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(54) **UTILITY OF SNP MARKERS ASSOCIATED WITH MAJOR SOYBEAN PLANT MATURITY AND GROWTH HABIT GENOMIC REGIONS**

NUTZEN VON SNP-MARKERN IN ZUSAMMENHANG MIT GENOMISCHEN BEREICHEN FÜR REIFE UND WACHSTUMSGEWOHNHEIT WICHTIGER SOJABOHNENARTEN

UTILITÉ DE MARQUEURS SNP ASSOCIÉS AVEC DES RÉGIONS MAJEURES DU PORT ET DE LA MATURITÉ DE PLANTES DE SOJA

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Description

Field of the Invention

[0001] The invention includes methods for screening plants and seeds from the genus *Glycine* with markers associated with genomic regions that are related to the plant maturity and plant growth habit of *Glycine* plants.

Background of the Invention

[0002] The soybean, *Glycine max* (L.) Merril, is a major economic crop worldwide and is a primary source of vegetable oil and protein (Sinclair and Backman, Compendium of Soybean Diseases, 3rd Ed. APS Press, St. Paul, MN, p. 106. (1989)). The growing demand for low cholesterol and high fiber diets has also increased importance of soybean as a health food.

[0003] Soybean varieties grown in the United States have a narrow genetic base. Six introductions, 'Mandarin,' 'Manchu,' 'mandarin' (Ottawa), "Richland,' 'AK' (Harrow), and 'Mukden,' contributed nearly 70% of the germplasm represented in 136 cultivar releases. The genetic base of cultivated soybean could be widened through the use of exotic species. In addition, exotic species may possess such key traits as disease and stress resistance. At present, the traits of many exotic species are inaccessible in part due to limitations with crossing soybean plants from extremely different maturity groups. Most soybean variety development crosses are made between parents within 10 maturity days of each other. If the parents differ greatly in maturity, the progeny plants segregate widely for maturity. In order for breeders to obtain and select for soybean plants of the desired maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive.

[0004] Plant maturity and yield are closely associated in soybean. An increase of one day in maturity may be equivalent to a ~0.7 bu/A increase in yield. Conversely, a decrease in maturity is often penalized with a ~0.7 bu/A decrease in yield. The correlation of plant maturity and yield confounds the evaluation of potential quantitative trail loci (QTLs) and candidate genes associated with yield. The ability to genetically fix maturity within a soybean plant would be helpful and assist in elucidating traits associated with yield.

[0005] Soybean plants are short day plants, therefore flowering is initiated by short days due to a decrease in photoperiod (Garner & Allard, J. Agric. Res. 18, 553-606 (1920)). Consequently, photoperiod (day length) and temperature response of the soybean plant determine areas of plant adaptation. Due to photoperiod sensitivity, soybean genotypes are often grown in narrow zones of latitude to optimize yield. Northern soybean varieties, in contrast to Southern varieties, initiate flowering with longer days. Northern varieties planted south of their adaptation zone exhibit accelerated flowering, limited plant growth and reduced yield. Southern soybean varieties planted north of their adaptation zone will have delayed flowering with a potential for frost damage that may reduce yield.

[0006] Soybean plant varieties are classified based on bands of adaptation that are determined by latitude and day length. In North America, soybeans are categorized into 13 maturity groups with the designations ranging from maturity groups 000, 00, 0, and I through X. The earliest maturity group 000 soybeans are adapted to the north (45° latitude), while the latest maturity group X soybeans are adapted to regions near the equator. Soybean plants in maturity groups 000 to IV have indeterminate plant structure, while soybean plants in maturity groups V through X have determinate plant structure. Determinate varieties cease vegetative growth after the main stem terminates in a cluster of mature pods. Indeterminate varieties develop leaves and flowers simultaneously throughout a portion of their reproductive period, with one to three pods at the terminal apex. Early maturity varieties (000 to III) are adapted to northern latitudes with the maturity designation increasing in southern latitudes. The maturity group is determined by the maturity date. Plants are considered mature when 95% of the pods have reached their mature color. The maturity date is typically described as a measurement of days after August 31st in the northern hemisphere.

[0007] US 2006/288444 suggests the use of SNPs to identify soy bean plants with a certain trait value for maturity.

[0008] There is a need in the art of plant breeding to identify genomic regions associated with the maturity group of a soybean plant. At present, soybean breeders are limited to crossing plants within similar maturity groups. In addition, a number of traits, like oil levels, are influenced by latitude and maturity growing region. Therefore, there is a need for a rapid, cost-efficient method to pre-select for maturity group of soybean plants. The present invention includes a method for screening and selecting a soybean plant for a preferred plant maturity using single nucleotide polymorphism (SNP) technology.

Brief Description of Figures

[0009]

Figure 1: Influence of maturity group on percent oil in commercial soybeans.

Figure 2: Correlation of stearidonic acid (SDA) levels and GLA (gamma-linolenic acid) and latitude for mature soybean seeds. The soybean plants are transgenic and engineered to produce SDA and GLA.
Figure 3: Correlation of stearidonic acid (SDA) levels and latitude for mature soybean seeds over three trials. The soybean plants are transgenic and engineered to produce SDA.

Summary of the Invention

[0010] The present invention relates to a method of screening and selecting a soybean plant or soybean seed for maturity group association comprising:

(a) assaying genomic nucleic acids of said soybean plant or soybean seed for the presence of a genomic maturity marker genetically linked to a genomic region, wherein said genomic region is associated with a plant maturity group, said genomic maturity marker is within 10 cM, or within 10,000 kilobases of any of SEQ ID NOs: 143-213;
(b) determining whether said genomic maturity marker is homozygous or heterozygous;
(c) and selecting said soybean plant or seed based on said determination.

Brief Description of Nucleic Acid Sequences

[0011]

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Definitions

[0012] A "maturity group value" can be any indicative number, symbol, or combination of both that provides an indication of when a plant will mature.

[0013] A "dominant maturity allele" is an allele that, when present either in single copy (heterozygous) or two copies (homozygous), affects the maturity of the plant.

[0014] A "recessive maturity allele" is an allele that, when present in one copy (heterozygous), does not affect the maturity of a plant.

[0015] As used herein, determinate growth habit refers to ceasing of vegetative growth after the main stem terminates in a cluster of mature pods.

[0016] As used herein, indeterminate growth habit refers to the development of leaves and flowers simultaneously throughout a portion of their reproductive period, with one to three pods at the terminal apex.

[0017] As used herein, an allelic combination is the combination of alleles present at more than one characterized location or loci. An example of an allelic combination is allelic combination 10, which is homozygous dominant at maturity genomic region 1; homozygous recessive at maturity genomic region 2; and homozygous dominant at maturity genomic region 3.

[0018] As used herein, "line" refers to a group of individual plants from the similar parentage with similar traits. An "elite line" is any line that has resulted from breeding and selection for superior agronomic performance. Additionally, an elite line is sufficiently homogenous and homozygous to be used for commercial production. Elite lines may be used in the further breeding efforts to develop new elite lines. An elite plant is any plant from an elite line.

[0019] As used herein, "a trait" refers to an observable and/or measurable characteristic of an organism, such as a trait of a plant, *for example,* tolerance to an herbicide, insect and microbe. A trait can be conventional and transgenic. Non-limiting examples of traits include herbicide tolerance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance, altered oils production, high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistant, increased digestibility, industrial enzymes, pharmaceutical proteins, peptides and small molecules, improved processing traits, improved flavor, nitrogen fixation, hybrid seed production, reduced allergenicity, biopolymers, and biofuels.

[0020] As used herein, "a transgene" refers to a foreign gene that is placed into an organism by the process of plant transformation. In certain aspects, a soybean plant provided by the invention may comprise one or more transgene(s).

[0021] As used herein, "altered" means increased or decreased at maturity. In this aspect, a mature seed as defined by a seed that is harvested in the field for commercial agricultural practices, such as sale for feed. In an aspect, a soybean plants are selected for preferred geographies for expression of at least one phenotypic trait. The phenotypic trait includes altered levels of a substance or a molecule, such as proteins, oils, or gamma linolenic acid. "Altered" can include any relative increase or decrease of function or production of a gene product of interest, in an aspect up to and including complete elimination of function or production of that gene product. When levels of a gene product are compared, such a comparison is preferably carried out between organisms with a similar genetic background. Preferably, a similar genetic background is a background where the organisms being compared share 50% or greater, more preferably 75% or greater, and, even more preferably 90% or greater sequence identity of nuclear genetic material. In another aspect, a similar genetic background is a background where the plants are isogenic except for one or more of the disclosed markers.

[0022] As used herein, a "cultivar" is a race or variety of a plant that has been created or selected intentionally and maintained through cultivation.

[0023] As used herein, the term "tissue culture" indicates a composition comprising isolated cells of the same or a different type or a collection of such cells organized into parts of a plant.

Detailed Description of the Invention

[0024] Determination of the maturity group value of a soybean plant or seed is important in selecting where a soybean plant should be grown. An aspect of the present invention provides for a method of establishing where a plant or seed should be grown. A suitable region of a soybean plant or seed can be established. Establishment of a region can include selection of a suitable maturity belt region. Maturity belts range in the United States from 000 in the extreme northern U.S. to VIII in the southern Gulf Coast states. The present invention can also be used to determine other maturity belts including IX and X. The present invention can further be utilized to determine whether a plant is suitable for one, two, or more maturity belts or regions.

[0025] A suitable geographic region can be selected using a method of the present invention. In addition to maturity belts, other geographic regions that can be selected include maturity group 0 regions, such as and without limitation, Western Maine, North Dakota, Central Montana, Northwestern Oregon; maturity group 1 regions, such as and without limitation, northern Wisconsin, South Dakota; maturity group 2 regions, such as and without limitation, Vermont, Southern Massachusetts, Northern Connecticut, New York, Central Florida, Michigan, Northern Illinois, Southern Wisconsin, Iowa, Nebraska, Colorado, Central California; maturity group 3 regions, such as and without limitation, Western New Hampshire, Pennsylvania, Ohio, Indiana, Southern Illinois, Northern Missouri, Kansas, Southeast Wyoming, Colorado; maturity group 4 regions, such as and without limitation, Maryland, Northern Virginia, Kentucky, Western West Virginia, Central Missouri, Texas, Western Oklahoma; maturity group 5 regions, such as and without limitation, Central Virginia, North Carolina, Central and Western North Carolina, Mississippi, Louisiana, Tennessee; maturity group 6 regions, such as and without limitation, North Carolina, Eastern South Carolina; and maturity group 7 regions, such as and without limitation, Georgia, and Alabama. In another aspect, a disclosed seed can be sent to a geographic region that is desirable to optimize a trait, such as yield.

[0026] The present invention also provides methods of selecting a suitable geographic region and methods for determining the maturity group of a soybean plant or seed by genotypic analysis. One aspect of the present invention includes a method of establishing where a soybean plant should be grown by obtaining DNA from the soybean plant; and determining if an allele within maturity genomic region 1 is homozygous or heterozygous using marker SEQ ID NO: 151.

[0027] The present invention allows the determination of allelic combinations. Allelic combinations can be any combination of alleles. In one aspect, it can be a combination of 2, 3, 4, 5, 6, 7, or 8 pairs of alleles that occupy a genetic locus. In another aspect, the alleles can be located within 2, 3, 4, 5, 6, 7, or 8 or more maturity genomic regions. Such maturity regions can be selected from maturity genomic region 1, maturity genomic region 2, maturity genomic region 3, maturity genomic region 4, maturity genomic region 5, maturity genomic region 6, maturity genomic region 7, or maturity genomic region 8.

[0028] Alleles at any combination of maturity regions can be determined individually or in combination. One illustrative combination is a combination of more than one pair of alleles at maturity regions 1, 2, and 3. Another illustrative combination is a combination of more than one pair of alleles at maturity regions 1 and 2. "Allelic combinations" is intended to include, without limitation, any of homozygous dominant, homozygous recessive, and heterozygous alternatives at a particular locus.

[0029] Determination of an allele or the combination of alleles at a locus or loci can be carried out by any appropriate methodology. In an aspect, various assays can be used, such as a Taq-Man® assay, Real Time PCR, and nucleic acid sequencing, and simple sequence repeat mapping, to detect the genotype. In an aspect of the present invention, the assay includes a disclosed nucleic acid molecule. Nucleic acids include deoxynucleic acids (DNA) and ribonucleic acids (RNA) and functionally equivalent analogues thereof.

[0030] Nucleic acids for use in the present invention can be obtained from a plant, such as from a plant part which

includes a leaf, vascular tissue, flower, pod, seed, root, stem, or a portion of any.

[0031] In one aspect, nucleic acids are obtained from a plant or plant part using a non-destructive method. In an aspect, the plant part is a seed. In an aspect, the nucleic acids are obtained from a seed in a non-destructive manner, which provides for a seed that is viable. For example, DNA can be obtained from a seed by chipping the seed with a sharp knife at a part furthest away from the 'eye' or by pricking carefully with a needle to puncture the seed. Any method that will obtain DNA for analysis or allow *in situ* analysis of the DNA can be used provided that the plant or plant part retains the ability to grow. If DNA is taken from a seed and the seed is still viable, the method can be considered non-destructive. Exemplary methods to sample seeds without affecting the germination viability of the seeds are detailed in US Patent Application Publication 2006/0042527. In an aspect, seeds are sampled by feeding the seeds individually to a sampling station, removing a sample from the seed in the sampling station, conveying the sample to a compartment in a sample tray and conveying the seed to a corresponding compartment in a seed tray.

[0032] In an aspect, the maturity genomic region associated with plant maturity and plant growth habit is introduced or selected within the genus *Glycine.* The genus *Glycine* includes the wild perennial soybeans and have a wide array of genetic diversity. For example, the cultivated soybean (*Glycine max* (L.) Merr.) and its wild annual progenitor (*Glycine soja* (Sieb. and Zucc.)) belong to the subgenus *Soja,* contain 2n = 40 chromosomes, are cross-compatible, usually produce vigorous fertile F_1 hybrids, and carry similar genomes. Crosses between cultivated *Glycine* species and wild perennial *Glycine* species have variable success among accessions. The present invention further provides that the selected plant is from the group consisting of members of the genus *Glycine,* more specifically from the group consisting of *Glycine arenaria, Glycine argyrea, Glycine canescens, Glycine clandestine, Glycine curvata, Glycine cyrtoloba, Glycine falcate, Glycine latifolia, Glycine latrobeana, Glycine max, Glycine microphylla, Glycine pescadrensis, Glycine pindanica, Glycine rubiginosa, Glycine soja, Glycine sp., Glycine stenophita, Glycine tabacina,* and *Glycine tomentella.* In an aspect the plant is selected from an elite *Glycine max* line.

[0033] The present invention also provides a soybean plant selected for a desired plant maturity by screening for a maturity marker in the soybean plant or seed, the selection comprising assaying genomic nucleic acids for the presence of a marker molecule that is genetically linked to a genomic region associated with a plant maturity in the soybean plant, where the genomic region is also located on a linkage group associated with a soybean plant of a preferred plant maturity. The disclosed methods include determining if a locus contains a polymorphism, or is homozygous or heterozygous at a maturity region selected from maturity genomic region 1, maturity genomic region 2, maturity genomic region 3, maturity genomic region 4, maturity genomic region 5, maturity genomic region 6, maturity genomic region 7, and/or maturity genomic region 8 by detecting a polymorphism within a nucleic acid molecule comprising a sequence or fragment thereof selected from the group consisting of SEQ ID NOs: 143-174, or complements thereof. The present invention includes the identification of alleles at eight maturity group regions. These regions are termed maturity genomic regions 1 through 8.

[0034] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 1 can be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 or more genetic markers selected from the group consisting of NS0093385, NS0093976, NS0096829, NS0097798, NS0098982, NS00995929, NS0099746, NS0103749, NS0123747, NS0124601, NS0125408, NS0128378, and NS0135390. SNP marker DNA sequences for region 1 include those presented as SEQ ID NO: 143 through SEQ ID NO: 155 and can be amplified using the primers indicated as SEQ ID NO: 1 through SEQ ID NO: 26 with probes indicated as SEQ ID NO: 214 through SEQ ID NO: 239. In another aspect, a maturity genomic region 1 is a region associated with SEQ ID NOs: 143-149, 154-155. In another aspect, a maturity genomic region 1 is a region associated with SEQ ID NO: 149 or SEQ ID NO: 151 or both. In an aspect, maturity genomic region 1 can span 1 centiMorgan (cM), 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 149 or SEQ ID NO: 151.

