asn Val Glu Ala Ala Gln Lys Ser Leu  
 290 295 300  
 Leu Ile Arg Ala Lys Ala Asn Ser Leu Ala Gln Leu Gly Arg Tyr Ser  
 305 310 315 320  
 Ala Glu Gly Glu Ser Glu Glu Ala Gln Lys Gly Met Phe Val Lys Gly  
 325 330 335  
 Tyr Thr Tyr

&lt;210&gt; SEQ ID NO 25

&lt;211&gt; LENGTH: 351

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Lotus japonicus

&lt;400&gt; SEQUENCE: 25

Ala Gly Ser Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Val Ala  
 1 5 10 15

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Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys  
           20                          25                          30  
 Gly Lys Arg Leu Ala Ser Ile Gly Leu Glu Asn Thr Glu Val Asn Arg  
           35                          40                          45  
 Gln Ala Tyr Arg Thr Leu Leu Val Ser Ala Pro Gly Leu Gly Gln Tyr  
           50                          55                          60  
 Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Thr  
           65                          70                          75                          80  
 Asp Gly Arg Lys Ile Val Asp Val Leu Ile Glu Gln Asn Ile Val Pro  
           85                          90                          95  
 Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Ala Gly Ser Asn Asp  
           100                         105                         110  
 Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Ala  
           115                         120                         125  
 Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser  
           130                         135                         140  
 Ile Pro Asn Gly Pro Thr Ala Leu Ala Val Lys Glu Ala Ala Trp Gly  
           145                         150                         155                         160  
 Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile  
           165                         170                         175  
 Val Glu Pro Glu Ile Leu Leu Asp Gly Glu His Asp Ile Glu Arg Thr  
           180                         185                         190  
 Phe Glu Val Ala Gln Lys Val Trp Ala Glu Val Phe Phe Tyr Leu Ala  
           195                         200                         205  
 Glu Asn Asn Val Leu Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val  
           210                         215                         220  
 Thr Pro Gly Ala Glu Ser Lys Asp Lys Val Ser Pro Gln Thr Val Ser  
           225                         230                         235                         240  
 Asp Tyr Thr Leu Lys Leu Leu Lys Arg Arg Ile Pro Pro Ala Val Pro  
           245                         250                         255  
 Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu  
           260                         265                         270  
 Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe  
           275                         280                         285  
 Ser Phe Ala Arg Ala Leu Gln Asn Thr Ala Leu Lys Thr Trp Gly Gly  
           290                         295                         300  
 Arg Ala Glu Asn Val Lys Ala Ala Gln Asp Ala Leu Leu Phe Arg Ala  
           305                         310                         315                         320  
 Lys Ser Asn Ser Leu Ala Gln Leu Gly Lys Tyr Asn Gly Asp Gly Glu  
           325                         330                         335  
 Ser Glu Glu Ala Lys Lys Glu Leu Phe Val Lys Gly Tyr Ser Tyr  
           340                         345                         350

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 351

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Lotus japonicus

&lt;400&gt; SEQUENCE: 26

Ala Gly Ser Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Val Ala  
 1                          5                          10                          15

Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys

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20					25					30					
Gly	Lys	Arg	Leu	Ala	Ser	Ile	Gly	Leu	Glu	Asn	Thr	Glu	Val	Asn	Arg
		35					40					45			
Gln	Ala	Trp	Arg	Thr	Leu	Leu	Val	Thr	Ala	Pro	Gly	Leu	Gly	Gln	Tyr
	50					55					60				
Val	Ser	Gly	Ala	Ile	Leu	Phe	Glu	Glu	Thr	Leu	Tyr	Gln	Ser	Thr	Thr
65					70					75					80
Asp	Gly	Arg	Lys	Ile	Val	Asp	Val	Leu	Ile	Glu	Gln	Asn	Ile	Val	Pro
				85					90					95	
Gly	Ile	Lys	Val	Asp	Lys	Gly	Leu	Val	Pro	Leu	Ala	Gly	Ser	Asn	Asp
			100					105						110	
Glu	Ser	Trp	Cys	Gln	Gly	Leu	Asp	Gly	Leu	Ala	Ser	Arg	Thr	Ala	Ala
		115					120					125			
Tyr	Tyr	Gln	Gln	Gly	Ala	Arg	Phe	Ala	Lys	Trp	Arg	Thr	Val	Val	Ser
	130					135					140				
Ile	Pro	Asn	Gly	Pro	Thr	Ala	Leu	Ala	Val	Lys	Glu	Ala	Ala	Trp	Gly
145					150					155					160
Leu	Ala	Arg	Tyr	Ala	Ala	Ile	Ala	Gln	Asp	Asn	Gly	Leu	Val	Pro	Ile
				165					170						175
Val	Glu	Pro	Glu	Ile	Leu	Leu	Asp	Gly	Glu	His	Gly	Ile	Glu	Arg	Thr
			180					185					190		
Phe	Glu	Val	Ala	Gln	Lys	Val	Trp	Ala	Glu	Val	Phe	Phe	Tyr	Leu	Ala
		195					200					205			
Glu	Asn	Asn	Val	Leu	Phe	Glu	Gly	Ile	Leu	Leu	Lys	Pro	Ser	Met	Val
	210					215					220				
Thr	Pro	Gly	Ala	Glu	Ser	Lys	Asp	Lys	Val	Ser	Pro	Gln	Gln	Val	Ser
225					230					235					240
Asp	Tyr	Thr	Leu	Lys	Leu	Leu	Gln	Arg	Arg	Ile	Pro	Pro	Ala	Val	Pro
				245					250						255
Gly	Ile	Met	Phe	Leu	Ser	Gly	Gly	Gln	Ser	Glu	Val	Glu	Ala	Thr	Leu
			260					265					270		
Asn	Leu	Asn	Ala	Met	Asn	Gln	Ser	Pro	Asn	Pro	Trp	His	Val	Ser	Phe
		275					280					285			
Ser	Phe	Ala	Arg	Ala	Leu	Gln	Asn	Thr	Ala	Leu	Lys	Thr	Trp	Gly	Gly
	290					295					300				
Arg	Ala	Glu	Asn	Val	Lys	Ala	Ala	Gln	Asp	Ala	Leu	Leu	Phe	Arg	Ala
305					310					315					320
Lys	Ser	Asn	Ser	Leu	Ala	Gln	Leu	Gly	Lys	Tyr	Thr	Gly	Asp	Gly	Glu
				325					330					335	
Ser	Glu	Glu	Ala	Lys	Lys	Glu	Leu	Phe	Val	Lys	Gly	Tyr	Ser	Tyr	
			340					345						350	

&lt;210&gt; SEQ ID NO 27

&lt;211&gt; LENGTH: 353

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Oryza sativa

&lt;400&gt; SEQUENCE: 27

Ala	Ala	Ala	Val	Ser	Tyr	Ala	Asp	Glu	Leu	Val	Ser	Thr	Ala	Lys	Ser
1				5					10					15	

Val	Ala	Ser	Pro	Gly	Arg	Gly	Ile	Leu	Ala	Ile	Asp	Glu	Ser	Asn	Ala
			20					25						30	



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Thr Cys Gly Lys Arg Leu Ala Ser Ile Gly Leu Asp Asn Thr Glu Val  
           35                                  40                                  45  
 Asn Arg Gln Ala Tyr Arg Gln Leu Leu Leu Thr Thr Ala Gly Leu Gly  
           50                                  55                                  60  
 Glu Tyr Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser  
           65                                  70                                  75                                  80  
 Thr Thr Asp Gly Lys Lys Phe Val Asp Cys Leu Lys Asp Gln Asn Ile  
                                   85                                  90                                  95  
 Met Pro Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Pro Gly Ser  
                                   100                                  105                                  110  
 Asn Asn Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Cys  
                                   115                                  120                                  125  
 Ala Glu Tyr Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val  
           130                                  135                                  140  
 Val Ser Ile Pro Cys Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala  
   145                                  150                                  155                                  160  
 Trp Gly Leu Ala Arg Tyr Ala Ala Ile Ala Gln Asp Asn Gly Leu Val  
                                   165                                  170                                  175  
 Pro Ile Val Glu Pro Glu Ile Leu Leu Asp Gly Asp His Ala Ile Glu  
                                   180                                  185                                  190  
 Arg Thr Leu Glu Val Ala Glu Lys Val Trp Ser Glu Val Phe Phe Tyr  
           195                                  200                                  205  
 Leu Ala Gln Asn Asn Val Leu Phe Glu Gly Ile Leu Leu Lys Pro Ser  
           210                                  215                                  220  
 Met Val Thr Pro Gly Ala Glu His Lys Gln Lys Ala Thr Pro Glu Ala  
   225                                  230                                  235                                  240  
 Ile Ala Lys His Thr Leu Thr Met Leu Arg Arg Arg Val Pro Pro Ala  
                                   245                                  250                                  255  
 Val Pro Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala  
                                   260                                  265                                  270  
 Thr Leu Asn Leu Asn Ala Met Asn Gln Glu Pro Asn Pro Trp His Val  
           275                                  280                                  285  
 Ser Phe Ser Tyr Ala Arg Ala Leu Gln Asn Ser Val Leu Lys Thr Trp  
           290                                  295                                  300  
 Gln Gly Arg Pro Glu Asn Val Glu Ala Ala Gln Lys Ala Leu Leu Val  
   305                                  310                                  315                                  320  
 Arg Ala Lys Ala Asn Ser Leu Ala Gln Leu Gly Arg Tyr Thr Gly Glu  
                                   325                                  330                                  335  
 Gly Glu Ser Asp Glu Ala Lys Lys Gly Met Phe Gln Lys Gly Tyr Thr  
                                   340                                  345                                  350