[0035] An aspect of the method of the present invention includes a method of determining if a soybean seed will grow into a soybean plant having a maturity group of III-VI by determining a homozygous or heterozygous marker within the soybean seed using a marker with the nucleic acid sequence of SEQ ID NO: 151. In a preferred aspect, the homozygous marker can be recessive or dominant. In another preferred aspect, the maturity of the plant is delayed where the marker is homozygous dominant.

[0036] Another aspect of the method of the present invention includes a method of determining if a soybean seed will grow into a soybean plant having a maturity group between 0.0 - III.0 comprising determining if an 11-basepair insertion within the nucleic acid sequence of SEQ ID NO: 149 exists in the soybean seed.

[0037] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 2 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, or 6 or more genetic markers including those selected from the group consisting of NS0118907, NS0122182, NS0126989, NS097952, NS0123506 and NS0095677. SNP marker DNA sequences for region 2 include those presented as SEQ ID NO: 156 through SEQ ID NO: 161 and can be amplified using the primers indicated as SEQ ID NO: 27 through SEQ ID NO: 38 with probes indicated as SEQ ID NO: 240 through SEQ ID NO: 251. In another aspect, a maturity genomic region 2 is a region associated with SEQ ID NO: 158. In another aspect, a maturity genomic region 2 is a region associated with SEQ ID NOs: 156-161. In an aspect, maturity genomic region 2 can span 1 cM, 5 cM, 10 cM, 15cM, 20 cM, or 30 cM either side of SEQ ID NO: 158.

[0038] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 3 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 or more genetic markers including those selected from the group consisting of NS0098853, NS0092561, NS0093197, NS0094891, NS0096225, NS0103853, NS0113929, NS0115535, NS0121511, NS0136544, NS0119569, NS0123708, and NS0114317. SNP marker DNA sequences for region 3 including those presented as SEQ ID NO: 162 through SEQ ID NO: 174 and can be amplified using the primers indicated as SEQ ID NO: 39 through SEQ ID NO: 64 with probes indicated as SEQ ID NO: 252 through SEQ ID NO: 277. In another aspect, a maturity genomic region 3 is a region associated with SEQ ID NOs: 164, 167, 171-174. In another aspect, a maturity genomic region 3 is a region associated with SEQ ID NO: 169. In an aspect, maturity genomic region 3 can span 1 cM, 5 cM, 10 cM, 15cM, 20 cM, or 30 cM either side of SEQ ID NO: 169.

[0039] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 4 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, or 6 or more genetic markers including those selected from the group consisting of NS0092743, NS0098176, NS0100078, NS0137415, NS0095530, and NS0129004. SNP marker DNA sequences for region 4 are presented as SEQ ID NO: 175 through SEQ ID NO: 180 and can be amplified using the primers indicated as SEQ ID NO: 65 through SEQ ID NO: 76 with probes indicated as SEQ ID NO: 278-289. In another aspect, a maturity genomic region 4 is a region associated with SEQ ID NO: 178. In an aspect, maturity genomic region 4 can span 1 cM, 5 cM, 10 cM, 15cM, 20 cM, or 30 cM either side of SEQ ID NO: 178. An aspect of the method of the present invention includes a method of detecting maturity genomic region 4 by detecting an allele using a marker selected from any of SEQ ID NO: 175-180.

[0040] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 5 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, or 9 or more genetic markers including those selected from the group consisting of NS0120015, NSO113878, NS0101863, NS0115066, NS0123168, NS0119165, NS0123724, NS0103446, and NS0099024. SNP marker DNA sequences for region 5 including those presented as SEQ ID NO: 181 through SEQ ID NO: 189 and can be amplified using the primers indicated as SEQ ID NO: 77 through SEQ ID NO: 94 with probes indicated as SEQ ID NO: 290 through SEQ ID NO: 307. In another aspect, a maturity genomic region 5 is a region associated with SEQ ID NO: 187. In an aspect, maturity genomic region 5 can span 1 cM, 5 cM, 10 cM, 15cM, 20 cM, or 30 cM either side of SEQ ID NO: 187. An aspect of the method of the present invention includes a method of detecting maturity genomic region 5 by detecting an allele using a marker selected from any of SEQ ID NO: 181-189.

[0041] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 6 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, or 7 or more genetic markers including those selected from the group consisting of NS0116125, NS0125770, NS0103755, NS0125713, NS0124590, NS0119281, and NS0102717. SNP marker DNA sequences for region 6 including those presented as SEQ ID NO: 190 through SEQ ID NO: 196 and can be amplified using the primers indicated as SEQ ID NO: 95 through SEQ ID NO: 108 with probes indicated as SEQ ID NO: 308 through SEQ ID NO: 321. In another aspect, a maturity genomic region 6 is a region associated with SEQ ID NO: 192. In an aspect, maturity genomic region 6 can span 1 cM, 5 cM, 10 cM, 15cM, 20 cM, or 30 cM either side of SEQ ID NO: 192. An aspect of the method of the present invention includes a method of detecting maturity genomic region 6 by detecting an allele using a marker selected from any of SEQ ID NO: 190-196.

[0042] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 7 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, or 7 or more genetic markers including those selected from the group consisting of NS0095211, NS0099531, NS0099417, NS0097307, NS0103004, NS0102630, and NS0102915. SNP DNA sequences for region 7 including those presented as SEQ ID NO: 197 through SEQ ID NO: 203 and can be amplified using the primers indicated as SEQ ID NO: 109 through SEQ ID NO: 122 with probes indicated as SEQ ID NO: 322 through SEQ ID NO: 335. In another aspect, a maturity genomic region 7 is a region associated with SEQ ID NO: 202. In an aspect, maturity genomic region 7 can span 1 cM, 5 cM, 10 cM, 15cM, 20 cM, or 30 cM either side of SEQ ID NO: 202. An aspect of the method of the present invention includes a method of detecting maturity genomic region 7 by detecting an allele using a marker selected from any of SEQ ID NO: 197-203.

[0043] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 8 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more genetic markers including those selected from the group consisting of N0102362, NS0100652, NS0117716, NS0119574, NS0127728, NS0099639, NS0103255, NS0119106, NS0101020, and NS0101779. SNP DNA sequences for region 8 including those presented as SEQ ID NO: 204 through SEQ ID NO: 213 and can be amplified using the primers indicated as SEQ ID NO: 123 through SEQ ID NO: 142 with probes indicated as SEQ ID NO: 336 through SEQ ID NO: 355. In another aspect, a maturity genomic region 8 is a region associated with SEQ ID NO: 204. In an aspect, maturity genomic region 8 can span 1 cM, 5 cM, 10 cM, 15cM, 20 cM, or 30 cM either side of SEQ ID NO: 204. An aspect of the method of the present invention includes a method of detecting maturity genomic region 8 by detecting an allele using a marker selected from any of SEQ ID NO: 204-213.

[0044] The disclosed nucleic acid molecules or fragments thereof are capable of specifically hybridizing to other nucleic acid molecules, also included in the present invention, under certain circumstances. In an aspect, the nucleic acid molecules may contain any of SEQ ID NO: 143-213, complements thereof and fragments of any. In another aspect, the

nucleic acid molecules include nucleic acid molecules that hybidize, for example, under high or low stringency, substantially homologous sequences, or that have both to .these molecules. As used herein, two nucleic acid molecules are capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook et al., In: Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989)), and by Haymes et al., In: Nucleic Acid Hybridization, A Practical Approach, IRL Press, Washington, DC (1985).

[0045] Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. In order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

[0046] As used herein, a substantially homologous sequence is a nucleic acid sequence that will specifically hybridize to the complement of the nucleic acid sequence to which it is being compared under high stringency conditions. The disclosed nucleic-acid probes and primers can hybridize under stringent conditions to a target DNA sequence. The term "stringent hybridization conditions" is defined as conditions under which a probe or primer hybridizes specifically with a target sequence(s) and not with non-target sequences, as can be determined empirically. The term "stringent conditions" is functionally defined with regard to the hybridization of a nucleic-acid probe to a target nucleic acid (i.e., to a particular nucleic-acid sequence of interest) by the specific hybridization procedure discussed in Sambrook *et al.*, 1989, at 9.52-9.55. See also, Sambrook *et al.*, 1989 at 9.47-9.52, 9.56-9.58; Kanehisa, Nucl. Acids Res. 12:203-213, 1984; and Wetmur and Davidson, J. Mol. Biol. 31:349-370, 1968. Appropriate stringency conditions that promote DNA hybridization are, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45° C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y., 1989, 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

[0047] For example, hybridization using DNA or RNA probes or primers can be performed at 65°C in 6x SSC, 0.5% SDS, 5x Denhardt's, 100 μg/mL nonspecific DNA (e.g., sonicated salmon sperm DNA) with washing at 0.5x SSC, 0.5% SDS at 65°C, for high stringency.

[0048] It is contemplated that lower stringency hybridization conditions such as lower hybridization and/or washing temperatures can be used to identify related sequences having a lower degree of sequence similarity if specificity of binding of the probe or primer to target sequence(s) is preserved. Accordingly, the disclosed nucleotide sequences can be used for their ability to selectively form duplex molecules with complementary stretches of DNA, RNA, or cDNA fragments. Detection of DNA segments via hybridization is well-known to those of skill in the art, and thus depending on the application envisioned, one will desire to employ varying hybridization conditions to achieve varying degrees of selectivity of probe towards target sequence and the method of choice will depend on the desired results.

[0049] As used herein, an agent, be it a naturally occurring molecule or otherwise may be "substantially purified", if desired, referring to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state. The agents will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

[0050] The agents may also be recombinant. As used herein, the term recombinant means any agent (e.g. DNA, peptide), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

[0051] The agents may be labeled with reagents that facilitate detection of the agent (*e.g.* fluorescent labels (Prober et al., Science 238:336-340 (1987); European Patent No. 144914), chemical labels (U.S. Patent no. 4,582,789; U.S. Patent No. 4,563,417), modified bases (European Patent No. 119448)).

[0052] In an aspect, an agent will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ

ID NO: 143 through SEQ ID NO: 213 or complements thereof or fragments of either under moderately stringent conditions, for example at about 2.0 x SSC and about 65°C. In an aspect, a nucleic acid will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complements or fragments of either under high stringency conditions.

[0053] Agents include genetic markers. Examples of such markers include nucleic acid molecules comprising nucleic acid sequences selected from the group consisting of SEQ ID NOs: 143-213. Examples of public marker databases include, for example: Soybase, an Agricultural Research Service, and United States Department of Agriculture. Other genetic markers are disclosed within.

[0054] Agents include fragment nucleic acid molecules. Fragments can contain significant portions of, or indeed most of, SEQ ID NOs: 143-213. In an aspect, the fragments are between 100 and 200 consecutive residues, 150 and 300 consecutive residues, 50 and 150 consecutive residues, or 20 and 50 consecutive residues long of a nucleic molecule. In another aspect, the fragment comprises at least 50, 100, 200, 300, 400, or 500 consecutive residues of SEQ ID NOs: 143-213. In an aspect, a fragment nucleic acid molecule is capable of selectively hybridizing to SEQ ID NOs: 143-213.

[0055] In one aspect, a preferred marker nucleic acid molecule has the nucleic acid sequence set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complements thereof or fragments of either. In another aspect, a preferred marker nucleic acid molecule shares between 80% and 100% or 90% and 100% sequence identity with the nucleic acid sequence set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complement thereof or fragments of either. In a further aspect, a preferred marker nucleic acid molecule shares between 95% and 100% sequence identity with the sequence set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complement thereof or fragments of either. In an aspect, a preferred marker nucleic acid molecule shares between 98% and 100% sequence identity with the nucleic acid sequence set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complement thereof or fragments of either.

[0056] The percent identity is preferably determined using the "Best Fit" or "Gap" program of the Sequence Analysis Software Package™ (Version 10; Genetics Computer Group, Inc., University of Wisconsin Biotechnology Center, Madison, WI). "Gap" utilizes the algorithm of Needleman and Wunsch to find the alignment of two sequences that maximizes the number of matches and minimizes the number of gaps. "BestFit" performs an optimal alignment of the best segment of similarity between two sequences and inserts gaps to maximize the number of matches using the local homology algorithm of Smith and Waterman. The percent identity calculations may also be performed using the Megalign program of the LASERGENE bioinformatics computing suite (default parameters, DNASTAR Inc., Madison, Wisconsin). The percent identity is most preferably determined using the "Best Fit" program using default parameters.

[0057] The present invention further discloses one or more single nucleotide polymorphism (SNP) markers. The detection of polymorphic sites in a sample of DNA, RNA, or cDNA may be facilitated through the use of nucleic acid amplification methods. Such methods include those that specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

[0058] A method of achieving such amplification employs the polymerase chain reaction (PCR) (Mullis et al. 1986 Cold Spring Harbor Symp. Quant. Biol. 51:263-273; European Patent Nos. 50,424; 84,796; 258,017; 237,362; 201,184; U.S. Patent Nos. 4,683,202; 4,582,788; and 4,683,194), using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

[0059] Alleles that associate with plant maturity can be determined based on linkage analysis of plants and nucleic acid molecules. A number of molecular genetic maps of *Glycine* have been reported (Mansur et al., Crop Sci. 36: 1327-1336 (1996); Shoemaker et al., Genetics 144: 329-338 (1996); Shoemaker et al., Crop Science 32: 1091-1098 (1992), Shoemaker et al., Crop Science 35: 436-446 (1995); Tinley and Rafalski, J. Cell Biochem. Suppl. 14E: 291 (1990); Cregan et al., Crop Science 39:1464-1490 (1999)). *Glycine max, Glycine soja* and *Glycine max x. Glycine soja* share linkage groups (Shoemaker et al., Genetics 144: 329-338 (1996)). A linkage group (LG) is a set of genes that tend to be inherited together from generation to generation. As used herein, reference to the linkage groups (LG), D1b; C2; O; L; and I and of *Glycine max* refers to the linkage group that corresponds to linkage groups, D1b, C2, O, L; and I from the genetic map of *Glycine max* (Mansur et al., Crop Science. 36: 1327-1336 (1996)); Cregan et al., Crop Science 39: 1464-1490 (1999), and Soybase, Agricultural Research Service, United States Department of Agriculture.

[0060] Genome-wide surveys revealed SNP markers associated with maturity genomic region 1 are located on linkage group (LG) C2, maturity genomic region 2 is located on LG O, maturity genomic region 3 is located on LG L, maturity genomic region 4 is located on LG I, maturity genomic region 5 is located on LG L, maturity genomic region 6 is located on LG D1b+W, maturity genomic region 7 is located on LG G, and maturity genomic region 8 is located on LG M.

[0061] In an aspect, the present invention can be used to identify additional markers associated with maturity genomic regions 1-8. Disclosed is a maturity marker within 1 cM, 5 cM, 10 cM, 15 cM, or 30 cM of SEQ ID NO: 143 - 213. Similarly, one or more markers mapped within 1, 5, 10, 20 and 30 cM or less from the marker molecules can be used for the selection or introgression of the region associated with maturity and/or plant growth habit. The present invention includes a maturity marker that is linked with SEQ ID NO: 143 - 213 and delays maturity. The present invention includes a substantially purified nucleic acid molecule comprising a maturity marker within 5 kilobases, 10 kilobases, 20 kilobases,

30 kilobases, 100 kilobases, 500 kilobases, 1,000 kilobases, 10,000 kilobases, 25,000 kilobases, or 50,000 kilobases of a marker selected from the group consisting of SEQ ID NO: 143 - 213. The present invention includes a maturity marker within 5 kilobases, 10 kilobases, 20 kilobases, 30 kilobases, 100 kilobases, 500 kilobases, 1,000 kilobases, 10,000 kilobases, 25,000 kilobases, or 50,000 kilobases of any of SEQ ID NO: 143 - 213 that cosegregates with any of SEQ ID NO: 143 - 213. Similarly, one or more markers mapped within 5 kilobases, 10 kilobases, 20 kilobases, 30 kilobases, 100 kilobases, 500 kilobases, 1,000 kilobases, 10,000 kilobases, 25,000 kilobases, or 50,000 kilobases or less from the marker molecules can be used for the selection or introgression of the region associated with maturity and/or plant growth habit.