Tyr

&lt;210&gt; SEQ ID NO 28

&lt;211&gt; LENGTH: 351

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Oryza sativa*

&lt;400&gt; SEQUENCE: 28

Ala Gly Ala Tyr Asp Asp Glu Leu Val Lys Thr Ala Lys Thr Ile Ala  
 1                                  5                                  10                                  15  
 Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys  
           20                                  25                                  30

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Gly Lys Arg Leu Ala Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn Arg  
           35                                  40                                  45  
 Gln Ala Tyr Arg Thr Leu Leu Val Thr Ala Pro Gly Leu Gly Gln Tyr  
           50                                  55                                  60  
 Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Val  
   65                                  70                                  75                                  80  
 Asp Gly Lys Lys Ile Val Asp Ile Leu Thr Glu Gln Lys Ile Val Pro  
           85                                  90                                  95  
 Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Ala Gly Ser Asn Asn  
           100                                  105                                  110  
 Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Glu Ala Ala  
           115                                  120                                  125  
 Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser  
           130                                  135                                  140  
 Ile Pro Asn Gly Pro Ser Glu Leu Ala Val Lys Glu Ala Ala Trp Gly  
   145                                  150                                  155                                  160  
 Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile  
           165                                  170                                  175  
 Val Glu Pro Glu Ile Leu Leu Asp Gly Glu His Gly Ile Asp Arg Thr  
           180                                  185                                  190  
 Phe Glu Val Ala Gln Lys Val Trp Ala Glu Thr Phe Phe Tyr Met Ala  
           195                                  200                                  205  
 Glu Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val  
           210                                  215                                  220  
 Thr Pro Gly Ala Glu Cys Lys Asp Arg Ala Thr Pro Glu Gln Val Ser  
   225                                  230                                  235                                  240  
 Asp Tyr Thr Leu Lys Leu Leu His Arg Arg Ile Pro Pro Ala Val Pro  
           245                                  250                                  255  
 Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Gln  
           260                                  265                                  270  
 Asn Leu Asn Ala Met Asn Gln Gly Pro Asn Pro Trp His Val Ser Phe  
           275                                  280                                  285  
 Ser Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Gly Gly  
           290                                  295                                  300  
 Gln Pro Glu Asn Val Lys Ala Ala Gln Asp Ala Leu Leu Leu Arg Ala  
   305                                  310                                  315                                  320  
 Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Ser Asp Gly Glu  
           325                                  330                                  335  
 Ala Ala Glu Ala Lys Glu Gly Met Phe Val Lys Asn Tyr Val Tyr  
           340                                  345                                  350

&lt;210&gt; SEQ ID NO 29

&lt;211&gt; LENGTH: 351

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Picea sitchensis

&lt;400&gt; SEQUENCE: 29

Ala Gly Ser Tyr Ala Glu Glu Leu Val Gln Thr Ala Lys Thr Val Ala  
   1                  5                                  10                                  15  
 Ser Pro Gly Arg Gly Ile Leu Ala Ile Asp Glu Ser Asn Ala Thr Cys  
           20                                  25                                  30  
 Gly Lys Arg Leu Ala Ser Ile Gly Leu Glu Asn Asn Glu Thr Asn Arg  
           35                                  40                                  45

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Gln Ala Tyr Arg Gln Leu Leu Leu Thr Thr Pro Gly Leu Gly Glu Tyr  
 50 55 60  
 Ile Ser Gly Ser Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Thr  
 65 70 75 80  
 Asp Gly Arg Lys Phe Val Asp Cys Leu Arg Glu Gln Asn Ile Met Pro  
 85 90 95  
 Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Pro Gly Ser Asn Asn  
 100 105 110  
 Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Glu  
 115 120 125  
 Tyr Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser  
 130 135 140  
 Ile Pro Asn Gly Pro Ser Asp Leu Ala Val Lys Glu Ala Ala Trp Gly  
 145 150 155 160  
 Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile  
 165 170 175  
 Val Glu Pro Glu Ile Leu Leu Asp Gly Asp His Ser Ile Asp Arg Thr  
 180 185 190  
 Leu Glu Val Ala Glu Lys Val Trp Ala Glu Val Phe Phe Tyr Leu Ala  
 195 200 205  
 Glu Asn Asn Val Phe Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val  
 210 215 220  
 Thr Pro Gly Ala Glu His Lys Glu Lys Ala Thr Pro Gln Gln Val Ala  
 225 230 235 240  
 Asp Tyr Thr Leu Lys Met Leu Lys Arg Arg Val Pro Pro Ala Val Pro  
 245 250 255  
 Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu  
 260 265 270  
 Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe  
 275 280 285  
 Ser Tyr Ala Arg Ala Leu Gln Asn Thr Ser Leu Lys Thr Trp Lys Gly  
 290 295 300  
 Leu Pro Glu Asn Ile Glu Ala Ala Gln Arg Ala Leu Leu Ile Arg Ala  
 305 310 315 320  
 Lys Ala Asn Ser Leu Ala Gln Leu Gly Arg Tyr Ser Ala Glu Gly Glu  
 325 330 335  
 Ser Glu Glu Ser Lys Lys Gly Met Phe Val Lys Gly Tyr Thr Tyr  
 340 345 350

&lt;210&gt; SEQ ID NO 30

&lt;211&gt; LENGTH: 351

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Picea sitchensis

&lt;400&gt; SEQUENCE: 30

Ala Gly Ala Tyr Ser Glu Glu Leu Ile Lys Thr Ala Lys Arg Val Ala  
 1 5 10 15  
 Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys  
 20 25 30  
 Gly Lys Arg Leu Ala Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn Arg  
 35 40 45  
 Gln Ala Tyr Arg Gln Leu Leu Val Ser Ala Pro Gly Leu Gly Gln Tyr



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Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Thr
65          70          75          80

Asp Gly Lys Lys Phe Val Asp Cys Leu Arg Asp Glu Asn Ile Val Pro
          85          90

Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Pro Gly Ser Asn Asn
          100          105          110

Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Glu
          115          120          125

Tyr Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser
          130          135          140

Ile Pro Cys Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp Gly
145          150          155          160

Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile
          165          170          175

Val Glu Pro Glu Ile Leu Leu Asp Gly Asp His Pro Ile Asp Arg Thr
          180          185          190

Leu Glu Val Ala Glu Lys Val Trp Ser Gly Val Phe Tyr Tyr Leu Ala
          195          200          205

Glu Asn Asn Val Val Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val
210          215          220

Thr Pro Gly Ala Glu His Lys Glu Lys Ala Ser Ala Asp Thr Ile Ala
225          230          235          240

Lys Tyr Thr Leu Thr Met Leu Lys Arg Arg Val Pro Pro Ala Val Pro
          245          250          255

Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Gln Ala Thr Leu
          260          265          270

Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe
          275          280          285

Ser Tyr Ala Arg Ala Leu Gln Asn Thr Val Leu Lys Thr Trp Gln Gly
290          295          300

Arg Pro Asp Asn Val Glu Ala Ala Gln Lys Ser Leu Leu Val Arg Ala
305          310          315          320

Lys Ala Asn Ser Leu Ala Gln Leu Gly Arg Tyr Ser Ala Glu Gly Glu
          325          330          335

Ser Glu Glu Ala Thr Lys Gly Met Phe Val Lys Gly Tyr Thr Tyr
          340          345          350

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&lt;210&gt; SEQ ID NO 32

&lt;211&gt; LENGTH: 351

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Populus trichocarpa

&lt;400&gt; SEQUENCE: 32

```

Ala Gly Ser Tyr Ala Asp Glu Leu Val Lys Thr Ala Lys Thr Ile Ala
1          5          10

Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys
          20          25          30

Gly Lys Arg Leu Ala Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn Arg
          35          40          45

Gln Ala Tyr Arg Thr Leu Leu Val Thr Val Pro Gly Leu Gly Asn Tyr
          50          55          60

Val Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Thr
65          70          75          80

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Asp Gly Lys Lys Met Val Asp Val Leu Val Glu Gln Lys Ile Val Pro  
                   85                                  90                                  95  
 Gly Ile Lys Val Asp Lys Gly Leu Val Pro Leu Ala Gly Ser Asn Asp  
                   100                                  105                                  110  
 Glu Ser Trp Cys Gln Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Ala  
                   115                                  120                                  125  
 Tyr Tyr Gln Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser  
                   130                                  135                                  140  
 Ile Pro Asn Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp Gly  
                   145                                  150                                  155                                  160  
 Leu Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile  
                                   165                                  170                                  175  
 Val Glu Pro Glu Ile Leu Leu Asp Gly Glu His Gly Ile Glu Arg Thr  
                                   180                                  185                                  190  
 Phe Glu Val Ala Gln Lys Val Trp Ala Glu Val Phe Tyr Tyr Met Ala  
                   195                                  200                                  205  
 Glu Asn Asn Val Met Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val  
                   210                                  215                                  220  
 Thr Pro Gly Ala Glu Cys Lys Asp Arg Ala Ser Pro Asp Gln Val Ala  
                   225                                  230                                  235                                  240  
 Glu Tyr Thr Leu Lys Leu Leu His Arg Arg Ile Pro Pro Ala Val Pro  
                                   245                                  250                                  255  
 Gly Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu  
                   260                                  265                                  270  
 Asn Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe  
                   275                                  280                                  285  
 Ser Tyr Ala Arg Ala Leu Gln Asn Thr Cys Leu Lys Thr Trp Gly Gly  
                   290                                  295                                  300  
 Arg Pro Glu Asn Val Gln Asp Ala Gln Glu Thr Leu Leu Ile Arg Ala  
                   305                                  310                                  315                                  320  
 Lys Ala Asn Ser Leu Ala Gln Leu Gly Lys Tyr Thr Gly Glu Gly Glu  
                                   325                                  330                                  335  
 Ser Asp Asp Ala Lys Lys Gly Met Tyr Val Lys Asn Tyr Ser Tyr  
                                   340                                  345                                  350

&lt;210&gt; SEQ ID NO 33

&lt;211&gt; LENGTH: 351

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Populus trichocarpa

&lt;400&gt; SEQUENCE: 33

Thr Gly Ser Tyr Ala Glu Glu Leu Val Lys Thr Ala Lys Thr Ile Ala  
 1                  5                                  10                                  15  
 Ser Pro Gly Arg Gly Ile Leu Ala Met Asp Glu Ser Asn Ala Thr Cys  
                   20                                  25                                  30  
 Gly Lys Arg Leu Ala Ser Ile Gly Leu Glu Asn Thr Glu Ala Asn Arg  
                   35                                  40                                  45  
 Gln Ala Tyr Arg Thr Leu Leu Val Thr Val Pro Gly Leu Gly Asp Tyr  
                   50                                  55                                  60  
 Val Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Thr  
                   65                                  70                                  75                                  80  
 Asp Gly Lys Lys Met Val Asp Val Leu Val Glu Gln Lys Ile Val Pro

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				85						90										95
Gly	Ile	Lys	Val	Asp	Lys	Gly	Leu	Val	Pro	Leu	Ala	Gly	Ser	Asn	Asp					
				100						105					110					
Glu	Ser	Trp	Cys	Gln	Gly	Leu	Asp	Gly	Leu	Ala	Ser	Arg	Thr	Ala	Ala					
			115					120					125							
Tyr	Tyr	Gln	Gln	Gly	Ala	Arg	Phe	Ala	Lys	Trp	Arg	Thr	Val	Val	Ser					
	130					135						140								
Ile	Pro	Asn	Gly	Pro	Ser	Ala	Leu	Ala	Val	Lys	Glu	Ala	Ala	Trp	Gly					
145					150					155					160					
Leu	Ala	Arg	Tyr	Ala	Ala	Ile	Ser	Gln	Asp	Asn	Gly	Leu	Val	Pro	Ile					
				165						170					175					
Val	Glu	Pro	Glu	Ile	Leu	Leu	Asp	Gly	Glu	His	Gly	Ile	Asp	Arg	Thr					
			180					185					190							
Phe	Glu	Val	Ala	Gln	Lys	Val	Trp	Ala	Glu	Val	Phe	Phe	Tyr	Met	Ala					
		195						200					205							
Glu	Asn	Asn	Val	Met	Phe	Glu	Gly	Ile	Leu	Leu	Lys	Pro	Ser	Met	Val					
	210					215						220								
Thr	Pro	Gly	Ala	Glu	Cys	Lys	Asp	Arg	Ala	Thr	Pro	Glu	Gln	Val	Ala					
225					230					235					240					
Glu	Tyr	Thr	Leu	Lys	Leu	Leu	Gln	Arg	Arg	Ile	Pro	Pro	Ser	Val	Pro					
				245						250					255					
Gly	Ile	Met	Phe	Leu	Ser	Gly	Gly	Gln	Ser	Glu	Val	Glu	Ala	Thr	Leu					
			260						265					270						
Asn	Leu	Asn	Ala	Met	Asn	Gln	Ser	Ala	Asn	Pro	Trp	His	Val	Ser	Phe					
		275						280					285							
Ser	Tyr	Ala	Arg	Ala	Leu	Gln	Asn	Thr	Cys	Leu	Lys	Thr	Trp	Gly	Gly					
	290					295					300									
Arg	Pro	Glu	Asn	Val	Asn	Ala	Ala	Gln	Glu	Ala	Leu	Leu	Ile	Arg	Ala					
305					310					315					320					
Lys	Ala	Asn	Ser	Leu	Ala	Gln	Leu	Gly	Lys	Tyr	Thr	Gly	Glu	Gly	Glu					
				325						330					335					
Ser	Asp	Glu	Ala	Lys	Lys	Gly	Met	Phe	Val	Lys	Asn	Tyr	Ala	Tyr						
		340						345						350						

&lt;210&gt; SEQ ID NO 34

&lt;211&gt; LENGTH: 245

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Zea mays

&lt;400&gt; SEQUENCE: 34

His	Glu	Gly	Ser	Asn	Asn	Glu	Ser	Trp	Cys	Gln	Gly	Leu	Asp	Gly	Leu					
1				5						10					15					
Ala	Ser	Arg	Cys	Ala	Glu	Tyr	Tyr	Lys	Gln	Gly	Ala	Arg	Phe	Ala	Lys					
			20					25					30							
Trp	Arg	Thr	Val	Val	Ser	Ile	Pro	Cys	Gly	Pro	Ser	Ala	Leu	Ala	Val					
		35					40					45								
Lys	Glu	Ala	Ala	Trp	Gly	Leu	Ala	Arg	Tyr	Ala	Ala	Ile	Ala	Gln	Asp					
		50				55					60									
Asn	Gly	Leu	Val	Pro	Ile	Val	Glu	Pro	Glu	Ile	Leu	Leu	Asp	Gly	Asp					
65					70					75					80					
His	Gly	Ile	Glu	Arg	Thr	Leu	Glu	Val	Ala	Glu	Lys	Val	Trp	Ser	Glu					
				85					90						95					

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Val Phe Phe Tyr Leu Ala Gln Asn Asn Val Leu Phe Glu Gly Ile Leu  
 100 105 110

Leu Lys Pro Ser Met Val Thr Pro Gly Ala Asp His Lys Glu Lys Ala  
 115 120 125

Ser Pro Glu Ala Ile Ala Lys Tyr Thr Leu Thr Met Leu Arg Arg Arg  
 130 135 140

Val Pro Pro Ala Val Pro Gly Ile Met Phe Leu Ser Gly Gly Gln Ser  
 145 150 155 160

Glu Val Glu Ala Thr Leu Asn Leu Asn Ala Met Asn Gln Ser Pro Asn  
 165 170 175

Pro Trp His Val Ser Phe Ser Tyr Ala Arg Ala Leu Gln Asn Ser Val  
 180 185 190

Leu Lys Thr Trp Gln Gly Arg Pro Glu Asn Val Glu Ala Ala Gln Lys  
 195 200 205

Ala Leu Leu Val Arg Ala Lys Ala Asn Ser Leu Ala Gln Leu Gly Arg  
 210 215 220

Tyr Thr Gly Glu Gly Glu Ser Asp Glu Ala Lys Lys Gly Met Phe Gln  
 225 230 235 240

Lys Gly Tyr Thr Tyr  
 245

&lt;210&gt; SEQ ID NO 35

&lt;211&gt; LENGTH: 350

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Glycine max

&lt;400&gt; SEQUENCE: 35

Ala Ser Ser Tyr Gln His Glu Leu Val Gln Thr Ala Lys Ser Ile Ala  
 1 5 10 15

Ser Pro Ser Arg Gly Ile Leu Ala Ile Asp Glu Ser Asn Ala Thr Cys  
 20 25 30

Gly Lys Arg Leu Ala Ser Ile Gly Leu Asp Asn Thr Glu Val Asn Arg  
 35 40 45

Gln Ala Tyr Arg Gln Leu Leu Leu Thr Thr Pro Gly Leu Gly Glu Tyr  
 50 55 60

Ile Ser Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Ser Thr Thr  
 65 70 75 80

Asp Gly Asn Lys Phe Val Asp Cys Leu Arg Asp Gln Asn Ile Val Pro  
 85 90 95

Asp Ile Lys Val Asp Lys Gly Leu Val Pro Leu Pro Gly Ser Asn Asn  
 100 105 110

Glu Ser Trp Cys Gly Leu Asp Gly Leu Ala Ser Arg Ser Ala Glu Tyr  
 115 120 125

Tyr Lys Gln Gly Ala Arg Phe Ala Lys Trp Arg Thr Val Val Ser Ile  
 130 135 140

Pro Cys Gly Pro Ser Ala Leu Ala Val Lys Glu Ala Ala Trp Gly Leu  
 145 150 155 160

Ala Arg Tyr Ala Ala Ile Ser Gln Asp Asn Gly Leu Val Pro Ile Val  
 165 170 175

Glu Pro Glu Ile Leu Leu Asp Gly Asp His Pro Ile Glu Arg Thr Leu  
 180 185 190

Glu Val Ala Glu Lys Val Trp Ser Glu Val Phe Phe Tyr Leu Ala Glu  
 195 200 205



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Asn Asn Val Leu Phe Glu Gly Ile Leu Leu Lys Pro Ser Met Val Thr
 210          215          220
Pro Gly Ala Glu His Thr Glu Lys Ala Ser Pro Glu Thr Ile Ala Lys
 225          230          235          240
Tyr Thr Leu Thr Met Leu Arg Arg Arg Val Pro Pro Ala Leu Pro Gly
          245          250          255
Ile Met Phe Leu Ser Gly Gly Gln Ser Glu Val Glu Ala Thr Leu Asn
          260          265          270
Leu Asn Ala Met Asn Gln Ser Pro Asn Pro Trp His Val Ser Phe Ser
          275          280          285
Tyr Ala Arg Ala Leu Gln Asn Thr Val Leu Lys Thr Trp Gln Gly His
          290          295          300
Pro Glu Asn Val Glu Ala Ala Gln Lys Ser Leu Leu Val Arg Ala Lys
 305          310          315          320
Ala Asn Ser Leu Ala Gln Leu Gly Arg Tyr Ser Ala Glu Gly Glu Ser
          325          330          335
Glu Glu Ala Lys Lys Gly Met Phe Val Lys Gly Tyr Thr Tyr
          340          345          350

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&lt;210&gt; SEQ ID NO 36

&lt;211&gt; LENGTH: 358

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 36