[0062] A maturity genomic region is a physical region of a plant chromosome that has been associated with determining a plant's maturity date. A plant is considered mature when 95% of its pods have reached their mature color. In one aspect, the maturity date of a plant is the number of days after August 31st in the northern hemisphere. Alleles of maturity genomic regions 1-8 can influence the maturity date of a plant.

[0063] In one aspect, the maturity date of a plant can determine the maturity group of a plant. Herein, relative maturity refers to a soybean plant maturity group subdividing a maturity group into tenths, *for example* III.5. Relative maturity provides a more exact description of plant maturity. The number following the decimal point refers to the relative earliness or lateness with a maturity group*, for example,* IV.2 is an early group IV variety and IV.9 is a late group IV.

[0064] In another aspect, maturity group can be determined by reference to a commercialized strain for a maturity group. For example, a commercialized strain with a known maturity group is grown in an experiment with a new soybean line and the relative maturity of the new soybean line is ascertained by counting the number of days after Aug 31 st and comparing to the commercialized strain. Maturity group refers to an industry division of groups of varieties based on a range in latitudes which the plant is best adapted and most productive. Soybean varieties are classified into 13 recognized maturity groups with the designations ranging from maturity groups 000, 00, 0, and I through X, where 000 represents the earliest maturing variety and X represents the latest maturing variety. The maturity groups have corresponding maturity belts.

[0065] Soybean plants in maturity groups 000 to IV have an indeterminate plant habit, while soybean plants in maturity groups V through X have a determinate plant habit. Early maturity varieties (000 to III) are adapted to northern latitudes with longer day lengths with the maturity designation increasing in southern latitudes with shorter day lengths.

[0066] An increase in maturity can correlate with an increase in yield or other traits such as oil concentration. The correlation of plant maturity and other traits confounds the evaluation of potential markers and candidate genes associated with other traits such as yield. Identification of genomic regions associated with plant maturity, but not with another trait, can allow breeders to genetically fix plant maturity within a soybean plant and separately elucidate other traits, such as those associated with yield.

[0067] Disclosed is a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1, 2, and 3; and assigning a maturity group value to the soybean plant or soybean seed. In a preferred aspect, determining if alleles at a locus are homozygous or heterozygous includes detecting a polymorphism with a nucleic acid molecule having a sequence of any of SEQ ID NOs: 143-174, or complements thereof.

[0068] Further disclosed is a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1, 2, 3 and 4; and assigning a maturity group value to the soybean plant or soybean seed.

[0069] Further disclosed is a method of providing information about the maturity of a soybean plant or soybean seed by obtaining DNA from the soybean seed or soybean plant and determining the allelic profile at a locus of genomic region 4.

[0070] The present invention also includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and determining the allelic combination of the alleles within maturity genomic regions 1, 2, and 3.

[0071] In a preferred aspect, the soybean plant or soybean seed is homozygous for the alleles within maturity genomics regions 1, 2, and 3. In a preferred aspect, the homozygous alleles are either dominant or recessive. In another aspect, the soybean plant or soybean seed is homozygous for the alleles within maturity genomics regions 1 and 2. In a preferred

aspect, the homozygous alleles are either dominant or recessive. In another aspect, the soybean plant or soybean seed is homozygous for the alleles within maturity genomics regions 2 and 3. In a preferred aspect, the homozygous alleles are either dominant or recessive. In another aspect, the soybean plant or soybean seed is heterozygous for the alleles within maturity genomics regions 1, 2, and 3. In another aspect, the soybean plant or soybean seed is heterozygous for the alleles within maturity genomics regions 1 and 2. In another aspect, the soybean plant or soybean seed is heterozygous for the alleles within maturity genomics regions 2 and 3. In a preferred aspect, the allelic combination is allelic combination 10, allelic combination 11, allelic combination 12, allelic combination 13, allelic combination 14, allelic combination 15, allelic combination 16, allelic combination 17, allelic combination 18, and allelic combination 19.

[0072] An aspect of the method of the present invention the method is suitable for establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant by obtaining DNA from a soybean plant or soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1 and 2; and assigning a maturity growth value to the soybean plant or soybean seed. In a preferred aspect, determining whether an allele is homozygous or heterozygous includes detecting a polymorphism from any of SEQ ID NOs: 143-161. In a preferred aspect, the allelic combination is allelic combination 1, allelic combination 2, allelic combination 3, allelic combination 4, allelic combination 5, allelic combination 6, allelic combination 7, allelic combination 8, and allelic combination 9. In a preferred aspect, the soybean plant or soybean seed is obtained from a cross of an early maturity group parent soybean plant and a mid-maturity parent soybean plant. In a preferred aspect, the early maturity group parent soybean plant is between 00.0 - 1.0 and the mid-maturity parent soybean plant is between III.0-IV.9

[0073] An aspect includes a method to determine if a soybean plant has a maturity group of 0.0-III.9 by determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; and assigning a maturity group value for the soybean plant between 0.0-III.9. In a preferred aspect, maturity in the soybean plant is reached at least 5 days before a soybean plant that is homozygous dominant within maturity genomic region 1, homozygous dominant within maturity genomic region 2 and is grown under the same environmental conditions.

[0074] Another aspect includes a method to determine if the maturity of a soybean plant is in a 00.0 - III.0 maturity group by determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; and assigning a maturity group value for the soybean plant between 00.0 - III.0. In a preferred aspect, a selected soybean seed is homozygous recessive at maturity genomic region 1 and homozygous recessive at maturity genomic region 2 and has a maturity group between 0.5 - II. 0. In a preferred aspect, a soybean seed is selected that is homozygous recessive at maturity genomic region 1 and heterozygous dominant at maturity genomic region 2 and has a maturity group between 1.5 - II.9.

[0075] Also disclosed is a method where the maturity group of a progeny plant is predicted by whether an allele in maturity genomic region 1 is homozygous dominant, homozygous recessive, or heterozygous and whether an allele in maturity genomic region 2 is homozygous dominant, homozygous recessive, or heterozygous. In an aspect, if the maturity group of a plant is between 0 and II, the maturity group can be identified by determining the allelic combination of maturity genomic regions 1 and 2 in a plant or seed. See, for example, Table 9.

[0076] In an alternate aspect, if the maturity group of a plant is between III and V, the maturity group can be identified by determining the allelic combination of maturity genomic regions 1, 2 and 3 in a plant or seed. See, for example, Table 9. In an aspect, if the maturity group of a plant is between IV and V, the maturity group can be identified by determining the allelic combination of maturity genomic regions 1, 2 and 3 in a plant or seed. See, for example, Table 9.

[0077] In another aspect, the maturity group of the parent plants is known. In an aspect, the maturity groups of the parent plants are different by more than 10 days, between 10 days - 20 days, between 10 days - 30 days, more than 2 maturity groups, less than 2 maturity groups, between maturity groups 000 and VI. In an aspect, the maturity group of a progeny plant resulting from a cross with at least one parent having a maturity group of 0-II is identified by determining the allelic combination of maturity genomic regions 1 and 2. In another aspect, the maturity group of a progeny plant resulting from a cross with parent plants having a maturity group of III, IV, V, or III-V is identified by determining the allelic combination of maturity genomic regions 1, 2 and 3.

[0078] In an aspect, more dominant alleles at a locus in a maturity group region correlate with a delay in maturity. In another aspect, an increase in the number of dominant alleles correlates with a delay in maturity.

[0079] In an aspect, parent plants with a difference in maturity group greater than 1.5, 2, 2.5, 3, 3.5 are crossed and their maturity group identified by determining the allelic combination. In an aspect, parent plants with a difference in maturity group between 1 and 3, between 1 and 4, between 2 and 3, between 2 and 5, between 2 and 6, between 2 and 7 are crossed and their maturity group identified by determining the allelic combination of the progeny. In an aspect, parent plants with a difference in maturity group greater than 1.5, 2, 2.5, 3, 3.5 are crossed and their maturity group identified by determining the allelic combination.

[0080] In an aspect, a progeny plant has a maturity group earlier than one parent by 5, 10, or 15 days. In another

aspect a progeny plant has a maturity group later than one parent plant by 5, 10, or 15 days. In an aspect, a progeny plant has a maturity group earlier than both parents by 5, 10, or 15 days. In another aspect, a progeny plant has a maturity group later than both parent plants by 5, 10, or 15 days.

[0081] In an aspect, an early parent of maturity group 0.1 is crossed with a later maturity parent plant that is a 1.9, and the progeny plants with allelic combination 1 are 0.1 - 0.5 maturity. In another aspect, an early parent with maturity of 0.9 is crossed with a plant having 3.5 maturity, and the plants having allelic combination 1 are maturity group 1.0 - 1.5.

[0082] In an aspect, the maturity group of a progeny seed is determined from a cross between a very early maturity parent plant with a later maturity parent plant. In an aspect, the very early maturity parent plant is a maturity group 00.0 - 0.9 and the later maturity parent plant is a maturity group III.5 - IV.5. In an aspect, the very early maturity parent plant is a maturity group 00 and the later maturity parent plant is a maturity group III or IV. In an aspect, DNA can be obtained from plants or plant parts such as seeds in the F_1, F_2, F_3, F_4 or later populations. In an aspect, one or more plants or plant parts are genotyped for alleles in genomic regions 1 and 2. In an aspect, the alleles are determined using the SNP markers NS0128378 (genomic maturity region 1) and NS0118907 (genomic maturity region 2).

[0083] In an aspect, the plants are phenotyped for maturity by counting the number of days after August 31st until a plant matures. In an aspect, a plant is considered mature when 95% of the pods are brown. In an aspect, when alleles from markers associated with maturity genomic regions 1 and 2 are homozygous recessive, the progeny plant will reach maturity 15, 14, 12, 11, 10, 9, or 8 days sooner than the maturity group if the alleles from markers associated with maturity genomic regions 1 and 2 are homozygous dominant. In an aspect, if an allele from a marker associated with maturity genomic region 1 is homozygous dominant and an allele from a marker associated with maturity genomic region 2 is heterozygous, then the progeny plant will reach maturity between 1 day, 1-2 days, 2-3 days, 2-4 days, or 3-5 days earlier than if the alleles from markers associated with maturity genomic regions 1 and 2 are homozygous dominant.

[0084] In another aspect, multiple seeds can be selected or bulked. Multiple seeds may include greater than or equal to 2, 3, 4, 5, 6, 10, 50, 100, 500, 1000, 5,000, 10,000 or more seeds. One or multiple seeds can be distributed to a geographic region suitable for growth of one or multiple plants. In this aspect, seeds selected can be distributed or shipped to an appropriate region.

[0085] The present invention also provides multiple soybean seeds in which greater than 50%, 60%, 70%, 80%, 90%, 95%, or 99% of the seeds will grow into plants where the variation in maturity group is within one maturity group, not more than 2 groups or 20 days after August 31st, not more than 1 group or 10 days after August 31st, not more than 0.9 group or nine days after August 31st, not more than 5 days after August 31st or 0.5 group, or with a maturity group between 0.0 - II.0, 000.0 - III.9. The multiple soybean seeds can grow into soybean plants having indeterminate soybean plant habit or having determinate soybean plant habit. One aspect includes a method to select a soybean seed based on indeterminate or determinate growth habit comprising determining if maturity genomic region 3 is homozygous or heterozygous. In one aspect, 85% of the multiple soybean seeds can reach maturity within 10 days, 5 days, 3 days of each other. In another aspect, 95% of the multiple soybean seeds can reach maturity within 10 days, 5 days, 3 days of each other.

[0086] In another aspect the method of the present invention is suitable to isolate indeterminate-early maturity soybean seeds by obtaining DNA from the soybean seed using a non-destructive method; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; and determining if an allele within maturity genomic region 2 is homozygous or heterozygous.

[0087] Such multiple seeds may be in a container. The container of soybean seeds can contain any number, weight, or volume of seeds. For example, a container can contain at least, or greater than, about 10, 25, 50, 100, 200, 300, 400, 500, 600, 700, 80, 90, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 5000, 7500, or 10,000 or more seeds. In another aspect, a container can contain about, or greater than about, 1 gram, 5 grams, 10 grams, 15 grams, 20 grams, 25 grams, 50 grams, 100 grams, 250 grams, 500 grams, or 1000 grams of seeds. Alternatively, the container can contain at least, or greater than, about 0 ounces, 1 ounce, 5 ounces, 10 ounces, 1 pound, 2 pounds, 3 pounds, 4 pounds, 5 pounds, 10 pounds, 15 pounds, 20 pounds, 25 pounds, 30 pounds, 40 pounds, 50 pounds, 60 pounds, 70 pounds, 80 pounds, 100 pounds, 200 pounds, 300 pounds, 500 pounds, or 1000 pounds or more seeds.

[0088] Containers of soybean seeds can be any container available in the art. For example, a container can be a box, a bag, a can, a packet, a pouch, a tape roll, a pail, or a tube.

[0089] In another aspect, the seeds contained in the containers of soybean seeds can be treated or untreated soybean seeds. In one aspect, the seeds can be treated to improve germination, for example, by priming the seeds, or by disinfection to protect against seed-born pathogens. In another aspect, seeds can be coated with any available coating to improve, for example, plantability, seed emergence, and protection against seed-born pathogens. Seed coating can be any form of seed coating including, but not limited to, pelleting, film coating, and encrustments. One aspect includes a method of distributing a soybean plant based on maturity group by obtaining DNA from a soybean plant; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and assigning a maturity growth value to the soybean plant; and shipping the soybean plant to a

preferred geographic region.

[0090] A plant may also comprise a gene that confers resistance to insect, pest, viral or bacterial attack. Such a gene may be a transgene. For example, a gene conferring resistance to a pest, such as soybean cyst nematode was described in US Patent Nos. 7,154,021.

[0091] Transgenes may also be used to alter protein metabolism. For example, U.S. Patent No. 5,545,545 describes lysine-insensitive maize dihydrodipicolinic acid synthase (DHPS), which is substantially resistant to concentrations of L-lysine which otherwise inhibit the activity of native DHPS. Similarly, EP 0640141 describes sequences encoding lysine-insensitive aspartokinase (AK) capable of causing a higher than normal production of threonine, as well as a subfragment encoding antisense lysine ketoglutarate reductase for increasing lysine.

[0092] In another aspect, a transgene may be employed that alters plant carbohydrate metabolism. For example, fructokinase genes are known for use in metabolic engineering of fructokinase gene expression in transgenic plants and their fruit (see U.S. Patent No. 6,031,154). A further example of transgenes that may be used are genes that alter grain yield. For example, U.S. Patent No. 6,486,383 describes modification of starch content in plants with subunit proteins of adenosine diphosphoglucose pyrophosphorylase ("ADPG PPase"). In EP0797673 transgenic plants are discussed in which the introduction and expression of particular DNA molecules results in the formation of easily mobilized phosphate pools outside the vacuole and an enhanced biomass production and/or altered flowering behavior. Still further known are genes for altering plant maturity. U.S. Patent No. 6,774,284 describes DNA encoding a plant lipase and methods of use thereof for controlling senescence in plants. U.S. Patent No. 6,140,085 discusses FCA genes for altering flowering characteristics, particularly timing of flowering. U.S. Patent No. 5,637,785 discusses genetically modified plants having modulated flower development such as having early floral meristem development and comprising a structural gene encoding the LEAFY protein in its genome.

[0093] In another aspect, the present invention provides methods and compositions for the preferred deployment of conventional and transgenic traits related to fatty acid synthesis and oil content. Using present invention, breeders can tailor trait integration to geographies for preferred trait expression, whether the trait is conventional (for example, a mutation) or transgenic. For example, a transgene may be employed that alters plant oil biosynthesis and oil composition. In particular, linoleic acid (LA) (18:2, Δ9, 12) is produced from oleic acid (18:1, Δ9) by a Δ12-desaturase (encoded by FAD2) while alpha linolenic acid (ALA) (18:3, Δ9, 12, 15) is produced from LA by a Δ15-desaturase (encoded by FAD3). Moreover, stearidonic acid (SDA) (18:4, Δ6, 9, 12, 15) and gamma linolenic acid (GLA) (18:3, Δ6, 9, 12) are polyunsaturated fatty acids (PUFAs) produced from LA and ALA by a Δ6-desaturase. Various genes encoding desaturases have been described. For example, U.S. Pat. No. 5,952,544 describes nucleic acid fragments isolated and cloned from *Brassica napus* that encode fatty acid desaturase enzymes. Expression of the *B. napus* Δ15-desaturase of the '544 patent resulted in accumulation of ALA. U.S. Pat. Publication 2006/0156435 describes the expression of fungal Δ15-desaturases to increase omega-3 fatty acid profiles in plants. WO05/021761 discusses genetically engineered plants which produce both SDA and GLA as a result of expressing a Δ6-desaturase and a Δ15-desaturase. Long chain PUFAs such as EPA and DHA can be produced in plants as disclosed in US Pat. Publication 2004/0172682.