```

Met Ser Ala Phe Val Ser Lys Tyr Glu Asp Glu Leu Ile Lys Thr Ala
 1          5          10          15
Lys Tyr Ile Ala Thr Pro Gly Arg Gly Ile Leu Ala Ala Asp Glu Ser
          20          25          30
Thr Glu Thr Ile Gly Lys Arg Phe Ala Gly Ile Asn Val Glu Asn Thr
          35          40          45
Glu Ser Asn Arg Gln Ala Tyr Arg Glu Leu Leu Phe Thr Ser Pro Gly
 50          55          60
Ser Tyr Pro Cys Leu Ser Gly Val Ile Leu Phe Glu Glu Thr Leu Tyr
 65          70          75          80
Gln Lys Thr Ser Asp Gly Lys Pro Phe Val Asp Leu Leu Met Glu Asn
          85          90          95
Gly Val Ile Pro Gly Ile Lys Val Asp Lys Gly Leu Val Asp Leu Ala
          100          105          110
Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp Ser Leu Gly Ala
          115          120          125
Arg Cys Gln Gln Tyr Tyr Glu Ala Gly Ala Arg Phe Ala Lys Trp Arg
          130          135          140
Ala Phe Phe Lys Ile Gly Ala Thr Glu Pro Ser Val Leu Ser Ile Gln
          145          150          155          160
Glu Asp Ala Arg Val Leu Ala Arg Tyr Ala Ile Ile Cys Gln Glu Asn
          165          170          175
Gly Leu Val Pro Ile Val Glu Pro Glu Val Leu Thr Gly Gly Ser His
          180          185          190
Asp Ile Lys Lys Cys Ala Ala Val Thr Glu Thr Val Leu Ala Ala Val
          195          200          205
Phe Lys Ala Leu Asn Tyr His His Val Leu Leu Glu Gly Thr Leu Leu

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210	215	220			
Lys Pro Asn Met Val Thr	Pro Gly Ser Asp Ser	Pro Lys Val Ala Pro			
225	230	235			240
Glu Leu Ile Ala Glu Tyr Thr	Val Thr Ala Leu Arg Arg Thr	Val Pro			
	245	250			255
Pro Ala Ile Pro Gly Ile Val	Phe Leu Ser Gly Ile Gln Arg Glu Glu				
	260	265			270
Gln Ala Thr Leu Asn Leu Asn	Ala Met Asn Lys Leu Asp Val Leu Lys				
	275	280			285
Pro Trp Thr Leu Thr Phe Ser	Phe Gly Gly Ala Leu Gln Gln Ser Ala				
	290	295			300
Ile Lys Ala Trp Ala Gly Lys	Pro Glu Asn Val Ala Lys Ala Gln Ala				
305	310	315			320
Lys Phe Leu Thr Arg Cys Lys	Ala Asn Lys Asp Ala Thr Leu Gly Lys				
	325	330			335
Tyr Thr Gly Trp Ala Ser Gly	Asp Ser Ala Ala Phe Glu Asn Leu Val				
	340	345			350
Val Ile Gly Tyr Arg Tyr					
	355				

<210> SEQ ID NO 37  
 <211> LENGTH: 1056  
 <212> TYPE: DNA  
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 37

```

gccggtgctt actccgacga gcttgtaa accgcaaaa gcattgcatc cctgggaga      60
ggtatcttgg cgatcgatga gtccaatgca acctgtggga agaggcttgc ttctatcggc      120
ttggataaca cggaggacaa cgtcaggcc tacaggcaac ttctgcttac cactcctggc      180
ctggcgatt acatctctgg ttccattctc ttcgaggaga ctctttacca gtccaccaag      240
gacggtaaga ctttgtcga ttgcttgcgc gatgccaaca tcgtccctgg catcaaagtt      300
gacaagggct tgtctccct agccggttcc aacgaagagt cttggtgcca aggcttggat      360
ggattggcct cacgctctgc tgagtactac aagcaaggcg ctcgtttgc caagtgagg      420
acagtgggta gtgttccctg cggctcttca gcactggctg tgaaggaagc tgcgtggggg      480
ctggctcgct atgcagccat ctctcaggat aatggtcttg tcccattgt ggagccagag      540
atccttctgg acggggacca cccaatagag aggactctgg aggtggcaga gaaagtgtgg      600
tcagaggtgt tcttctactt ggcacagaac aacgtcatgt ttgagggcat tctgttgaag      660
ccgagcatgg tcaccccagg cgctgagcac aagaacaagg cctctcccga gaccgttgca      720
gatttcacgc tcaccatgct gaaaaggagg gttcctccgg ctgtcccagg gatcatgttt      780
ctgtcaggag gacaatcaga ggcagaggcc acaactgaacc tgaacgcat gaaccagagc      840
ccaaacccat ggcattgtgc cttctcatac gcacgtgccc tgcagaactc cgtgctcaga      900
acatggcaag gcaagccgga gaagattgag gctcgcaga aggcactggt ggtgagggca      960
aaggccaact cactggccca gctcggcaaa tactcagccg agggagagaa cgaggatgcc      1020
aagaaaggaa tgtttgcata gggttacacc tactga                               1056
    
```

<210> SEQ ID NO 38  
 <211> LENGTH: 1059

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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 38

```

gccgcttctg cttacgccga tgagctcgtc aaaaccgcta aaacaatcgc gtctccggga    60
cacggaatta tggcgatgga tgagtccaac gcgacttggt gaaagcgttt ggcgtcaatt    120
gggctagaga acacggaggc taaccgtcaa gcttacagga cgttgcttgt gtcggctcca    180
ggacttgac agtacatctc cggagctatc ctgttcgagg agactctgta ccaatccacc    240
actgatggca agaaaatggt tgatgttctc gtcgagcaga acatcgtccc tggcatcaaa    300
gtcgacaagg gtttgggtgcc acttgttggg tcttacgacg agtcatgggt ccaaggactt    360
gacggtttag cctctcgcac cgctgcttac taccaacaag gtgctcgttt cgccaaatgg    420
cgtactgttg tgagcattcc aaatggacce tctgctttgg ctgttaaaga agcagcttgg    480
ggacttgctc gctacgcagc tatttctcaa gacagcggtc tgggtccgat tgtggagcca    540
gagattatgt tggacggaga acacggcatt gacaggacat acgacgttgc agagaaggtt    600
tgggctgagg tcttcttcta cctcgcctcag aacaacgtca tgttcgaagg tatttctctg    660
aagccaagca tggttactcc aggagctgag gccacagaca gagctactcc tgagcaggtt    720
gcttcctaca ctctcaagct ccttcgcaac agaatccctc ctgctgtccc cggaatcatg    780
ttcttgctcg gtggacagtc cgagttggag gcgaccttga acttgaacgc aatgaaccag    840
gcaccgaacc catggcacgt gtccttctcc tacgcacgtg ccttcgagaa cacttgcttg    900
aagacatggg gaggcaagga agagaacgtg aaggcggctc aggacattct cttggccaga    960
gccaagcca attcgtctggc tcagctcggg aaatacactg gagaaggcga gtctgaggaa   1020
gccaaggagg gtatgtttgt aaaaggctac acctactaa                               1059

```

&lt;210&gt; SEQ ID NO 39

&lt;211&gt; LENGTH: 1059

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 39

```

gccgcttctc cctacgccga tgagcttgtt aagacagcga aaactattgc gtctcccgga    60
cgtggaatct tggcgatgga cgagtcaaac gcgacttgcg ggaaacgttt ggattcgata    120
gggctagaga aactgagggc aaatcgtcaa gcttcccgga ctttgcgtgt ctctgcaccg    180
ggactcggac agtacgtctc cggcgcgaat ctatttgagg agactctgta ccagtctacc    240
accgaaggca agaaaatggt cgacgtctc gtcgagcaga acattgtccc tggtatcaaa    300
gtcgacaagg gtttgggtgcc acttgttggg tccaacaatg agtcatgggt ccaaggacta    360
gatggtctat catctcgaac tgetgcttac tatcaacagg gtgcgctgtt cgccaaatgg    420
cgtactgtcg tgagcattcc taacggctcg tctgcctcgc ccgtcaaaga agctgcttgg    480
ggtcttgctc gatacgtgac catttcacag gacagcgggt tggttccgat tgttgagcca    540
gagatcttgt tggatggaga acacgacatt gacagaacat acgacgtagc agagaaggtt    600
tgggctgagg ttttcttcta ccttgcctcag aacaatgtca tgtttgaagg tatectcta    660
aaaccgagca tgggtgactcc cggagctgag tctaagaca gagctactcc tgaacaagtt    720
gccgcctaca cctcaagct cctccgcaac agagtccctc ccgcagtcgc cggaatcatg    780
ttttgtccg gaggacagtc ggaggtggag gcaacactca acttgaacgc aatgaaccag    840

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gcaccaaacc catggcacgt gtccttctcc tacgcacgtg cgttgcagaa cacttgctctg    900
aaaacatggg ggggcagacc cgagaacgtg aacgcagctc agaccactct cttggcccgt    960
gccaaaggcca attcgttggc tcagctcgga aaatacaccg gtgagggtga gtccgaagag    1020
gctaaggagg gcatgttctg caaagggtag acctattga                                1059

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<210> SEQ ID NO 40
<211> LENGTH: 1062
<212> TYPE: DNA
<213> ORGANISM: Hordeum Vulgare

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<400> SEQUENCE: 40

```

```

gcctccggcg gctcctacgc cgacgagctc gtctccaccg cgaaaactgt tgcttcccct    60
ggccgtggga tccttgcat cgacgagctc agtgcaacat gtggaaagag attggcatcc    120
attgggttgg acaacaccga agttaaccgc caggcttaca ggcagctggt gctgaccact    180
gctggtcttg gtgaatata ctctggtgct attctcttg aggaaactct ctaccagtcc    240
actacagatg gcaagacctt tgttgatgtc ttgaaggacc agaatatcat gectggtatc    300
aaggttgaca agggtttggg tccattgccc ggatccaaca atgaatcctg gtgccaaggt    360
cttgatggtt tggcctcaag gtgtgctgag tactacaagc aggggtgcacg cttcgcaaag    420
tggcggactg ttgtagcat cccttgggt cctactgcat tagctgtcaa ggaagcggca    480
tggggacttg ctgcgtatgc tgctattgct caggacaatg gtttagtgcc aattgtggag    540
ccagagatcc tcctcgacgg tgacctggc atcgagagaa ctcttgaggt cgccgagaag    600
gtgtggtccg aggtgttctt ctacctggc gaaaacaatg ttcttttga gggcatcctg    660
ctgaagccca gcatggttac ccctggtgct gaggacaagg agaaggcttc tccagaagcc    720
attgcaaga acaccctcac aatgctgagg aggagagtag cggccgctgt ccctggaatc    780
atgttccttt ctggcgggca gtcogaactg gaggcgacga tgaacctgaa cgcgatgaac    840
cagtcgccca acccgtggca cgtgtccttc tcgtaacgccc gggccctcca gaactcggtg    900
ctgaagacat ggcaggggca gcccgagaac atcgaggcgg cgcagaaggg cctgctggtc    960
cgcgccaagg ccaactcgtt ggcgcagctc ggcagctaca cgggcgaggg cgagagcgac    1020
gaggccaaga agggcatggt ccagaagggc tacacctact ga                                1062

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```

<210> SEQ ID NO 41
<211> LENGTH: 732
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

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<400> SEQUENCE: 41

```

```

gccagcgcgt acgccgatga gcttgtgaaa accgcgaaaa ccatcgcate gectggcagg    60
ggtatccttg ccatggatga gtcgaatgct acctgtggca agagacttgc ctcgattggc    120
cttgagaaca ccgaggctaa ccgccaggct taccggacct tccttgtcac tccaccaggc    180
ttgggaaact acatctctgg tgctatcttc tttgaggaga ccctctacca gtegactggt    240
gatggcaaga agattgttga catccttgc gaggcgggga tcgttcccgg tatcaaggtt    300
gacaagggtc ttgtgccaat tgttgggtcc aacgatgagt catggtgcca aggcctcgat    360
ggccttgct cccgtgaagc agcatactgc cagcaaggcg cccgcttgcg caagtggcgc    420
actgttgcga gcattcctaa cggaccatct gagcttgcgt tcaaggaagc tgctgggggt    480

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cttccccgtt acgcgccat ctcacaggac aatgggctgg tgccgattgt ggagcctgag 540
atcatgctcg atggtgagca cggcatcgag aggaccttcg aggtggcgca gaaggtgtgg 600
gcgagacct tttactacat ggcccagaac aacgtcatgt ttgagggcat cctcctgaag 660
ccaagcatgg tgaccctgg tgccgagtgc aaggacaggg ccaccctga ggaagtagcc 720
agccctcaag tg 732

```

```

<210> SEQ ID NO 42
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