[0094] Inhibition of the endogenous soy FAD2 gene through use of transgenes that inhibit the expression of FAD2 has been shown to confer a desirable mid-oleic acid (18:1) phenotype (i.e. soybean seed comprising about 50% and 75% oleic acid by weight). Transgenes and transgenic plants that provide for inhibition of the endogenous FAD2 gene expression and a mid-oleic phenotype are disclosed in U.S. Patent 7,067,722. In contrast, wild type soybean plants that lack FAD2 inhibiting transgenes typically produce seed with oleic acid compositions of less than 20%. Inhibition of the endogenous FAD3 gene gene through use of transgenes that inhibit the expression of FAD3 has been shown to confer a desirable linolenic acid (18:3) phenotype. A *"FATB"* or "palmitoyl-ACP thioesterase" gene encodes an enzyme (FATB) capable of catalyzing the hydrolytic cleavage of the carbon-sulfur thioester bond in the panthothene prosthetic group of palmitoyl-ACP as its preferred reaction. Hydrolysis of other fatty acid-ACP thioesters may also be catalyzed by this enzyme. Representative *FATB-1* sequences include, without limitation, those set forth in U.S Pat. Publication 2004/0006792 and U.S. Patent Nos. 5,955,329; 5,723,761; 5,955,650; and 6,331,664. When the amount of FATB is decreased in a plant cell, a decreased amount of saturated fatty acids such as palmitate and stearate may be provided. Thus, a decrease in expression of FATB may result in an increased proportion of unsaturated fatty acids such as oleic acid (18:1). The simultaneous suppression of *FAD2, FAD3,* and *FATB* expression thereby results in driving the FAS pathway toward an overall increase in mono-unsaturated fatty acids of 18-carbon length, such as oleic acid (C18:1). *See* U.S. Patent No. 5,955,650.

[0095] In an aspect, the present invention provides methods and compositions for the preferred deployment of conventional and transgenic traits related to fatty acid synthesis and oil content. Soybean seed oil levels are highly impacted by environment. Oil concentration increases with decreasing latitude, therefore, soybeans in maturity groups 00-I generally have lower oil levels than later maturing soybeans (Yaklich et al. 2002. Crop Sci 42:1504-1515). The decrease in oil concentrations is attributed to lower temperatures and shorter growing season (Piper and Boote 1999 J. Am. Oil Chem. Soc. 76:1233-124). In addition, soybeans cultivated under drought stress tend to produce seeds with decreased protein and increased oil (Specht et al. 2001 Crop Sci 41:493-509). Using present invention, breeders can tailor trait

integration to geographies for preferred trait expression, whether the trait is conventional (for example, a mutation) or transgenic.

[0096] Genes for altering plant morphological characteristics are also known and may be used in accordance with the invention. U.S. Patent No. 6,184,440 discusses genetically engineered plants which display altered structure or morphology as a result of expressing a cell wall modulation transgene. Examples of cell wall modulation transgenes include a cellulose binding domain, a cellulose binding protein, or a cell wall modifying protein or enzyme such as endoxyloglucan transferase, xyloglucan endo-transglycosylase, an expansin, cellulose synthase, or a novel isolated endo-1,4-ß-glucanase.

[0097] Methods for introduction of a transgene, for instance to soybean, are well known in the art and include biological and physical plant transformation protocols. See, for example, Miki *et al.* (1990), Clemente *et al.* (Clemente et al., Crop Sci., 40:797-803, 2000), and U.S. Patent 7,002,058. A further aspect of the invention relates to tissue cultures of a soybean variety of the invention. Exemplary types of tissue cultures are protoplasts, calli and plant cells that are intact in plants or parts of plants. Plant parts include, but not limited to, embryos, pollen, flowers, leaves, roots, root tips, anthers, vascular tissue, pod, stem, seed, or a portion thereof, or a cell isolated from the plant. In an aspect, the tissue culture comprises plant parts such as embryos, protoplasts, meristematic cells, pollen, leaves or anthers. In these ways, plants or parts thereof can be grown in culture and regenerated. Exemplary procedures for preparing tissue cultures of regenerable soybean cells and regenerating soybean plants therefrom, are disclosed in U.S. Patent Nos. 4,992,375; 5,015,580; 5,024,944, and 5,416,011. An important ability of a tissue culture is the capability to regenerate fertile plants. For transformation to be efficient and successful, DNA must be introduced into cells that give rise to plants or germ-line tissue. In particular, methods for the regeneration of *Glycine max* plants from various tissue types and methods for the tissue culture of *Glycine max* are known in the art (See, for example, Widholm et al., In Vitro Selection and Culture-induced Variation in Soybean, In Soybean: Genetics, Molecular Biology and Biotechnology, Eds. Verma and Shoemaker, CAB International, Wallingford, Oxon, England (1996). Regeneration techniques for plants such as *Glycine max* can use as the starting material a variety of tissue or cell types. With *Glycine max* in particular, regeneration processes have been developed that begin with certain differentiated tissue types such as meristems, Cartha et al., Can. J. Bot. 59:1671-1679 (1981), hypocotyl sections, Cameya et al., Plant Science Letters 21: 289-294 (1981), and stem node segments, Saka et al., Plant Science Letters, 19: 193-201 (1980); Cheng et al., Plant Science Letters, 19: 91-99 (1980). Regeneration of whole sexually mature *Glycine max* plants from somatic embryos generated from explants of immature *Glycine max* embryos has been reported (Ranch et al., In Vitro Cellular & Developmental Biology 21: 653-658 (1985)). Regeneration of mature *Glycine max* plants from tissue culture by organogenesis and embryogenesis has also been reported (Barwale et al., Planta 167: 473-481 (1986); Wright et al., Plant Cell Reports 5: 150-154 (1986)). Once a transgene is introduced into a variety it may readily be transferred by crossing. By using backcrossing, essentially all of the desired morphological and physiological characteristics of a variety are recovered in addition to the locus transferred into the variety *via* the backcrossing technique. Backcrossing methods can be used with the present invention to improve or introduce a characteristic into a plant (Poehlman and Sleper, In: Breeding Field Crops, Iowa State University Press, Ames,1995; Fehr, Principles of Cultivar Development Vol. 1, pp. 2-3 (1987)). Disclosed is a method of soybean plant breeding by crossing at least two different parent soybean plants, where the parent soybean plants differ in plant maturity by over 10 days, 10days - 20 days, 10 days - 30 days; obtaining a progeny seed from the cross; genotyping a progeny seed of the cross with a genetic marker; and selecting a soybean seed possessing a genotype for preferred maturity. Also disclosed is a method of soybean plant breeding by assaying a soybean plant for the presence of a marker sequences selected from SEQ ID NO: 143 through SEQ ID NO: 213; and associating the soybean plant with a maturity group. The present invention also includes a method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent soybean plant, where the parent soybean plants differ in soybean plant maturity by over 10 days, 10 days - 20 days, 10 days - 30 days, by crossing a parent soybean plant comprising a desired trait with a second parent soybean plant; obtaining progeny soybean seed from the cross; screening a progeny soybean seed for the trait; screening a progeny soybean seed for a desired maturity group using a marker selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213 to determine the desired geographical growing region; and selecting a progeny soybean seed containing the desired trait and desired soybean plant maturity.

[0098] The method of soybean plant breeding includes crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group. In a preferred aspect, the maturity phenotype of the progeny soybean plant or soybean seed is unknown. In another preferred aspect, the progeny is grown under conditions that are unsuitable for determining maturity of the soybean plant. In another preferred aspect, the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days - 20 days, 10 days - 30 days. herein a maturity phenotype of at least one of the two different parent soybean plants is unknown. In a preferred aspect, the maturity phenotype of both of the two different parent soybean plants is unknown. In a preferred aspect, the progeny soybean plant is not photoperiod sensitive. In another preferred aspect, at least one parent soybean plant is not photoperiod sensitive. In a preferred

aspect, both parent soybean plants are not photoperiod sensitive. In a preferred aspect, the maturity genomic region is characterized by a dominant allele identified in Table 6. In a preferred aspect, the maturity genomic region is characterized by a recessive allele identified in Table 6.

[0099] In an aspect, at least one or both parent soybean plant are an elite variety. In an aspect, a progeny soybean plant is an exotic soybean plant or one or both parent soybean plants are exotic soybean plants.

[0100] An aspect includes a method of selecting a soybean plant for germplasm improvement by determining a maturity group by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group; and incorporating the selected soybean plant into a use selected from the group consisting of using the soybean plant for breeding, advancement of the soybean plant through self-fertilization, trait integration, use of soybean plant or parts thereof for transformation, and use of soybean plants or parts thereof for mutagenesis.

[0101] Another aspect of the method of the present invention includes a method of co-selecting a soybean plant for expression of a non-maturity phenotypic trait and a maturity trait by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group; and to determine the desired geography for the progeny soybean plant growth, and a method for determining the non-maturity phenotype.

[0102] In a preferred aspect, the method for detecting the non-maturity phenotype is a genotypic or phenotypic method. In a preferred aspect, the non-maturity phenotypic trait is any of herbicide tolerance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance, altered oils production, high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistant, increased digestibility, industrial enzymes, pharmaceutical proteins, peptides and small molecules, improved processing traits, improved flavor, nitrogen fixation, hybrid soybean seed production, reduced allergenicity, biopolymers, and biofuels.

[0103] In another preferred aspect, a phenotypic trait is any of altered protein and oil composition, altered levels of a molecule selected from the group consisting of protein, oil, linolenic acid, stearic acid, palmitic acid, oleic acid, linoleic acid, stearidonic acid, alpha-linolenic acid, gamma linolenic acid, docosahexaenoic acid, eicosapentaenoic acid, docosapentaenoic acid, and combinations thereof.

[0104] In one aspect, plants can be used in activities related to germplasm improvement, non-limiting examples of which include using the plant for breeding, advancement of the plant through self-fertilization, trait integration, use of plant or parts thereof for transformation, and use of plants or parts thereof for mutagenesis. Non-limiting examples of breeding decisions include progeny selection, parent selection, and recurrent selection for at least one haplotype. In another aspect, breeding decisions relating to development of plants for commercial release comprise advancing plants for testing, advancing plants for purity, purification of sublines during development, variety development, and hybrid development. In yet other aspects, breeding decisions and germplasm improvement activities comprise transgenic event selection, making breeding crosses, testing and advancing a plant through self-fertilization, using plants or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plants or parts thereof for mutagenesis. The choice of breeding method depends on the mode of plant reproduction, the heritability of the trait (s) being improved, and the type of cultivar used commercially (*e.g.*, F_1 hybrid cultivar, pureline cultivar).

[0105] Descriptions of breeding methods that are commonly used for soybeans can be found in one of several reference books (*e.g.* Fehr, Principles of Cultivar Development Vol. 1, pp. 2-3 (1987)). In one aspect disclosed is a method of soybean plant breeding by assaying a soybean plant for the presence of a marker sequences selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213; and associating the soybean plant with a maturity group.

[0106] In another aspect disclosed is a method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent soybean plant, wherein the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days - 20 days, or 10 days - 30 days, by crossing a parent soybean plant comprising a desired trait with a second parent soybean plant; obtaining progeny soybean seed from the cross; screening a progeny soybean seed for the trait; screening a progeny soybean seed for a desired maturity group using a marker selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213 to determine the desired geographical growing region; and selecting a progeny soybean seed containing the desired trait and desired soybean plant maturity. In a preferred aspect, the desired trait is transgenic.

[0107] An aspect includes a method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days - 20 days, or 10 days - 30 days; obtaining a progeny soybean seed from the cross; genotyping a progeny soybean seed of the cross with a genetic marker; and selecting a soybean seed possessing a genotype for preferred maturity.

[0108] Another aspect includes a method of screening soybean seeds based on soybean plant maturity group by obtaining DNA from a soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heter-

ozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and assigning a maturity growth value to the soybean seed.

[0109] One aspect is a method of introgressing an allele into a soybean plant by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; screening the progeny soybean plant of the cross for the allele; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; and selecting a soybean seed, wherein the soybean seed comprises the allele and a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-213. In a preferred aspect, the selected soybean seed further has a second sequence selected from the group consisting of SEQ ID NOs: 143-213. In another preferred aspect, the allele is selected from any or both of SCN resistance and root rot resistance. Another aspect includes a method of introducing a desired trait into a soybean plant by crossing at least two different parent soybean plants, wherein at least one parent soybean plant has a desired trait; obtaining a progeny soybean seed from the cross; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; assaying the progeny soybean seed of the cross for evidence of the desired trait; and selecting the soybean seed with the desired trait and a desired maturity group. In a preferred aspect, the desired trait is transgenic.

[0110] A further aspect includes a method of introgressing an allele into a soybean plant by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; and selecting a soybean seed with the allele and a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-174.

[0111] Another aspect includes a method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 10 days; obtaining progeny soybean seed from the cross; genotyping the progeny soybean seed of the cross with a genetic marker selected from the group consisting of SEQ ID NOs: 143-213; and selecting a soybean seed with a desired maturity group. A further aspect includes a soybean plant comprising within its genome an introgressed haplotype associated with maturity, wherein the introgression is facilitated by at least one of the markers from SEQ ID NO: 143-213 or of the markers 143-162.

[0112] Having now generally described the invention, the same will be more readily understood through reference to the following examples.

Examples

Example 1: Discovery of molecular markers associated with genomic regions affecting plant maturity

[0113] Soybean is a short day plant, therefore flowering is initiated by short days due to a decrease in photoperiod (Garner & Allard, J. Agric. Res. 18, 553 - 606 (1920)). Consequently, photoperiod (day length) and temperature response of the soybean plant determines areas of plant adaptation. Due to photoperiod sensitivity, soybean genotypes are grown to narrow zones of latitude to optimize yield. Northern soybean varieties, in contrast to Southern varieties, initiate flowering with longer days. Northern varieties planted south of their adaptation zone exhibit accelerated flowering, limited plant growth and reduced yield. Southern soybean varieties planted north of their adaptation zone will have delayed flowering with a potential for frost damage that may reduce yield. Most soybean variety development crosses are made between parents within 10 maturity days of each other. If the parents differ greatly in maturity, progeny plants segregate widely for maturity. In order for breeders to obtain and select for soybean plants of a desire maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive. Identification of genomic regions associated with plant maturity facilitated crosses between parents outside 10 maturity days of each other without maintain a large number of progeny plants.

[0114] To identify genomic regions associated with plant maturity, 258 soybean lines (129 pairs of differing maturity groups) are genotyped with one thousand, four hundred single nucleotide polymorphism (SNP) markers, distributed across the 20 linkage groups of the soybean genetic linkage map. In addition, 258 soybean lines are phenotyped for yield and plant maturity. Associations between SNP marker genotype and plant maturity phenotype are then evaluated. This was done in multiple environments (Tables 2-3).

Table 1: Initial identification of maturity genomic regions via marker assisted breeding

Region	Marker	SEQ ID NO:	Effect (Δ d)	P- value
1	NS0125408	148	-0.05071	0.009068
1	NS0098982	155	1.242281	0.01081
2	NS0123506	156	-0.57638	0.021863
3	NS0093197	164	1.274868	1.92E-09

(continued)

Region	Marker	SEQ ID NO:	Effect (Δ d)	P- value
3	NS0136544	171	1.162352	1.33E-10
3	NS0119569	172	-1.87063	3.79E-15
3	NS0114317	174	1.419675	3.01E-08
5	NS0123168	188	-0.21704	0.025498
6	NS0103755	190	-0.02572	0.011701
7	NS0095211	199	-0.09176	2.99E-07
7	NS0097307	200	-0.09023	6.66E-07
7	NS0102630	202	-0.08407	2.26E-06
7	NS0102915	203	-0.08226	5.19E-06
8	NS0100652	206	1.75824	3.92E-06
8	NS0119574	207	0.446757	0.045212
8	NS0101020	212	0.829784	0.000462

Table 2: Estimated effect in days of maturity genomic regions

Region	Marker	SEQ ID NO:	Est. effect on plant maturity (Δ d)	Effect (Δd)	P-value
1	NS0124601	143	4.7	0.309636	0.156883
1	NS0096829	145	4.8	0.444689	0.022932
1	NS0099746	146	4.7	0.315142	0.191492
1	NS0123747	147	4.9	0.714394	0.011568
1	NS0125408	148	4.8	0.538569	0.015846
1	NS0128378	149	4.9	0.757069	0.01699
1	NS0093976	154	5.1	0.989792	0.061019
1	NS0098982	155	5.2	1.242281	0.01081
2	NS0123506	156	4.1	0.911763	0.007307
2	NS0097952	157	5.6	4.069668	5.06E-30
2	NS0118907	158	6.3	5.477999	1.01E-33
2	NS0126989	160	4.6	1.994585	0.000191
2	NS0095677	161	3.8	0.473053	0.10136
3	NS0093197	164	5.2	1.274868	1.92E-09
3	NS0103853	167	6	2.937938	3.78E-09
3	NS0136544	171	6.4	3.765493	3.23E-11
3	NS0119569	172	5.8	2.409513	1.72E-21
3	NS0123708	173	6	2.876505	3.44E-26
3	NS0114317	174	5.9	2.627908	1.69E-22
4	NS0098176	176	4.3	1.068684	6.45E-12
4	NS0100078	177	4	0.479955	0.073839
4	NS0095530	179	4.5	1.364994	2.50E-09
4	NS0129004	180	4.5	1.48424	8.04E-08
5	NS0099024	181	3.4	0.732455	0.112193
5	NS0101863	182	3.3	0.434912	0.078906
5	NS0103446	183	3.1	0.181809	0.058299
5	NS0123168	188	3.2	0.217041	0.025498
6	NS0103755	190	1.2	0.609071	0.140857
6	NS0116125	191	0.9	0.456086	0.152892
6	NS0125713	192	1.1	0.566084	0.036335
6	NS0125770	193	0.8	0.414212	0.009099
6	NS0119281	194	1.6	0.797885	0.038077
6	NS0124590	195	1.4	0.706375	0.000889

(continued)

Region	Marker	SEQ ID NO:	Est. effect on plant maturity (Δ d)	Effect (Δd)	P-value
6	NS0102717	196	1.5	0.749548	0.000246
7	NS0099531	197	1.3	0.636575	0.000701
7	NS0099417	198	2.4	1.181523	0.015954
7	NS0095211	199	1.7	0.835736	0.099501
7	NS0097307	200	0.2	0.090232	6.66E-07
7	NS0102630	202	2.1	1.029761	0.046938
7	NS0102915	203	2.5	1.231387	4.37E-09
8	NS0102362	204	4.8	2.23831	1.23E-09
8	NS0117716	205	4.3	1.171503	9.09E-06
8	NS0100652	206	4.6	1.75824	3.92E-06
8	NS0119574	207	4.3	1.195594	4.79E-05
8	NS0127728	208	4.5	1.630904	3.33E-07
8	NS0099639	209	4.2	1.037891	0.015656
8	NS0103255	210	4.2	0.975115	0.001037
8	NS0119106	211	4.3	1.18298	0.023909
8	NS0101020	212	4.1	0.829784	0.000462
8	NS0101779	213	4.2	1.000886	0.000563

[0115] The approximate locations of informative markers indicating a state of dominance or recessivity of genomic regions 1, 2, 3, 4, 5, 6, 7, and 8 are determined based upon a survey of polymorphisms among a panel of 258 soybean lines (Table 3 and 4). One factor in choosing these informative markers is based on which marker has the largest effect or is associated with the largest delay in maturity such that it is indicative of the maturity phenotype. Another factor in choosing these informative markers is based on the lowest P value, such that the marker does not get lost in the event of recombination. The markers with lower P value are more likely to be consistently associated with the maturity phenotype across different soybean populations (different parents, different pedigrees). Markers with strong association and predictive of introgression of the genomic region are listed in Table 5. For NS0128378, the SNP is actually an 11-bp indel, were "D" represents the deletion (**********) and "I" represents the insertion (TTCGAAGATTT).

Table 3: Position of SNP markers associated with regions 1, 2, 3, 4, 5, 6, 7 and 8.

Region	LG	Position (cM)	Marker	Polymorphism position on Consensus Sequence	SEQ ID NO:
1	C2	113.7	NS0124601	884	143
1	C2	121.9	NS0103749	96	144
1	C2	121.9	NS0096829	225	145
1	C2	121.9	NS0099746	330	146
1	C2	121.9	NS0123747	56	147
1	C2	121.9	NS0125408	133	148
1	C2	121.9	NS0128378	212	149
1	C2	129.3	NS0135390	108	150
1	C2	123	NS0099529	243	151
1	C2	124.3	NS0097798	325	152
1	C2	129.4	NS0093385	109	153
1	C2	134.7	NS0093976	242	154
1	C2	134.7	NS0098982	383	155
2	O	125.4	NS0123506	126	156
2	O	127.7	NS0097952	420	157

(continued)

Region	LG	Position (cM)	Marker	Polymorphism position on Consensus Sequence	SEQ ID NO:
2	O	134.9	NS0118907	450	158
2	O	151.4	NS0122182	104	159
2	O	150.8	NS0126989	251	160
2	O	158.5	NS0095677	202	161
3	L	99.4	NS0098853	82	162
3	L	111.5	NS0092561	190	163
3	L	99.4	NS0093197	225	164
3	L	100.4	NS0094891	83	165
3	L	99.4	NS0096225	471	166
3	L	136.2	NS0103853	341	167
3	L	114.2	NS0113929	685	168
3	L	114.2	NS0115535	433	169
3	L	113.6	NS0121511	512	170
3	L	132.9	NS0136544	208	171
3	L	143.1	NS0119569	262	172
3	L	145.8	NS0123708	530	173
3	L	155.9	NS0114317	331	174
4	I	48.3	NS0092743	217	175
4	I	49.6	NS0098176	92	176
4	I	66.4	NS0100078	1412	177
4	I	58.3	NS0137415	231	178
4	I	33.4	NS0095530	327	179
4	I	32.3	NS0129004	1014	180
5	L	40.1	NS0099024	69	181
5	L	35.7	NS0101863	381	182
5	L	40.1	NS0103446	69	183
5	L	35.9	NS0113878	375	184
5	L	36.8	NS0115066	298	185
5	L	36.9	NS0119165	181	186
5	L	36.8	NS0120015	449	187
5	L	36	NS0123168	75	188
5	L	38.8	NS0123724	42	189
6	D1b+W	172.5	NS0103755	45	190
6	D1b+W	164.1	NS0116125	409	191
6	D1b+W	176.3	NS0125713	392	192
6	D1b+W	165.4	NS0125770	1074	193
6	D1b+W	134.8	NS0119281	596	194

(continued)

Region	LG	Position (cM)	Marker	Polymorphism position on Consensus Sequence	SEQ ID NO:
6	D1b+W	157.6	NS0124590	1092	195
6	D1b+W	177.2	NS0102717	402	196
7	G	111.5	NS0099531	287	197
7	G	122.1	NS0099417	408	198
7	G	125.7	NS0095211	251	199
7	G	125.7	NS0097307	426	200
7	G	130.4	NS0103004	430	201
7	G	132.1	NS0102630	186	202
7	G	131.2	NS0102915	193	203
8	M	37.7	NS0102362	74	204
8	M	42.2	NS0117716	74	205
8	M	44.2	NS0100652	247	206
8	M	44.2	NS0119574	367	207
8	M	42.8	NS0127728	650	208
8	M	48.8	NS0099639	362	209
8	M	64.8	NS0103255	289	210
8	M	64.8	NS0119106	417	211
8	M	67.1	NS0101020	238	212
8	M	67.1	NS0101779	147	213

[0116] Allele-specific fluorescence-resonance-energy-transfer (FRET) probes are used in Real-Time PCR assays. Two FRET probes bearing different fluorescent reporter dyes are used, where a unique dye is incorporated into an oligonucleotide that can anneal with high specificity to only one of the two alleles. The reporter dyes are 2'-chloro-7'-phenyl-1,4-dichloro-6-carboxyfluorescein (VIC) and 6-carboxyfluorescein phosphoramidite (FAM).

Table 4: Listing of SNP markers associated with regions 1, 2, 3, 4, 5, 6, 7 and 8.

Region	Marker	SEQ ID NO:	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	SEQ ID NO: FAM Probe	FAM Allele	SEQ ID NO: VIC probe	VIC allele
1	NS0124601	143	1	2	214	T	215	G
1	NS0103749	144	3	4	216	G	217	A
1	NS0096829	145	5	6	218	C	219	A
1	NS0099746	146	7	8	220	G	221	A
1	NS0123747	147	9	10	222	T	223	A
1	NS0125408	148	11	12	224	T	225	C
1	NS0128378	149	13	14	226	TTCGAAGATTT	227	**********
1	NS0135390	150	15	16	228	T	229	G
1	NS0099529	151	17	18	230	T	231	A
1	NS0097798	152	19	20	232	G	233	A

(continued)

Region	Marker	SEQ ID NO:	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	SEQ ID NO: FAM Probe	FAM Allele	SEQ ID NO: VIC probe	VIC allele
1	NS0093385	153	21	22	234	T	235	C
1	NS0093976	154	23	24	236	G	237	C
1	NS0098982	155	25	26	238	C	239	*
2	NS0123506	156	27	28	240	T	241	G
2	NS0097952	157	29	30	242	G	243	A
2	NS0118907	158	31	32	244	C	245	A
2	NS0122182	159	33	34	246	T	247	C
2	NS0126989	160	35	36	248	T	249	A
2	NS0095677	161	37	38	250	T	251	C
3	NS0098853	162	39	40	252	AG	253	**
3	NS0092561	163	41	42	254	T	255	C
3	NS0093197	164	43	44	256	G	257	A
3	NS0094891	165	45	46	258	T	259	G
3	NS0096225	166	47	48	260	C	261	A
3	NS0103853	167	49	50	262	T	263	C
3	NS0113929	168	51	52	264	G	265	C
3	NS0115535	169	53	54	266	T	267	G
3	NS0121511	170	55	56	268	T	269	C
3	NS0136544	171	57	58	270	T	271	C
3	NS0119569	172	59	60	272	T	273	A
3	NS0123708	173	61	62	274	G	275	A
3	NS0114317	174	63	64	276	G	277	A
4	NS0092743	175	65	66	278	AGAA	279	****
4	NS0098176	176	67	68	280	T	281	C
4	NS0100078	177	69	70	282	T	283	G
4	NS0137415	178	71	72	284	T	285	C
4	NS0095530	179	73	74	286	T	287	A
4	NS0129004	180	75	76	288	G	289	A
5	NS0099024	181	77	78	290	G	291	A
5	NS0101863	182	79	80	292	G	293	A
5	NS0103446	183	81	82	294	G	295	A
5	NS0113878	184	83	84	296	G	297	A
5	NS0115066	185	85	86	298	T	299	A
5	NS0119165	186	87	88	300	G	301	A
5	NS0120015	187	89	90	302	G	303	C
5	NS0123168	188	91	92	304	T	305	C

(continued)

Region	Marker	SEQ ID NO:	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	SEQ ID NO: FAM Probe	FAM Allele	SEQ ID NO: VIC probe	VIC allele
5	NS0123724	189	93	94	306	G	307	A
6	NS0103755	190	95	96	308	T	309	A
6	NS0116125	191	97	98	310	T	311	C
6	NS0125713	192	99	100	312	G	313	A
6	NS0125770	193	101	102	314	G	315	A
6	NS0119281	194	103	104	316	G	317	A
6	NS0124590	195	105	106	318	T	319	C
6	NS0102717	196	107	108	320	G	321	A
7	NS0099531	197	109	110	322	AA	323	**
7	NS0099417	198	111	112	324	G	325	C
7	NS0095211	199	113	114	326	T	327	C
7	NS0097307	200	115	116	328	G	329	C
7	NS0103004	201	117	118	330	G	331	A
7	NS0102630	202	119	120	332	C	333	A
7	NS0102915	203	121	122	334	G	335	A
8	NS0102362	204	123	124	336	T	337	C
8	NS0117716	205	125	126	338	ACTT	339	****
8	NS0100652	206	127	128	340	T	341	A
8	NS0119574	207	129	130	342	G	343	A
8	NS0127728	208	131	132	344	G	345	A
8	NS0099639	209	133	134	346	T	347	C
8	NS0103255	210	135	136	348	T	349	C
8	NS0119106	211	137	138	350	G	351	A
8	NS0101020	212	139	140	352	G	353	C
8	NS0101779	213	141	142	354	G	355	C

Table 5: Most predictive markers for genomic regions associated with plant maturity and/or growth habit of soybean plants

Region	Marker	SEQ ID NO:	Rec. Allele	Dom. Allele
1	NS0099529	151	A	T
1	NS0128378	149	**********	TTCGAAGATTT
2	NS0118907	158	A	C
3	NS0115535	169	T	G
4	NS0137415	178	C	T
5	NS0120015	187	C	G
6	NS0125713	192	A	G

(continued)

Region	Marker	SEQ ID NO:	Rec. Allele	Dom. Allele
7	NS0102630	202	C	A
8	NS0102362	204	C	T

[0117] SNP markers associated with region 1 include SEQ ID NO: 143 through SEQ ID NO: 155. All of these SNP makers for region 1 map to a region on linkage group C2. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 1 through SEQ ID NO: 26, and probes indicated as SEQ ID NO: 214 through SEQ ID NO: 239.

[0118] SNP markers associated with region 2 include SEQ ID NO: 156 through SEQ ID NO: 161. All of these SNP makers for region 2 map to a region on linkage group O. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 27 through SEQ ID NO: 38, and probes indicated as SEQ ID NO: 240 through SEQ ID NO: 251.

[0119] SNP markers associated with region 3 include SEQ ID NO: 162 through SEQ ID NO: 174. All of these SNP makers for region 3 map to a region on linkage group L. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 39 through SEQ ID NO: 64, and probes indicated as SEQ ID NO: 252 through SEQ ID NO: 277.

[0120] SNP markers associated with region 4 include SEQ ID NO: 175 through SEQ ID NO: 180. All of these SNP makers for region 4 map to a region on linkage group I. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 65 through SEQ ID NO: 76 and probes indicated as SEQ ID NO: 278 through SEQ ID NO: 289.

[0121] SNP markers associated with region 5 include SEQ ID NO: 181 through SEQ ID NO: 189. All of these SNP makers for region 5 map to a region on linkage group L. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 77 through SEQ ID NO: 94, and probes indicated as SEQ ID NO: 290 through SEQ ID NO: 307.

[0122] SNP markers associated with region 6 include SEQ ID NO: 190 through SEQ ID NO: 196 of these SNP makers for region 6 map to a region on linkage group D1b. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 95 through SEQ ID NO: 108, and probes indicated as SEQ ID NO: 308 through SEQ ID NO: 321.

[0123] SNP markers associated with region 7 include SEQ ID NO: 197 through SEQ ID NO: 203. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 109 through SEQ ID NO: 122, and probes indicated as SEQ ID NO: 322 through SEQ ID NO: 333.

[0124] SNP markers associated with region 8 include SEQ ID NO: 204 through SEQ ID NO: 213 of these SNP makers map. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 123 through SEQ ID NO: 142 and probes indicated as SEQ ID NO: 336 through SEQ ID NO: 355.

Example 2: Identifying allelic combinations of genomic regions associated with plant maturity in early maturity group soybeans

[0125] Genomic regions 1 and 2 are used to predict the plant maturity of progeny plant resulting from a cross between early maturity and mid-maturity parents (III - V). In particular, the allelic combinations of genomic regions 1 and 2 are correlated with a delay in plant maturity. To determine the correlation between allelic combinations of region 1 and 2 and delay in plant maturity, three populations are developed from crossing an early maturity parent (maturity group 00) with a mid-maturity parent (maturity group III or IV) (Table 6). Populations 1-3 are used to determine the association of the composition of genomic regions 1 and 2 with delay in plant maturity.