```

```

<400> SEQUENCE: 42

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```

gccggcgct acgacgatga gctcgtcaag acagcgaaaa ccatcgcgct gccggggcgc 60
ggcatcctgg ccatggacga gtccaacgcc acctgcggga agcgctcga ctcgatcggc 120
ctggagaaca cggaggccaa ccggcaggcg ttccgcacgc tgctggtctc cgtacctggc 180
ctcggcaacc acatttcgg cgccatcctc ttccaggaga cgctctacca gtccaccgtc 240
gacggcaaga agattgtcga catcctggca gacgaggga tcgtgcccg gatcaaggtg 300
gacaagggcc tcgtgccgct caccggtcc aacgacgagt cttggtgtca gggcctcgac 360
ggcctcgct cccgggaggc cgcctactac cagcagggcg cccgcttcgc caagtggcgc 420
accgtggtca gcattcccaa cggcccctcc gagctcggcg tcaaggaggc cgcctggggc 480
ctcggccgct acgcccgat ctcgcaggac aacggcctgg tgcccatcgt ggagccggag 540
atcctgctgg acggggagca cggcatcggg cgcaccttcg aggtggcgca gaaggtgtgg 600
gccgagacat tctaccagat gtcccagaac aacgtcatgt tcgagggcat cctgctcaaa 660
cccagcatgg tcaccctgg cgtgagtgc aaggacaggg ctacgccgga gcaggtggcc 720
ggctacacc tcaagctcct cagccgccgc gtgccgcccg ccgtcccggg catcatgttc 780
ctgtcgggag ggcagtcga ggtggaggcc acgctcaacc tcaacgccat gaaccagggg 840
cccaaccctt ggcacgtctc cttctcctac gccaggcgcc tgcagaacac gtgcctcaag 900
acgtggggtg gccaccgga gaacgtcaag gcggcgagg aggcgctgtt gctgctgccc 960
aaggccaact cgctcgcga gctcggaaa tacaccagcg acggcgaggc cgcagggccc 1020
aaagagggca tgttcgtcaa aaactacagc tatta 1056

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```

<210> SEQ ID NO 43
<211> LENGTH: 1059
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum

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<400> SEQUENCE: 43

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```

gctgctggat cttacaccga tgagctcacc aaaaccgcta aaactattgc ttctcctgga 60
aggggcatcc ttgccattga tgaatcgaat gcaactgccg gaaagagact ggcgtcaatt 120
ggtctggaca acacagaagc aaacagacaa gcttaccgtc aactcttgtt gaccactcct 180
ggcctaggtg attacatctc tggatccatt ctattogaag agacactttt ccagtccact 240
accgatggga agaagtttgt tgatgtcttg cgcgatcaga agattgtacc tggaatcaaa 300
gttgacaagg gtttggttcc cctaccagga tccaacaatg aatcctgggtg ccaaggattg 360
gatggattgg cttctaggtc tgctgaatac tacaagcaag gggcacgttt tgccaagtgg 420

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```

agaacagttg ttagcattcc ttgctgtcct tctgctttgg ctgtaaaaga agcagcttgg 480
ggtcttctgc gatatgctgc tatatctcag gacaatggtt tagtgccaat agtagagcct 540
gagattcttt tggatggtga ccaccaata gaacgaacct ttgaagtgc ggaactgtt 600
tgggcagaag tcttctacta cctagcagaa aacaatgtcg tttttgaagg tattttgctc 660
aaacctagca tggttactcc tgggtgctgaa cacaaagaga aggctacccc agaaccatt 720
gctaaataca cacttaccat gttgaggaga agagtccctc ctgcagtcc tggaatcatg 780
tttctgtccg gaggacaatc tgaagtggaa gcgacactca acctccacga aatgaaccag 840
agccccaacc catggcatgt atctttctca tatgcaagag cactccagaa cacagtgtc 900
aagacatggc aaggacgtcc tgagaatgtg gatgctgcac agagggcact cttgattcgt 960
gcaaaagcaa actccttggc tcagctcggg aaatactccg cagaaggtga aagtgaggaa 1020
gccaaagaagg gaatgtttgt caagggctac acctactaa 1059

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<210> SEQ ID NO 44
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum

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<400> SEQUENCE: 44

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```

gctagctcct atgctgatga gctcgtcaaa accgcgaaaa ctattgcatc ccttggtcgt 60
ggaattttgg ccatggatga gtccaatgct acctgtggga agcgttttagc ttcaatcgga 120
atggagaaca ctgaggctaa ccgccaggcg ttcaggacct tgctagtctc agttcctgga 180
ctaggggagt acatctctgg tgcaatcctc tttgaggaga cactttatca atcaaccgtc 240
gagggaaaga aaatggttga tgtgcttgtt gacgagaaca ttgttcctgg tattaaggtt 300
gacaagggtc ttgttccttt ggctggetca aacaatgaat catggtgcca aggtcttgat 360
ggccttgctc ctcgctctgc tgcttactac caacaaggcg cccggtttgc caaatggcgt 420
actgttgtga gcacccctaa tggctcctca gcacttcagc tgaaggaagc agcctggggt 480
cttgctcgtc acgctgctat ttctcaggac aatgggttgg taccatcgt tgagccagag 540
atcttacttg atggtgaaca caacattgat aggaccttg aagtgcgcaa gcaggtgtgg 600
gctgaagttt tcttctacct tgcccagaac aatgtcatgt ttgaaggtat cttgttgaag 660
cccagcatgg tcacccctgg agctgagtgc aaggacaggg ccaccccaca gcaagttgct 720
gactacacc ctagtctcct ccgccaaaga atccctcctg ccgtcccagg aatcatgttt 780
ttgtctggtg gacaatctga agttgaggca actcttaact tgaacgccat gaaccaaagt 840
cccaaccat ggcaagctgc gttctcatac gccagagccc ttcagaacac atgcctcaag 900
acttggagtg gaaggccaga aaatgtgaag gcagctcagg atgccttgc tgttagagca 960
aaggccaact ctcttgccca gctagggaaa tacaccggtg aaggtgagtc cgatgaggcc 1020
aagaagggaa tgttcgtgaa gggatacgtc tatta 1056

```

```

<210> SEQ ID NO 45
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum

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```

<400> SEQUENCE: 45

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```

gccagctcct acgctgatga gctcgtcaaa accgcgaaaa ctgttgcac tcttggtcgt 60

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ggaattttgg cgatggatga gtcgaatgct acctgtggga agcgtttaga ttcaatcgga 120
ctagagaaca cggaaagctaa tcgccaagca tacaggacc ttcttgtttc agctccagga 180
cttgtaact acatttcagg tgccatcctt ttgaggaga cactttacca gtccactgtt 240
gatggaaaga aaattgttga tgtacttctt gaacagaaca ttgttcctgg aattaagggt 300
gacaagggtt tagttccttt ggctggttca aacaatgaat cttggtgcca aggtcttgat 360
ggccttgct cgcgctctgc tgcttactac caacaaggcg ctcgttttgc taaatggcgt 420
actgtagtga gcattcccaa tggtccttct gcaactgcag ttaaggaggc agcctggggt 480
cttgctcgt atgctgcaat ttctcaggac aatgggttag taccaattgt tgagccagag 540
atthtgctag atggtgaaca caatatcgat aggaccttg aggttgetca acaggtgtgg 600
gctgaagttt tctctacct ggcgaaaaac aatgtcatgt ttgaaggat cttgttgaag 660
cctagcatgg tcaccccggg agcagaatgc aaggagaggc ccacccaga acaagttgct 720
gattataccc tcaagctcct ccaacgaaga attccccctg ctgtccctgg aatcatgttc 780
ttgtctggtg gacaatctga agtggaaagct actcttaact tgaacgcgat gaaccaatct 840
cccaaccat ggcacgtatc gttctcatat gcaagagccc ttcagaacac atgtctcaag 900
acatggggtg gaagaccaga aaatgttgag gcagctcaga aagctttgct tactagagca 960
agtccaact ctctcgcga actaggcaaa tacaccggtg aaggtgagtc tgaggaggcc 1020
aaggagggaa tgtttgtgaa aggatatgtc tactaa 1056

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&lt;210&gt; SEQ ID NO 46

&lt;211&gt; LENGTH: 1017

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Lotus japonicus

&lt;400&gt; SEQUENCE: 46

```

aaaactattg cgtctcctgg tcgtggaata cttgcaattg atgagtcaaa cgcgaccgct 60
gggaagcgtt tggcatcgat tggattggac aacacggaga ccaatcgcca ggcctacagg 120
caacttctgc tgaccacacc tggccttggg gaatacatct ctggtgccat tttttogag 180
gaaacccttt accagtcaac cactgatgga aagaagtttg tggactgtct tcgtgaggag 240
aacattgtac ctggaatcaa agttgataag ggtttggtcc ctctgccagg gtcaaacaa 300
gaatcttggg gccaaagggt ggatggattg gcttcaagat ctgctgaata ctacaagcaa 360
ggtgctagat ttgccaaagt gaggacagtt gtcagcattc cttgtggtcc ttctgcattg 420
gcogttaagg aagcagcatg gggacttgca cgttaoetg ctatctctca ggacaatggc 480
cttgttccaa ttgtagagcc tgaattctt cttgatgggg accaccaat cgagaggaca 540
ttggaagtgg ccgagaaggt ctggtctgaa gtcttctctc atttggctga aaacaatgtc 600
gtttttgagg gaattttgct caaacctagc atggttacgc ctggagcggg acacaagcaa 660
aaggcttctc cagaaactat tgccaataac aactaacca tgcttagaag gagagttcct 720
ccagcagtc ctggaatcat gttctgtctg ggtggacaat ctgaagtgga agccacacta 780
aatctcaatg ctatgaacca aagtccaaac ccatggcatg tttcgttctc gtatgaaga 840
gctctgcaga aactgtgct taagacttg caaggacgcc ctgaaaatgt ggaagctgct 900
cagaagtctc tcttgatccg cgttaaagca aactccttgg ctcaacttgg aagatactct 960
gctgagggtg aaagtgaaga agcacagaaa ggaatgtttg tcaagggcta cacctac 1017

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<210> SEQ ID NO 47  
 <211> LENGTH: 1056  
 <212> TYPE: DNA  
 <213> ORGANISM: Lotus japonicus

<400> SEQUENCE: 47

gctggttcct atgctgatga gcttgtaag actgcgaaaa ctggtgcttc accagggcgt	60
ggtatnttgg ccatggatga gtcaaatgct acctgtggga agcgtttggc ttcaattggg	120
ctagagaaca ccgaagttaa ccgccaagca taccgtactc ttcttggtgc tgctccaggc	180
cttgccagtg acatctctgg tgcattctc tttgaggaaa ctctctacca atccacaact	240
gatggcagga agattgttga tgtacttatt gaacagaaca tcgttcctgg tattaagtt	300
gacaagggtt tgggtaccact ggtggttcc aatgatgaat catggtgcca aggtctggat	360
ggtcttgctc ctgcctcagc agcatactac caacaagggtg cccgattcgc caaatggcgt	420
accggtgtga gcatcccaaa cggctccact gctttggcag ttaaggaagc agcctggggg	480
ctggctcgtt atgctgcaat ttctcaggac aatgggctag ttccaattgt ggagcctgag	540
atcctgcttg acggtgagca tgatattgaa aggacttttg aggtagccca aaaggtgtgg	600
gctgaggttt tctctacct tctgagaaac aatgtcctgt ttgaggggat tctcctcaag	660
cctagcatgg ttaccctcgg agctgagagc aaggacaagg tctctcctca gacggtttct	720
gattacacc ccaagctcct taaaaggaga attccccctg ctgtccctgg aatcatgttt	780
ttgtctggtg gacaactctga ggttgaagca accctgaact tgaatgcat gaaccaatct	840
ccaaaccat ggcatgtgct gttctcgttt gcaagagctc tccaaaatac cgccttgaag	900
acatgggggg gtcgcgcgga gaacgtgaag gcagcacaag atgcactcct tttcctgct	960
aagagcaact cactggctca gcttgggaag tacaatggtg atggtgaatc tgaggaggcc	1020
aagaaggagt tgttcgtcaa aggatactcc tatta	1056

<210> SEQ ID NO 48  
 <211> LENGTH: 1056  
 <212> TYPE: DNA  
 <213> ORGANISM: Lotus japonicus

<400> SEQUENCE: 48

gctggttcct atgctgatga gcttgtaag actgcgaaaa ctggtgcttc accagggcgt	60
ggcattttgg ccatggatga gtccaatgct acctgtggga agcgtttggc ttcaattggg	120
ctagagaaca ccgaagttaa ccgccaagca tggcgtactc ttcttggtgc tgctcctggc	180
cttggtcagt acgtctctgg ggccattctc tttgaagaaa ctctctacca atccacaacc	240
gatggcagga agattgttga tgttcttatt gagcaaaaaa tcgttccggg tattaagtt	300
gacaagggtt tgggtccctt ggtggttcc aatgatgagt catggtgtca aggtctggat	360
ggtcttgctc ctgcacagc tgcatactac cagcaagggtg cccgattcgc caaatggcgt	420
actggtgtga gcatcccaaa cggctccact gctttggcag ttaaggaagc agcttggggg	480
ctggctcgtt atgctgcaat tgctcaggac aatgggctag tccaattgt ggagcctgag	540
atcctgcttg atggtgaaca tggattgaa aggacttttg aagtagccca aaaggtttgg	600
gctgaggttt tctctacct tctgagaaac aatgtctgt ttgaggggat tctcctcaag	660
cctagcatgg ttaccctcgg agctgagagc aaggataagg tctctcctca gcaagtttct	720



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gattacaccc tcaagctcct tcagaggaga attccccag ctgtccctgg aatcatgttt 780
ttgtcaggag gacaatctga ggttgaagca accctgaact tgaatgccat gaaccaatct 840
ccaaacccat ggcattgttc attctcattt gccagagctc tccaaaacac cgccctgaag 900
acatgggggg gccgcgcaga gaatgtgaag gcagcacaag atgcactcct tttccgcgct 960
aagagcaact cattggctca gcttggaaag taaactgggtg atggtgaatc tgaggaagcc 1020
aagaaggagt tgttcgtcaa aggctactcc tatta 1056

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<210> SEQ ID NO 49
<211> LENGTH: 1062
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

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<400> SEQUENCE: 49

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gccgcgccgg tctctacgc cgaagagctc gtctccaccg cgaaatctgt tgcttcccca 60
gggcgtggtg tctctgcaat tgatgagtcg aatgccacat gcgaaagag attagcatcc 120
attggtttgg acaacacaga agttaaccgc caggcttaca ggcagctttt actgaccact 180
gctggtcttg gtgaatatat tctctggtct atcctttttg aggaaactct ttatcagtca 240
accactgatg gtaagaagtt tgttgactgc ttgaaggatc agaatatcat gcccggtatc 300
aaggtcgaca agggcttggg tccattgcct gggccaaca atgaatcttg gtgccaaggc 360
ctagatggtt tggcttcaag gtgtgctgag tactacaagc agggggcagc cttcgctaag 420
tggcggactg ttgtagcat cccttggtgt ccctcagcat tagcagtaa ggaagcggca 480
tggggacttg ctcgatatgc tgccattgct caggacaatg gcttagtgcc aattggtgag 540
ccagagatcc ttcttgatgg tgaccatgcy atcgagagaa ctcttgaagt ggcagagaaa 600
gtgtggtctg aggtattctt ctacctggcc caaaacaatg ttctttttga gggatctctg 660
ctgaaacca gcatgggtgac ccctggagct gaacacaagc agaaggccac tccagaagcc 720
attgcgaagc acacccttac aatgctgagg aggagagtgc cgctgctgt ccctggaatc 780
atgttctctt ctggtgggca atctgaggtg gaggcaaccc tgaacctgaa cgcgatgaac 840
caagaaccaa acccatggca tgtgtccttc tcatacgccc gggctctcca gaactcgggtg 900
ctgaagacat ggcagggggc ccccgagAAC gtggaggcag cgcagaagcc actgctgggtc 960
cgtgccaagg cgaactcgct ggctcagctc ggtcgtctaca ccggcgaggg cgagagcgat 1020
gaggccaaga agggaatggt ccagaaggcc tacacttact ga 1062

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<210> SEQ ID NO 50
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

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<400> SEQUENCE: 50

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```

gctggtgcct acgacgatga gcttgtcaag accgcgaaaa ccattgcac accaggaagg 60
ggtatccttg ccatggatga gtcgaacgcg acctgcggtg agaggcttgc gcaattggc 120
cttgagaaca ccgaggccaa ccgccaggct taccggacct tcttgtcac cgcaccgggc 180
ttgggacagt acatctccgg tctatctctc ttcgaggaga ctctgtacca gtcaactgta 240
gatggcaaga agattgtcga catcctcact gagcagaaaa tcgttccagg tatcaaggtc 300
gacaagggtc ttgtgccctt tgctggctcc aacaacgagt catggtgcca aggtctcgac 360

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```

ggccttgect cgcgcgaggc ggcatactac cagcagggcg ctgccttcgc caagtggcgc 420
actgttgtea gcatacccaa cggcccatct gaactcgccg tgaaggaggc tgccctggggc 480
cttgcccgcg acgcccgcct ttctcaggac aacgggctgg tgccgatgtg cgagcctgag 540
atcctcctcg acggtgagca tggcatcgac aggaccttcg aggtggcgca gaaggtgtgg 600
gcgagagcct tcttctacat ggcgagaaac aatgtgatgt tgcagggcat cctcctcaag 660
ccaagcatgg tgacaccocg tgccgagtgc aaggacaggg ccaccocctga gcaagtatct 720
gactacaccc tcaagctcct ccacagaagg atccccctcg ccgtccccgg catcatgttc 780
ttgtcgggtg ggcagtcgga ggtggaggcg acgcagaacc tgaacgcgat gaaccagggg 840
cccaaccocg ggcacgtgtc gttctcgtac gcgagggcgc tgcagaacac gtgcctcaag 900
acgtggggcg ggcagccgga gaacgtgaag gcggcgcagg acgcgctgct cctccgcgcc 960
aaggccaact cgctggcgca gctcggcaag tacaccagcg acggcagagg cgccgagggc 1020
aaggagggca tgttcgtcaa gaactacgtc tactaa 1056

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```

<210> SEQ ID NO 51
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Picea sitchensis

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```

<400> SEQUENCE: 51
gcccgatcgt atgccgagga gcttgttcaa accgcgaaaa ctgttgcatc tcttggtcgt 60
ggtattcttg ccatagatga gtccaatgcc acttgtggga agaggttgc ttccattgga 120
ctgaaaaaca atgaaccaa ccgccaaagca tacagacaac tcttgttgac cacaccagga 180
cttggggaat atatttccgg ttccatcctt ttgaagaaa ccctctacca gtccacaact 240
gatgggagga aatttgttga ttgtttgcgc gacgagaata ttatgcctgg catcaaagt 300
gacaagggtt tagtccatt gccaggatca aacaatgaat cttggtgcca gggctctggat 360
ggattagcct caagatctgc cgagtactac aaacagggtg caagatttgc taaatggcga 420
actgttgtea gcataccaaa cgggcatct gacttagctg tcaaggaaag tgccctggga 480
cttgcacgtt atgctgcat ttctcaggac aatggtcttg tgccattgt ggagccagag 540
attcttctgg atggagacca ttccattgat agaacccttg aagtggcaga gaaagtctgg 600
gctgaagttt tcttctactt ggcagagaaac aatgtgtttt tgcaggggat tttgttaaag 660
cccagtatgg tgactcctgg tgctgagcac aaggagaaag caaccocaca acaggttgca 720
gattacactc ttaaaatgct caagaggagg gtgccaccag ctgttccctgg gattatgttc 780
ttgtctggag gacagtccga ggttgaggca actttgaatt tgaatgcaat gaaccaaagc 840
ccaaatccat ggcagtgttc cttttcatat gcacgagcct tgcagaacac atctctcaag 900
acctggaagg gtctccaga gaatattgaa gcagctcaga gggcacttct tattcgtgcc 960
aaggtaatt ctctggccca gcttggcgca tactccgctg aaggtgaaag tgaggagtcc 1020
aagaagggaa tgtttgtcaa gggatacaca tattaa 1056

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```

<210> SEQ ID NO 52
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Picea sitchensis