Table 6: Maturity group phenotype of parents in soybean populations

Population	Maturity Group of Female Parent	Maturity Group of Female Parent
1	00.9	3.1
2	00.9	3.4
3	00.9	4.1
4	5.9	4.7
5	5.9	5.1
6	5.8	4.7
7	4.1	00.9
8	3.1	00.9
9	3.4	00.9

[0126] The three populations segregate widely for maturity and are polymorphic at genomic regions 1 and 2. F_3 seed are obtained by selecting one pod per F_2 plant (modified single seed descent). The F_3 populations are planted in Guelph,

ON and 1,214 F_3 individuals from all three populations are phenotyped for genomic regions 1 and 2 with the SNP markers NS0128378 (genomic region 1) and NS0118907 (genomic region 2). Individual plants in the F_3 populations are also genotyped for maturity by counting the number of days after August 31st until plant matures; plants are considered mature when 95% of the pods were brown. The procedure is repeated with 1055 of the individual plants where each plant row is grown in Chile and phenotyped for maturity by counting the number of days after March 1st until plant matures; plants are considered mature when 95% of the pods are brown. The procedure is repeated with experimental breeding lines developed from 88 of the 1055 individual plants. Table 8 compares the days to maturity of individual plants across all three populations and the genotype of the individuals at genomic regions 1 and 2. The markers associated with 1 and 2 explain 64% of the variation in plant maturity in year 1 and 94% of the variation in plant maturity in year 2.

Table 7: The association of days to maturity with composition of regions 1 and 2. Presence (1) or absence (0) of dominant allele indicated. Homozygous allele states are 0,0 and 1,1. Heterozygous allele state is 0,1.

Allelic Combination	Region 1	Region 2	Days to Maturity (D after August 31st) Year 1	Year 2
1	0,0	0,0	19.2	9.5
2	0,0	0,1	25.7	13.5
3	0,0	1,1	33.6	15.5
4	0,1	0,0	26.2	16.4
5	0,1	0,1	40.3	ND
6	0,1	1,1	49.1	19.5
7	1,1	0,0	34.2	17.11
8	1,1	0,1	49.3	22.7
9	1,1	1,1	53.5	23.9
		Correlation:	64%	94%

Example 3: Identifying allelic combinations of genomic regions associated with plant maturity in late maturity group soybeans

[0127] Genomic regions 1, 2, and 3 are used to predict the plant maturity of progeny plant resulting from a cross between late maturity and mid-maturity parents. In particular, some of the allelic combinations of genomic regions 1, 2 and 3 are correlated with a delay in plant maturity (Table 8 and 9). To determine the correlation between allelic combinations of region 1, 2 and 3 and delay in plant maturity, three F_3 populations are developed from crossing a late maturity group V with a late maturity group IV. The populations 4-6 following crosses are used to determine the association of the composition of genomic regions 1, 2 and 3 with delay in plant maturity.

[0128] The three segregate widely for maturity and are polymorphic at genomic regions 1, 2, and 3. F_3 seed are obtained by selecting one seed per F_2 plant (single seed descent). 5,984 F_3 individuals from all three population are genotyped with the SNP markers NS0099529 (genomic region 1), NS0118907 (genomic region 2), and NS0115535 (genomic region 3) and seeds with the same marker haplotype are bulked. F_3 seeds are planted.

Table 8: Summary of days to flowering for soybean lines containing various compositions of genomic regions 1, 2, and 3 for plant maturity. Presence (1) or absence (0) of dominant allele indicated. Homozygous allele states are 0,0 and 1,1. Heterozygous allele state is 0,1. ND = no data.

Allelic Combination	Region 1	Region 2	Region 3	Days to flowering (DAP) Pop. 4	Pop. 5	Pop. 6
10	1,1	0,0	1,1	57	57	57
11	1,1	1,0	1,1	58	57	58
12	1,1	1,1	0,0	58	59	55
14	1,1	0,0	0,0	ND	ND	54

(continued)

Allelic Combination	Region 1	Region 2	Region 3	Days to flowering (DAP) Pop. 4	Pop. 5	Pop. 6
15	0,1	0,1	0,1	59	57	56
16	0,0	1,1	1,1	43	36	41
17	0,0	0,0	1,1	44	38	45
18	0,0	1,1	0,0	44	39	44
19	0,0	0,0	0,0	44	38	43

[0129] The individuals are also phenotyped for maturity by counting the number of days after August 31st until plant matures; plants are considered mature when 95% of the pods were brown. Genomic region 3 influences the time of maturity (Tables 8 and 9).

Table 9: Summary of days to plant maturity for soybean lines containing various compositions of genomic regions 1, 2, and 3 for plant maturity. ND = no data.

Allelic Combination	Days to Maturity (D after Aug Pop. 4	Pop 5	Pop 6
10	59	58	58
11	54	58	58
12	59	57	59
14	ND	ND	58
15	54	54	53
16	41	35	37
17	37	35	38
18	44	44	43
19	38	42	43

Example 4: Discovery of molecular markers associated with genomic regions affecting plant growth habit

[0130] Plant growth habit is an important characteristic for late maturity group growing regions. To identify genomic regions associated with plant growth habit, three F_3 populations are developed from crossing a late maturity group V (determinate growth habit) with a late maturity group IV (indeterminate growth habit). Populations 4-6 are used to determine the association of the genomic region 3 with plant habit (Table 6). Seven hundred and seventy-four soybean lines are screened with the markers associated with genomic region 3. The three populations segregated widely for maturity and are polymorphic at genomic region 3. F_3 seed are obtained by selecting one seed per F_2 plant (single seed descent). 5,984 F_3 individuals from all three population were phenotyped with the SNP NS0115535 (genomic region 3) and seeds with the same marker haplotype are bulked. F_3 seeds are planted. A single marker, NS00115535, is determined to be most predictive and able to separate determinant group V varieties from indeterminant group IV and earlier varieties.

Example 5: Genomic regions associated with growth habit and maturity independent of yield

[0131] Plant maturity and yield are closely associated in soybean. An increase of one day in maturity may be equivalent to a -0.7 bu/A increase in yield. The correlation of plant maturity and yield confounds the evaluation of potential QTLs and candidate genes associated with yield. Identification of genomic regions associated with plant maturity allows breeders to genetically fix plant maturity within a soybean plant and elucidate traits associated with yield.

[0132] Three soybean populations are generated from crossing a maturity group 0 with a maturity group III or IV. Populations 7-9 are used (Table 5). The progeny seed planted in Chile and then harvested 52 seeds from those progeny plants are selected in Chile and the plants are grown in Ontario in 2006. Eighty-four progeny are screened with markers

associated maturity regions 1 and 2 and evaluated for maturity days and yield (Table 10-12). Markers associated with regions 1 and 2 select for maturity and are independent of yield. For example, Progeny 0430 has significantly higher yield than Progeny 0083 (Table 11). The higher yield of Progeny 0430 is not attributed to differences in plant maturity due similar days to maturity and allelic states of maturity genomic regions 1 and 2.

Table 10: Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity Days	Allelic combination
Population 8	0117	30.93	5.50	1
Population 8	0140	29.18	6.50	1
Population 8	0234	32.84	6.50	1
Population 8	0043	34.67	6.50	1
Population 8	0267	36.80	7.00	1
Population 8	0276	40.67	7.50	1
Population 8	0243	42.88	9.50	1
Population 8	0198	39.56	10.50	1
Population 8	0325	33.42	11.00	1
Population 8	0011	39.92	11.50	1
Population 8	0390	41.22	11.50	1
Population 8	0418	44.05	11.50	1
Population 8	0119	41.62	9.50	2
Population 8	0069	37.68	10.00	2
Population 8	0274	38.90	10.00	2
Population 8	0165	43.03	10.00	2
Population 8	0219	39.67	12.50	2
Population 8	0373	49.22	13.00	2
Population 8	0089	50.41	17.00	2
Population 8	0186	43.74	18.00	2
Population 8	0395	43.20	9.50	3
Population 8	0426	41.12	10.00	3
Population 8	0256	43.83	10.00	3
Population 8	0216	45.47	10.50	3
Population 8	0367	47.94	11.50	3
Population 8	0266	42.86	14.00	3
Population 8	0285	42.04	16.00	3
Population 8	0277	50.47	16.00	3
Population 8	0188	45.62	17.50	3
Population 8	0143	44.47	13.50	4
Population 8	0101	41.22	14.50	4
Population 8	0366	41.79	16.50	4
Population 8	0340	47.41	11.50	7
Population 8	0359	46.10	14.50	7
Population 8	0184	46.24	14.50	7
Population 8	0158	43.08	16.00	7
Population 8	0401	50.95	16.00	7
Population 8	0255	47.26	17.00	7
Overall Mean Non-Check		42.78	12.00	
Mean		42.60	12.38	
Check Mean		44.08	9.25	
# Locs		3	2	
# Reps		3	2	
CV		9.978	15.094	

(continued)

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity Days	Allelic combination
LSD(.05)		6.989	3.640	
F-Statistic		4.525	7.670	
P-Value		0.000	0.000	
Repeatability		0.781	0.870	
Root MSE		4.269	1.811	

Table 11: Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity (D)	Allelic Combination
Population 9	0381	38.46	11.00	1
Population 9	0473	40.89	12.50	1
Population 9	0371	36.86	9.00	2
Population 9	0380	31.86	10.00	2
Population 9	0263	43.01	11.00	2
Population 9	0396	38.97	12.00	2
Population 8	0083	29.01	15.00	2
Population 8	0430	42.65	15.00	2
Population 9	0299	39.96	16.00	2
Population 8	0076	42.95	22.00	2
Population 9	0142	32.31	11.50	3
Population 9	0487	27.86	14.00	3
Population 8	0240	43.66	15.50	3
Population 9	0317	46.74	16.50	3
Population 8	0392	38.21	18.50	3
Population 9	0206	45.77	19.00	3
Population 9	0254	44.06	19.50	3
Population 8	0280	48.22	26.50	3
Population 9	0262	41.41	17.50	4
Population 9	0173	43.17	23.50	4
Population 9	0032	33.65	13.50	6
Population 9	0166	40.72	11.50	7
Population 9	0188	42.19	16.50	7
Population 9	0117	47.98	19.00	7
Population 8	0229	45.34	20.00	7
Population 9	0437	43.25	20.50	7
Population 9	0077	34.05	10.50	8
Population 9	0078	47.66	17.00	8
Population 9	0187	37.18	27.00	8
Population 8	0230	47.26	20.50	9
Population 9	0368	46.49	21.50	9
Population 9	0505	34.06	23.50	9
Overall Mean		39.96	15.69	
Non-Check Mean		40.38	16.57	
Check Mean		37.07	9.50	
# Locs		3	2	
# Reps		3	2	
CV		15.453	13.984	
LSD(.05)		10.105	4.434	

(continued)

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity (D)	Allelic Combination
F-Statistic		2.546	10.862	
P-Value		0.000	0.000	
Repeatability		0.609	0.908	
Root MSE		6.176	2.194	

Table 12: Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity (D)	Allelic Combination
Population 7	0121	35.25	8.50	1
Population 7	0107	30.98	10.50	1
Population 7	0251	36.59	10.50	1
Population 7	0377	34.51	11.00	1
Population 7	0375	34.34	11.50	1
Population 7	0326	30.51	13.00	1
Population 7	0216	42.26	10.50	2
Population 7	0312	36.15	18.00	2
Population 7	0298	41.40	19.00	2
Population 7	0205	39.41	13.00	3
Population 7	0139	38.59	14.50	3
Population 7	0365	38.14	13.00	4
Population 7	0004	39.79	12.50	5
Population 7	0361	47.75	24.00	8
Overall Mean		39.37	12.55	
Non-Check Mean		37.79	13.57	
Check Mean		44.10	9.50	
# Locs		3	2	
# Reps		3	2	
CV		16.518	11.343	
LSD(.05)		10.749	2.979	
F-Statistic		3.074	16.491	
P-Value		0.002	0.000	
Repeatability		0.675	0.939	
Root MSE		6.503	1.423	

Example 6: Utilization of molecular markers associated with plant maturity to select geographic region for planting seed

[0133] Soybean genotypes are grown to narrow zones of latitude to optimize yield due to photoperiod sensitivity. Northern soybean varieties, in contrast to Southern varieties, initiate flowering with longer days. Northern varieties planted south of their adaptation zone exhibit accelerated flowering, limited plant growth and reduced yield. Southern soybean varieties planted north of their adaptation zone have delayed flowering with a potential for frost damage that may reduce yield. When the parents differ in plant maturity greater than 10 day, the progeny of the cross segregate widely for plant maturity. Molecular markers associated with plant maturity genomic regions allows breeders to cross with parents that differ in maturity greater than 10 days, select seed of the cross to grow in the appropriate maturity zone.

[0134] A BC_2F_1 soybean population is generated by crossing MG III.5 with MG 000 and the seed is selected for the appropriate maturity zone growing region using the molecular markers associated with plant maturity. Ninety-three BC_2F_1 plants are screened with 106 SNP markers to evaluate the genetic similarity to the recurrent MG III.5 parent (Table 13). Additionally, the SNP markers included markers associated with the maturity genomic regions 1, 2, 3, 4, and 5. Each individual is heterozygous for at least one maturity genomic region. Individual Progeny:0107 is heterozygous for 1, 2, 3, 4, and 5 and may be used to select for individual varieties adapted to each maturity group zone. Individuals selected

to move forward to the next generation based on adaptation to specific maturity group regions using the allelic combination for the genomic maturity regions.

Table 13: Summary of heterozygousity for maturity genomic regions with the F2 generation of MG III.5 parent/(MG III.5 parent*2/MG 000 parent). Individuals within the population are selected for a geographic maturity group region with SNP markers associated maturity genomic regions.

Plant	Similarity to MGIII.5 parent (%)	Heterozygous for genomic maturity region: 1	2	3	4	5
MG III.5 parent	98.7					
MG 000 parent	2.6					
Progeny: 0050	86.2	x			x	x
Progeny: 0107	85.8			x	x	
Progeny: 0050	84.9	x	x			
Progeny: 0093	84.9	x		x		
Progeny: 0050	82.8		x	x	x	x
Progeny: 0096	82.8			x	x	
Progeny: 0107	82.3		x			
Progeny: 0096	81.9	x			x	
Progeny: 0107	81.5	x	x	x	x	x
Progeny: 0066	60.8				x	
Progeny: 0096	84.1	x		x	x	
Progeny: 0093	82.8	x	x			
Progeny: 0050	81.9	x		x	x	
Progeny: 0050	81.9	x		x		
Progeny: 0096	81.0	x		x	x	
Progeny: 0046	80.6		x	x	x	x
Progeny: 0050	80.2	x	x	x		
Progeny: 0107	80.2	x		x	x	
Progeny: 0093	80.2	x			x	
Progeny: 0096	80.2		x			

(continued)

Plant	Similarity to MGIII.5 parent (%)	Heterozygous for genomic maturity region: 1	2	3	4	5
Progeny: 0093	79.7	x			x	
Progeny: 0063	79.7			x	x	
Progeny: 0093	79.3		x	x		x
Progeny: 0096	78.9	x		x		
Progeny: 0012	78.9	x			x	x
Progeny: 0085	78.4	x		x	x	
Progeny: 0096	78.0	x				
Progeny: 0107	77.6	x		x		
Progeny: 0063	74.6		x	x	x	
Progeny: 0063	74.1	x		x		
Progeny: 0012	61.2	x	x	x		
Progeny: 0036	61.2	x	x	x		
Progeny: 0012	61.2	x	x			
Progeny: 0093	61.2	x		x	x	x
Progeny: 0012	61.2	x		x		x
Progeny: 0050	61.2	x		x		
Progeny: 0036	61.2	x		x		
Progeny: 0063	61.2	x			x	x
Progeny: 0050	61.2	x			x	
Progeny: 0012	61.2	x			x	
Progeny: 0107	61.2	x				
Progeny: 0012	61.2	x				
Progeny: 0012	60.8	x		x	x	
Progeny: 0012	60.8	x		x	x	
Progeny: 0012	60.8	x		x	x	

(continued)

Plant	Similarity to MGIII.5 parent (%)	Heterozygous for genomic maturity region: 1	2	3	4	5
Progeny: 0050	60.8	x		x		
Progeny: 0012	60.8	x			x	
Progeny: 0036	60.8	x			x	
Progeny: 0012	60.8	x				
Progeny: 0012	60.8	x				
Progeny: 0036	60.8		x	x	x	
Progeny: 0012	60.8			x	x	
Progeny: 0012	60.3	x	x			
Progeny: 0093	59.9	x	x	x	x	
Progeny: 0096	59.9	x		x	x	
Progeny: 0012	59.9	x		x		
Progeny: 0050	59.9		x	x		x
Progeny: 0085	59.9		x	x		x
Progeny: 0050	59.5	x	x			
Progeny: 0096	59.5	x	x		x	
Progeny: 0036	59.5	x	x		x	
Progeny: 0096	59.5	x		x	x	x
Progeny: 0063	59.5	x		x		
Progeny: 0036	59.5	x		x		
Progeny: 0096	59.5		x			x
Progeny: 0093	58.6	x	x		x	
Progeny: 0050	58.6	x				x
Progeny: 0050	58.6	x				
Progeny: 0093	58.6		x	x	x	
Progeny: 0093	58.2	x	x			

(continued)

Plant	Similarity to MGIII.5 parent (%)	Heterozygous for genomic maturity region: 1	2	3	4	5
Progeny: 0012	58.2	x	x		x	
Progeny: 0012	58.2	x		x	x	x
Progeny: 0050	58.2	x		x	x	
Progeny: 0012	58.2	x		x	x	
Progeny: 0012	58.2	x		x		
Progeny: 0143	58.2	x		x		
Progeny: 0096	58.2	x			x	
Progeny: 0050	58.2	x			x	
Progeny: 0012	57.8	x	x		x	
Progeny: 0050	57.8	x	x		x	
Progeny: 0012	57.8	x		x		
Progeny: 0093	57.8	x			x	
Progeny: 0093	57.8	x				
Progeny: 0012	57.8		x		x	x
Progeny: 0012	57.8			x	x	
Progeny: 0012	57.8			x	x	
Progeny: 0096	57.3	x		x	x	
Progeny: 0050	56.9	x	x		x	
Progeny: 0093	56.9	x		x	x	
Progeny: 0050	56.9	x		x	x	
Progeny: 0050	56.9	x		x		
Progeny: 0050	56.9			x		x
Progeny: 0096	55.6	x	x		x	x

Example 7: Estimating effect of genomic regions associated with maturity

[0135] Each allele of each individual maturity genomic region is associated with a value that can either increase or

decrease the relative maturity of a given line. The relative maturity of a given line are predicted by using an additive or epistatic model. The example in Table 14 demonstrates predicting relative maturity based on the allelic combination of the maturity genomic regions. The maturity group of a soybean seed is predicted by the composition of maturity genomic region alleles.

Table 14: An example of predicting relative maturity based on additive model

Maturity genomic	Δ Days	Direction
1	10	10
2	5	-5
3	3	-3
4	2	2
5	6	6
6	4	4
7	5	-5
	Sum	9
	Constant	3
	Maturity Days	12
	Maturity Group	1.2

Example 8: Utilization of molecular markers associated with plant maturity to facilitate crosses with exotic germplasm

[0136] The genetic base of cultivated soybean is narrow compared to other field crops. Eighty to ninety percent of cultivated soybean gene pool are traced to 12 plant introductions in northern United State and seven plant introductions in southern United States. Due to the narrow genetic base, soybean is more likely to be impacted by disease and insect attacks. Exotic germplasm helps expand the genetic base of soybean. In addition, exotic germplasm possesses such key traits as disease resistance, insect resistance, nematode resistance, and tolerance to environmental stress. At present, many exotic species are inaccessible in part due to limitations with crossing soybean plants from extremely different maturity groups. Traditionally, breeders must produce and maintain large numbers of progeny plants from crosses between exotic and cultivated germplasm, in order for breeders to select for a small number soybean plants of the desired maturity group. It is often cost prohibitive to maintain the large number of plants required.

[0137] Molecular markers associated with plant maturity facilitate the used of exotic germplasm. Breeders create crosses between exotic and cultivated germplasm. The progeny seed is assayed for plant maturity without expending the resources required to plant and grow large numbers of progeny.

Example 9: Utilization of molecular markers associated with plant maturity to facilitate introgression of a transgene

[0138] After a transgene is introduced into a variety, it may readily be transferred to other varieties by crossing. Most soybean variety development crosses are made between parents within 10 maturity days of each other. When parents differ in plant maturity greater than 10 days, the progeny of the cross segregate widely for plant maturity. In order for breeders to obtain and select for soybean plants of the desire maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive. If a transgene is present in a maturity group III variety needs to be transferred to maturity group 0, a direct cross between a maturity group III variety and a maturity group 0 variety is not typically performed. Instead, the transgene is transferred through a series of intermediate crosses between varieties close in plant maturity. Molecular markers associated with plant maturity genomic regions allows breeders to cross parents that differ in maturity greater than 10 days, then select seed of the cross based on the presence of the transgene and the plant maturity phenotype.

Example 10: Utilization of molecular markers associated with plant maturity to facilitate introgression of a trait

[0139] If a variety possesses a desirable trait, it may readily be transferred to other varieties by crossing. Most soybean variety development crosses are made between parents within 10 maturity days of each other. When the parents differ in plant maturity greater than 10 days, the progeny of the cross segregate widely for plant maturity. In order for breeders to obtain and select for soybean plants of the desire maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive. If a trait is present in a maturity group III variety needs to be transferred to maturity group 0, a direct cross between a maturity group III variety and a maturity group 0 variety is

typically not performed. Instead, the trait is transferred through a series of intermediate crosses between varieties close in plant maturity. Molecular markers associated with plant maturity genomic regions allow breeders to cross with parents that differ in maturity by greater than 10 days and to select seed of the cross based on the presence of the trait and the plant maturity phenotype.

Example 11: Utilization of molecular markers associated with plant maturity to select environments to optimize expression of traits

[0140] Soybeans cultivated in different environments often perform differently. For instance, a soybean variety may produce seeds with a particular fatty acid profile in one environment and a different fatty acid profile in another environment. A number of environmental factors can influence the expression of traits, including soil type, soil conditions, temperature, photoperiod, geography and cultural practices. Variation in performance of genotypes across different environments is often referred to genotype x environment interactions.

[0141] Soybean seed oil levels are highly impacted by environment. Oil concentration increases with decreasing latitude, therefore, soybeans in maturity groups 00-I generally have lower oil levels than later maturing soybeans (Figure 1). Molecular markers associated with plant maturity assist breeders in selecting soybean genotypes and produce plants that are better adapted to a maturity group region to produce higher oil.

[0142] Soybean seed fatty acid composition is highly impacted by the latitude of cultivation. The present invention provides molecular markers associated with plant maturity which are useful for assisting plant breeders to select favorable soybean maturity genotypes to optimize the expression of particular traits in specific geographies, such as fatty acid synthesis, wherein the trait is conventional or transgenic. As used herein, conventional traits include those obtained by mutagenesis. For example, the profile of fatty transgenic soybean plants engineered to produce stearidonic acid (SDA) have a positive correlation with latitude for SDA production and have a negative correlation with latitude for oleic acid, stearic acid, palmitic acid and α-linolenic acid production (Table 15). The percent of SDA increases with increasing latitude (Figs. 2-3).

Table 15: Correlation of longitude and latitude on fatty acids for mature soybean seed

	Latitude			Longitude		
Fatty Acid	**R**	**P value**	**N**	**R**	**P value**	**N**
stearidonic acid	0.6625*	3.12E-10	71	-0.3748	0.001281263	71
γ-linolenic acid	0.1097	0.362504877	71	-0.0798	0.508051934	71
oleic acid	-0.4081 *	0.000411819	71	0.167	0.16389379	71
linoleic acid	-0.1581	0.187769857	71	0.0837	0.48752276	71
α-linolenic acid	-0.2403*	0.043495686	71	0.1901	0.112261464	71
palmitic acid	-0.7305*	4.82E-13	71	0.4592	5.62E-05	71
stearic acid	-0.258*	0.029810388	71	-0.1498	0.212583113	71
*signifcant at 0.05 level						

[0143] Latitude is closely related with maturity groups and growing regions. Soybeans are classified into 13 maturity groups (000, 00, 0, I-X) according to the range in latitude in which the plants are adapted and most productive. Group 000 are the earliest maturing and cultivated at the higher latitudes and Group X are the latest maturing and cultivated in lower latitudes. Molecular markers associated with plant maturity will assist breeders in selecting soybean genotypes that are adapted to latitudes known to be associated with preferred SDA production in the plants. As a result, the soybean breeders more efficiently produce plants that are better adapted to the environment and produce higher levels of SDA or other similar traits.

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<223> Synthetic Primer

<400> 76
gcaagaaata agatatagcc t t gggt at 28

<210> 77
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 77
tggcatcctc ttatcaacaa agc 23

<210> 78
<211> 22
<212> DNA
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<220>
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<400> 78
cctatcagtg ttggtggaag ca 22

<210> 79

<211> 22
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<220>
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<400> 79
ggtgagccaa ggaaagaaac ac 22

<210> 80
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<220>
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<400> 80
cgacgatatg aatcagggaa tagg 24

<210> 81
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<220>
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<400> 81
tggcatcctc ttatcaacaa agc 23

<210> 82
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<212> DNA
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<220>
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<400> 82
cctatcagtg ttggtggaag ca 22

<210> 83
<211> 25
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<220>
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<400> 83
gagaaggatg cttttgaaga gctta 25

<210> 84
<211> 24
<212> DNA
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<220>
<223> Synthetic Primer

<400> 84
acctgactcg gtttctcatt caat 24

<210> 85
<211> 30
<212> DNA
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<220>
<223> Synthetic Primer

<400> 85
ggtaaacatt t gtcttaccat tattgacatt 30

<210> 86
<211> 30
<212> DNA
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<220>
<223> Synthetic Primer

<400> 86
cat caact t g cat t acat aa agt ct gat t a 30

<210> 87
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 87
ttatgtttgt aat ct aat ca ggctatgttt tt 32

<210> 88
<211> 28
<212> DNA
<213> Artificial sequence

<220>
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<400> 88
aaaaggaaga aaagaagaac aaattttg 28

<210> 89
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 89
agcagaat cc tcacttcaaa gtacag 26

<210> 90
<211> 25
<212> DNA
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<220>
<223> Synthetic Primer

<400> 90
accaagagga gaaaatctgc t t agg 25

<210> 91
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 91
ccaacaaggg t gcagaaatg a 21

<210> 92
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 92
gggt t gcct t gat agt t gaa t ct g 24

<210> 93
<211> 26
<212> DNA
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<220>
<223> Synthetic Primer

<400> 93
cactcatct tcaggcatat act cca 26

<210> 94
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 94
tcttcaaggc t ggt t ggat g a 21

<210> 95
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 95
tgatggt gaa tatgaagggt ct ca 24

<210> 96
<211> 27
<212> DNA
<213> Artificial sequence

<220>
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<400> 96
aatggaactg ggatttctta ct acaaa 27

<210> 97
<211> 23
<212> DNA
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<220>
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<400> 97
tggcaaaagc tagagagcat gat 23

<210> 98
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 98
aaccct aacc ttttcttctg ctctt 25

<210> 99
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 99
aactgaaaat tttacattcc tgtcaatg 28

<210> 100
<211> 33
<212> DNA

<213> Artificial sequence

<220>
<223> Synt het i Primer

<400> 100
ttctaactga tgacttcaca ctagttttct tat 33

<210> 101
<211> 26
<212> DNA
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<220>
<223> Synthetic Primer

<400> 101
ctcatgtcat cat ct t acac aaagca 26

<210> 102
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 102
cttgtggaga ataagaaaaa ggttcttc 28

<210> 103
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 103
t ct at at cca aagtctttat atggacacct 31

<210> 104
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 104
ttaaaatcat t acacagtca ct ccacaa 28

<210> 105
<211> 28
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic Primer

<400> 105
gtcacaaagc aattccaatt t ataacact 28

<210> 106
<211> 24
<212> DNA
<213> Artificial sequence

<220>
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<400> 106
aacct t ggt a aggcaaaaat gcta 24

<210> 107
<211> 24
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<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 107
gggtgctgat tttcataaagttga 24

<210> 108
<211> 24
<212> DNA
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<220>
<223> Synthetic Primer

<400> 108
gccattctaa tttttgtgga caga 24

<210> 109
<211> 22
<212> DNA
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<220>
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<400> 109
t aacct ct cc t cccccaaac tt 22

<210> 110
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 110

gggt t gt cct agaactcctg aaga 24

<210> 111
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 111
t gt t ct t gt a atcatcaacc agct t aa 27

<210> 112
<211> 20
<212> DNA
<213> Artificial sequence

<220>
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<400> 112
gcct t ct ccg t t gcat acca 20

<210> 113
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 113
tcacatgcat tagggaattg ctt 23

<210> 114
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 114
agcattgtcc caact aagat ct tgt 25

<210> 115
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 115
at gt attcat tttgaatggg ct acaa 26

<210> 116

<211> 26
<212> DNA
<213> Art i f i ci al sequence

<220>
<223> Synthetic Primer

<400> 116
gttaaaaatt acaacgccac gaataa 26

<210> 117
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<220>
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<400> 117
ttgcaatttt ttatatcttg atttcacat 29

<210> 118
<211> 23
<212> DNA
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<220>
<223> Synthetic Primer

<400> 118
gcgaagaatc aaaactggtc aaa 23

<210> 119
<211> 27
<212> DNA
<213> Artificial sequence

<220>
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<400> 119
acaaggacaa ggctatgaga agtaaga 27

<210> 120
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 120
ggccatgaat caagccactt 20

<210> 121
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 121
gagttagatt t at ccggcaa cga 23

<210> 122
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 122
cccgaagaga t gt cat gt t a acaa 24

<210> 123
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 123
gcgaaaaaca aatttccatt gc 22

<210> 124
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 124
agtggtgatg gcatggttga 20

<210> 125
<211> 25
<212> DNA
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<220>
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<400> 125
tcactaagat ctggaattcc aaacc 25

<210> 126
<211> 30
<212> DNA
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<220>
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<400> 126
tggaggaaga taagttaaca attaatagca 30

<210> 127
<211> 26
<212> DNA
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<220>
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<400> 127
cctgaaaaag ccaat cat aa t ct aca 26

<210> 128
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 128
caggtaggga t gct t cagtgttg 23

<210> 129
<211> 28
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<220>
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<400> 129
tggaaaagga aagatgatat agcaattt 28

<210> 130
<211> 23
<212> DNA
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<220>
<223> Synthetic Primer

<400> 130
aaccaggaca accacat caa t ct 23

<210> 131
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 131
tgatcggatt tgactctttt gtcat 25

<210> 132
<211> 27
<212> DNA
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<220>
<223> Synthetic Primer

<400> 132
ttgcagtttt tgagtatacc act acca 27

<210> 133
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 133
at ggaagtgg atggaagtag tataatga 28

<210> 134
<211> 24
<212> DNA
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<220>
<223> Synthetic Primer

<400> 134
tttccacatt ttccaatagc ttga 24

<210> 135
<211> 25
<212> DNA
<213> Artificial sequence

<220>
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<400> 135
tggagctcta ccgaaagttt acaaa 25

<210> 136
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 136
caagaactac ctcaaagcca at cc 24

<210> 137
<211> 25
<212> DNA

<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 137
cttttaaatg gacccagttt gttca 25

<210> 138
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 138
t gggt t gaag tgaaatggtc aga 23

<210> 139
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 139
agcaacaatg actatttcaa ccatttt 27

<210> 140
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 140
ccacacctcc ccttggttt 19

<210> 141
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 141
cagcaaaatg aatgcaattg gt 22