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<400> SEQUENCE: 52

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```

gccggggcctt acagcgaaga actcatcaag acggcgaaaa gagtggcgtc tccggggaga      60
ggcatcctgg cgatggacga gtccaacgct acctgcgcca aacggctggc gtccatcggg      120
ctggagaaca cggaggcgaa ccgccaggca tacaggcagc ttctcgtcag cgctcccggc      180
ctgggacagt acatctccgg ctccattctc ttcgaggaga ccctctacca gtccaagacc      240
gacggcaaga agatggtaga tgtcctcgtg cagcaggaca tagtccccgg catcaaagtt      300
gacaagggtt tgggtccttt ggctggctca aacgacgaat cttggtgcca aggcctagac      360
ggcctcgcac cgagggtcgc tgcattattc cagcagggtg cccgcttcgc taaatggcgt      420
accgttgtga gcattcccaa cggcccctct gctctggccg tgaagaagc tgcattgggt      480
ctcgcctcgc acgcggaat tgctcaggac aacggtcttg ttcccatagt ggagccggag      540
atcctgttgg acggagagca cggccttgag aggacttttg aagtagcgt gaaggtttgg      600
gccgaggtgt tcttctactt agctgagaac aacgtgctgt tcgaaggcat tctgctgaag      660
ccgagcatgg ttaccccagg tgcgagtgcc aaggacaggc caagcccaga aactgttgcc      720
caataatact tcaaccttct tcgaagaaga gttccaccag ctgttcctgg tatcatgttc      780
ttgtctgggt ggcaatctga ggtggaggcg acgttgaact tgaacgcgat gaaccaggcg      840
ccgaaccctg ggcacgtatc attctcatac gctcgtgcac tgcaaaatac atgcttaaag      900
acatgggctg gcaggcccga aaacgtggac gcagcccaga agatcctggt ggttcgggca      960
aaggccaact cccttgcaaa gctcggcaaa tactctgctg aaggcgagtc tgcagagtcg     1020
aaggagggaa tggctcgtgaa gggctacact tactaa                                1056

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&lt;210&gt; SEQ ID NO 53

&lt;211&gt; LENGTH: 1056

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Populus trichocarpa

&lt;400&gt; SEQUENCE: 53

```

gccaaactctt aactgaagca gctcgtccaa accgctaaaa ctattgcac acctggctgt      60
ggtatccttg ccatagacga atcaaatgca acctgtggga agaggttggc atctattggc      120
ttggataaca ccgaaaccaa ccgacaagca tacagacaac ttttattgac tactcctagt      180
cttggcgaat acatttcttg tgccattctt ttcgaggaga cactttacca gtctacaact      240
gatgaaaga agttcgtgga ttgcctcgtg gatgagaaca ttgtacctgg catcaaagtt      300
gacaagggtt tagtcccct accaggttca aacaacgagt cttggtgcca aggtttggat      360
ggattggcct caagatctgc tgaatattac aagcaagggt cacgttttgc taagtggagg      420
actgttgta gcattccctg tggcccttct gctctggctg tcaaggaagc tgcattggga      480
cttgcaagat atgctgcaat ttctcaggat aacggtcttg tgcccatagt tgagcctgag      540
attctacttg atggggacca tccaattgac aggacccttg aagttgctga gaaggtctgg      600
tcaggagtct tttactatth ggctgaaaac aatgttgtgt ttgaggcat cctacttaag      660
cctagcatgg taacgccagg ggtgaaacac aaggagaagg catcagcaga taccatagcc      720
aaatatacac ttacgatgct taaaaggaga gtacctcctg cagttcctgg tatcatgttt      780
ttgtctggag ggcaatctga agtgcaagca accctcaacc tcaatgcaat gaaccaaagc      840
cccaaccat ggcattgttc cttctcatat gcacgtgcac tgcagaacac cgtgctcaag      900
acatggcaag gacgccctga taacgtggaa gctgctcaga agtcactttt ggtgcgtgcc      960

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```
aaggctaact ccttggtca gcttgaagg tattctgccc agggtgaaag cgaggaagct 1020
acgaaggga tggtcgtaaa gggctatacc tattga 1056
```

```
<210> SEQ ID NO 54
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Populus trichocarpa
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```
<400> SEQUENCE: 54
```

```
gctggttctt atgctgatga gcttgcaag accgcgaaaa ccattgcatc tcttggtcgt 60
ggtatttttg ccatggacga gtccaatgct acctgtggga aacgtctagc ctcaattggg 120
ctagagaaca ctgaggctaa ccgccaggca taccgaacct ttcttgtagc agtccctggt 180
cttggaatt acgtctctgg tgccatcctt ttgaggaga ctctctacca atccacaact 240
gatggcaaga agatggttga tgttcttgtt gagcagaaga ttgttccctgg tatcaaagtc 300
gacaagggtt tgggtcctct agctggttcc aatgacgagt cgtggtgcc aaggtcttgat 360
ggacttgct cccgctcagc tgcttactac cagcagggtg ctcgtttcgc caaatggcgt 420
actgttgtag gcattcccaa cggccatct gccttggcag tgaaggaggc tgcctggggt 480
cttccccgt atgctgcat ttctcaagac aacggattgg tccctattgt ggagccagaa 540
atcttacttg atggcgagca tggcattgag aggacttttg aagtagccca gaaggtgtgg 600
gctgaggttt tctactacat ggcagagAAC aatgtcatgt ttgagggtat cctcctcaag 660
cctagtatgg tcaactcctg cgctgaatgc aaggacaggg cctcccctga ccaagttgct 720
gaatacacc tcaagctcct ccacaggaga atccccccag ccgtccctgg aatcatgttt 780
ttgtctggtg ggcaatctga ggtcgaagca accctgaacc tcaacgcaat gaaccaatct 840
ccaaacccat ggcaagctgc attctcatat gccagagctc tccagaacac ttgtttgaaa 900
acatggggag gcaggccaga gaacgttcag gatgctcagg aaacacttct catccgtgcc 960
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<210> SEQ ID NO 55
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Populus trichocarpa
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<400> SEQUENCE: 55
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ctagagaaca ccgaggctaa ccgccaggca taccgtacct ttcttgtagc agtccctggc 180
cttggtgatt acgtctctgg tgccatcctt ttgaggaga ctctctacca atccaccact 240
gatggcaaga agatggttga tgttcttgtt gagcaaaaga ttgttcccgg catcaaagtt 300
gacaagggtt tgggtcctct agctggttcc aatgatgagt catggtgcc aaggtcttgat 360
ggactcgct cccgcacagc tgcttactac caacaggag ctcgttttgc caaatggcgt 420
actgttgtag gcattcccaa cggccatct gccttggcag tgaaggaggc tgcctggggt 480
cttccccgt atgctgcat ttctcaagac aatggattgg tcccaattgt ggagccagaa 540
atcttgcttg atggtgagca tggcattgac aggactttcg aagtagccca gaaggtttgg 600
```

- continued

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```

gctgaggttt tcttctacat ggcagagaac aatgtcatgt ttgagggtat tcttctcaag   660
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gagtacacac tcaagctcct tcagaggaga atccccccat ccgtccctgg aatcatgttt   780
ttgtctggtg ggcaatccga ggttgaagca accctgaacc tcaacgcaat gaaccagtct   840
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acatggggag gcaggccaga gaacgtgaat gcagctcagg aagcacttct catccgtgcc   960
aaggccaact ctcttgctca gcttggaag tacaccggtg agggagagtc agatgaagcc  1020
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```

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<210> SEQ ID NO 56
<211> LENGTH: 738
<212> TYPE: DNA
<213> ORGANISM: Zea mays

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<400> SEQUENCE: 56

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tgtggccat  ctgcattagc agtgaaggaa gcagcatggg gacttgctcg atatgctgct   180
attgctcagg ataatggctt agtgccaatt gtggagccag agatccttct tgatggagac   240
catgggatcg aaagaactct tgaggtggca gagaaagtgt ggtctgaggt gttcttctac   300
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gagaacgttg agggggcgca aaaggccctg ctggtgcgcg caaaggccaa ctcgctggca   660
cagctaggtc gctacactgg tgagggtgag agcgacgagg cgaagaaagg catgttcag   720
aagggtaca  cctactaa                               738

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1. A composition for producing a plant body having an improved sugar content, the composition comprising a substance (excluding hydrogen peroxide) for regulating an oxidation-reduction state of a cell.

2. The composition according to claim 1, wherein the substance is glutathione, a polynucleotide encoding  $\gamma$ -glutamyl-cysteine synthetase, or a polynucleotide encoding glutathione-binding plastid type fructose-1,6-bisphosphate aldolase.

3. The composition according to claim 1, wherein the substance is oxidized glutathione.

4. A kit for producing a plant body having an improved sugar content, the kit comprising a substance (excluding hydrogen peroxide) for regulating an oxidation-reduction state of a cell.

5. A method for producing a plant body having an improved sugar content, the method comprising the step of cultivating the plant body by using a substance (excluding hydrogen peroxide) for regulating an oxidation-reduction state of a cell.

6. A plant body obtained by a production method recited in claim 5.

\* \* \* \* \*