<210> 142
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic Primer

<400> 142
acat t gcaag aactggatgg ttt 23

<210> 143
<211> 1040
<212> DNA
<213> Glycine max

<400> 143

agaaagagag aagagt gaag agt gt t at t t t t t gt t t ga ct ct gaaaaa aaat t aagat 60
acaacacat g gcat gat t gg agccgt t t at at gat cct ac gcat gaaaat gt t t caact a 120
cacat ccggt t cccgt caag aat gggagag gat ccgt at g cgat gaact g aact t gaat t 180
gat t cat t t a at at agt gag agagaaaaaa gt t aaaccaa t caaaat ggt t gat t gct t t 240
agt t t t at at t t cct t t t t a caaat t aacc ct at t gt t aa cagat t aat t t ggt t aat ga 300
at at t t t at t t ct t t t t t at t ct ct t t aat t t caat caaa caat t t t at t t t t t act t t t 360
t t t ct at t ct gt ct cat t t a t t t t t cat t t ct cacgat ca aacagaggat t agt ct aaaa 420
aaat at t aaa t aat gct t ga t t t t at t gga act aat t ct t aat t t cat ga ccggaat at t 480
cacat gaat t aat t gaaaaa t gt gt aagat t ggt t agat t ggat t aat t t act t gact t t 540
ct t aat t gt c t t t t t at gaa t t t gact aac ct aat t ct t t at t t at t t t g cgaagaaaga 600
agt at t at t g t at ccgt gt g t gt at at at a aaat aaagt c at t caat cgg t cct aaat t a 660
cacaagat ac at gt caaat a t gcaaat gaa gt aact ct t t gat ct gaaaa aaaaaaaaaa 720
aaaaaacaat ccagt t t t cc ct t gt gaaaa aagagct cca aat agct t ca ggt t gaagca 780
aaaat aaaaa at t gaagaaa aggt t gaagc t aaacat aaa cct caaaaac t ggt gt acgt 840
cat t aacat g ggt gaccccg aagt t gccac gt act ccaag cgt gt gcggt t aacaacgt a 900
cgagagt at c gaat ct gcct ct gct t t ct t t caat t t caa cagaacccat cacacacaca 960
cagaccccat caaccaaaaa caaagaacaa t gat t ct gag at t t gcagca gct gcaggt c 1020
gact ct agga aagacccggg 1040

<210> 144
<211> 821
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1)..(821)
<223> unsure at all n locations; n = a, t, c, or g

<400> 144

attccataac ggtttgcaac tcttgaagat cgtgactctg gtcgtgtcac tcctgcgtat 60
cgcgcctggg agcaacaaga ttagttgttc ctctcatggc ttcaatccac cgtttctgct 120
cccattcttc gaaatttcat cggctgcact agtttgtggc ttctctagga caaaatccac 180
aactattttc atgctcatac aaatgcaaag gcacggccac ttcgtacaga gctgcatcaa 240
ctcactcttg aaggtcgtac tatttctgat tatttgactg agattcagaa tcttgttgat 300
tcttttactg ctattggtga tccaatttct atttgcgaac atgttgacat tattattgaa 360

gaatgtgtac cagaaaacta tgagtcctct gtttcgcaca tcaataatag atctgaacct 420
ctcactattg atgaaatcaa aactgttctt ctcggtcatg aggctcagat tgacaaattc 480
aggaagaagg cagtggtttc ggttaatgtt gcttccacat ccactgtgtc ttctgtgact 540
aatccatctc atgctaattt tggaggtttc agaatcagaa tcagagtcag tataaaaaca 600
gaggacgtag cagtattcag tgttacatct gtcagaagtt tggtcatgat gttgccaact 660
gctggcacag gccctcaact tcctatgctc tgctccttat cctatgttgg cacaatttcc 720
caccatgcct cagctttatt ccaatttctt tggagctgct ctgcatttcc ctcttatctg 780
tttatgcagg ctcctgtntc tcaacaatgc cagcagccac t 821

<210> 145
<211> 855
<212> DNA
<213> Glycine max

<400> 145

tagaattaca ggtctggaga agtatctgaa gactgtagat tcggtgcggg attggattct 60
gtttcatata tactttttta acaacataag ttaatttttc atatagtttt ttatttaatt 120
ttataaatat tttgaataaa accaaaaata tatgtaagtc gttcgtacat aagacgcgtt 180
aaacgtcagt acttaataat aataatatag tgtaagaaac tcaactgggg aagtgcataa 240
aaaaataaaa gtataaatac aagaaaaatg aactaagaaa gtgtgtactt atgtgctaat 300
tagcaagatc gttggaacaa aaagccaaat tgactggtac tttctcgtta atttcttcaa 360
ttttcattgt ttcgttaaat actagtggca tgtccgtcaa aagtcaaaag ccacatattg 420
atgaaattgt gttgttagaa taattaatta attacttgca gagcaaatct cctccacaat 480
ttttcttttt ttctctaccc aagagacttc ctttcaactc agatactctt tgattctctt 540
caggaaaaca tcaactaatt aaaatctaat tttgtctttg atactctttg tccgcggaat 600
tcaccacccc caccttctca atttgtttgc tttctgcttt cttacctctt ttttctcaga 660
tttcatttgg ttgatccttt cttcaattct tcttctgggt ttgtagttgt ttttttatct 720
gacttgtgtt tctaaaatcc atgaaccgta tgtgatttcc agtgtctttt tctttttcca 780
gattcccaga gagaaaaaag aaaaaatcct tttgtttgtg tgagactgta aggatcaatt 840
ggttgagttc tccta 855

<210> 146
<211> 1395
<212> DNA
<213> Glycine max

<400> 146

act t gcct ga gagt gt t gt t gct t ct gaac aggct gcat g t t cat cacat t t gaaagaaa 60
ct gt t ggaaa acct act ct t gat gcat ct c aacccagccc aact gct act cccagagat a 120
t t gaggct t t t ggccgat ct ct aagaccaa acat t gt t t t gaat cat aat t t ct cct t gt 180
t ggat caagt t caat ct gca agaaacat gg agact gat cc t agt aat cgg gat gt caaga 240

gat t gaaagt t t ct gat aat at ggt ggt gg acaaacagct ggt agat t cc aaccat gggc 300
aacagt t gt c at at gggt at gat aat gt gg t caaagat gg gt ggt caggt aat aat t cca 360
t gccat cat c agat cct aat at gct aagct t t t caacaaa gccact t gat ggacagt aca 420
caaat gcat c t t ct caagag gaggt t ggt t at ggt aaaaa aat t gct ct t aat gt t gct g 480
acagt aacaa agcagcct ct gt t aaaagt g at t at t ct ct ggt aaat cct caaat ggcac 540
cat cat ggt t t gagcgat at ggaact t t t a aaaat ggt aa gat gt t gcca at gt acaat g 600
cacagaaaat gact gct gct aagat aat gg accagcct t t cat t gt agca aaccaat t ca 660
gat agt t t gc gct t t cat aa t t cagt agag caaat t caga gt gt cagt ga t gct cagct a 720
agt aat gct a gt gaaagt cc aat gcct gct t t agct gcaa at aagcat gc agact ct cag 780
t t at cgacac ct gct gt t ga acct gact t a ct t at t at ga gaccgaagaa gcgaaaaagt 840
gccacat ct g aact cat acc at ggcat aaa gaact gt t ac agggt t ct ga aaggct t cga 900
gat at caggt ggt t gccaaa act aagt gat t t aat gt gct t at t t t t cgg t gt t gct at t 960
gt t ggt gt ag t aaaagat cc cat gt ct cca gt t gat at t g t gt t gt t t ca at t gt t t t ga 1020
aagaaaacgg t gt gt t t cca t agt gt cagt at gact at t t t aat at t gt t t t at gt t t at 1080
caat at at ca agt at t t gt t t t cct at aac t t aaaat t t c t t act at gt g gcagt gt ggc 1140
agaat t agac t gggct caaa gt gcaagcag at t gat t gaa aaggt t t gt t t at aat aaaa 1200
t cagt ct acg cat gaat ct a t aat t ct at a at t t at gagt t cact t t act ct gt at aat t 1260
at aat t at ag gt t gaagaca gt gt ggaggt agt t gaagat t t gccagcag t ggt gaagt c 1320
aaaaagaaga ct t gt ct t gt act act cagc t t at gcagca acaact t agt cct cct ccag 1380
ct gcaggcag gcgag 1395

<210> 147
<211> 618
<212> DNA
<213> Glycine max

<400> 147

atttcttata ctcaaatttt tggtacctct ctttccttca ataaaatttc ttcttttata 60
catgtgtgtg tgtgtgtttg gatgttggta ataaatttct gccagaggat ttgaagatga 120
agagtccata agtttgttga ttacttgata caatctaata gagtatttta accggcccat 180
tttttttctt gggctaaagt gatgtaacat ctaacaagtg ttgaggagat aaaacatttt 240
caaggagttt gattgttgga tatctagagc aattgtaggg ttttattgta ttcatgatgc 300
ttcttaatca ttcaaattgt ttgtgccttt tcatgttata gctttgtgaa gaggagttac 360
tcaaggaaga agcgcttttta gtaaaaaaac aacttatttc ctttagtttt attaatgact 420
tgtatgcaga ttggacaaca ctttagggat ggctacttgc ataaagaaga atttaagata 480
gtttatgttg ctccaatgaa ggtatgttga tgcttttgtt tttctttaca tttctctatt 540
cagatttgct ttttgttccc tgcatttgtg tgccattact catttctaag tatagattct 600

tgtcctttcc aggctttg 618

<210> 148
<211> 1066
<212> DNA
<213> Glycine max

<400> 148

gtatggggcg attcaggagg tggaatctgc aatacaagag cttgaaggga acaatgaggg 60
gaatgtaatg ttgacagaaa ctgttggacc tgaacacata gccgaggttg ttagccgttg 120
gactggtata cctgtgacaa ggcttggcca aaacgataaa gaaaggttga ttggtcttgc 180
tgacagattg caccagagag ttgtggggca agaccaagca gttaatgctg ttgctgaagc 240
tgtgctgaga tcaagagctg ggcttggaag acctcagcaa ccaactggtt ccttcttgtt 300
cttgggtcca actggtgttg gcaagactga gctttcaaag gcacttgctg agcaactctt 360
cgatgacgaa aatcaattgg tgagaattga catgtctgaa tacatggaac aacactctgt 420
ttcgcggttg attggtgcac caccagggtg tgtggattga cattttcaca tttcagttta 480
ttgttagttt tctgtatgaa ctacagataa ctgactcatt gtttcgactt tcaggtatgt 540
tggacatgaa gaaggaggtc aactaactga agctataagg cggaggcctt atagtgtggt 600
actctttgat gaagtggaaa aggcacacac atctgtgttt aacactctcc ttcaagtctt 660
ggatgatggg aggttaactg atggccaagg ccgtactgtg gacttccgaa acactgtcat 720
tatcatgacc tccaaccttg gtgcagagca tctcctcact ggactttcag gaaaatcttc 780
aatgcaagta gcccgtgata gagtgatgca agaggtatgt ctcttgacac catttgttta 840
atatgtatga caaaggtctt tgtgctgtgt tttgacttgt gaccttgtct gttgaatttg 900
ttgtaacagg tgaggaggca ttttaggcca gagttgttga accggctcga tgaaattgtt 960
gtatttgatc ctctttcaca cgagcaacta aggaaggtca caaggttaca aatgaaggac 1020
gttgctagtc gtcttgctga gagaggaata gccattggca gtgacc 1066

<210> 149
<211> 1052
<212> DNA
<213> Glycine max

<400> 149

aagttcactc ttaactaatg tttttcact gtattccta gctatatttc agactggtgt 60
gtgacagtct ttttttgttc atagatattg cggaagcttg aagaacgtgg ggctgacctа 120
gaccgcttgt atgagatgga ggaaaaagac attggggcat taattcgtta tgcgcctgga 180
ggaagggtat gcaacttttа ctagaatgat tttcgaagat ttccatcaga ggttggttcg 240
gatgttgaag aaatgctgat taatgttttc ttatcccttc ccctttttag ttggtcaagc 300
aacacctagg gtatttttcca tcacttcagt tatcagcaac tgtgagtcca attaccagaa 360
ctgtgttgaa ggtatttcat gatgaagatt tttttttcca gactgctcag ttgacatttt 420
ttcattgatt tcatcacatc aaaaagcctt gatacctaat tctgcatcac cactcattat 480

tttcaggttg atctggtcat tacgcctgtt ttcatttgga aagatcgttt tcatggtact 540
gctcaacgtt ggtggatttt ggtagaggtg aataaatttt catgtgatga ttggtcacat 600
tgtaaattcc ttggttttttg ttaaaaactc tgatctcttg ttataaaagg agaaattтat 660
caagatgaag agaaagactt tcaaagagaa aggaggatga ggaatcctcc taaacaaagg 720
aacaaaacag aaaacaacta ggaagaaaga gataatcaga gaaacaaatc ttcccagttg 780
ctcgatataa ctttcagtga aaatgctaaa gaaacccccct ttaaagcaaa tagatactga 840
gcacctgatc ttatаccaaa tcatgtgacg tgctaaagaa acctcctttа aaaatactag 900
aacagcttgt agcatatgta gcagatttat acaaaaaatt agcttctttа cttctgtcaa 960
aaccttgaaa accaatcatc gataattgtt tttgagactt aggacacacc caacattaac 1020
tgaaaatgct gaataagtaa tgccagggag gg 1052

<210> 150
<211> 742
<212> DNA
<213> Glycine max

<400> 150

tgaaccaggg tattgtgagc attcatgcta tagatgtgta gtttgctgga atcaaattcc 60
tcgagttatt ggtatgagat attttatgat taagaaattt gaagggtttt agcttattgc 120
tttggatgtt aaatataccg ttttttagtt ttcaatgatg aaaataagat aattgatgat 180
taataggttt tacttttttgg agcatagttt atattttcta tattagtgca tagtacttag 240
tagcctacca caacaatatg aggcttcaaa tatggtgatt tgcctgatcc cacaatgaaa 300
tagaatgtaa ctttttattt ttttttaaaac atagctatag aaagtaactt ttttttattg 360
aagtatgaac aaaccattgg ttaacaatgc atatattatt atcaactaaa agtgcacaaa 420
tttgtacggg aagtcagtgt cagccatgct tttgaggtaa tgtaactact gagcccaaat 480
gcaaatttttg aggtaatgta cagtacacgc catttatagta caatgttaaa tttgctaata 540
ctgtatttaa ttgcatacat atgtaaaagt atgtcgatga aatctttttgt accacttgta 600
ccatccgcgc cttgtatttg ttgaccactc attgatgatt tacctgcatt tttaattatt 660
aggtgttttc agacctaaat aatttgttct tttctttgta ggttggatta taatcctata 720
gtcaaggtgt cttgtatccc tt 742

<210> 151
<211> 681
<212> DNA
<213> Glycine max

<400> 151

agaaaacttc tctccgttca tcttctttct actcaatggc atcctcttat caacaaagcc 60
cttccatgaa gcaacaagat gcttccacca acactgatag gagcacccaa atcccagcat 120
ctacagtgac gactgttacg aacagaggac aaagctagct atgctaaact acactaatgg 180
ttaccttcgt aattcttcct tccttcttat ttcattactg ccatatttat aatgatttca 240
acaaaagata atatatggca ttccaaatgg ccataacaga aaggaaaata tcctaataac 300
agagtgagat gaagtttgtt ataacagaaa ggtatttttgg ggcaataaca gaattagtgg 360
agtgagtggt ggaatatcct gaagttggtg cccatgctgt ttatcctaca cttgagtcat 420
agcagcgttg ctatcaacga cgcagagaga aaggggctttt gaattaatac ttattcctgg 480
tcatgaagag gaacgcaaaa agtatgcgaa acacaggtac taattccagc ttctcttaac 540
aataaaaaca tatgttttga atgtccttat tgtccacagg tggattttaga gtccattaaa 600
agttggttcc caacacatga tgggagaaca ccctataatt cataaagata ctaccattag 660
ggagtgattt ttgaaagaaa a 681

<210> 152
<211> 993
<212> DNA
<213> Glycine max

<400> 152

atcattttca aagagtgtat attttttttt tttaaatcgc tgagttccta aatataatcc 60
aaacactgaa ttgaggagtc aagtgctgtg tgtgtaagac attgcaaaat aagttaccac 120
aaattcaccg aagtttcata gatattgtct tattgttatt tgatcctgaa acatgctagc 180
aggattaata aaaagaataa aaatgttacc agctgcacta gtatagtttt gatcctgtca 240
tcctttctag caatggttcc attccttgaa tacacttcat ctgaatgacc aattttattc 300
ttggcacctt cattctttttc aatggaatca atgttggtgg agctcacacc actggaatac 360
acttcacccg aatgaccaat tttattcttg gaaccttcat tcttttcaat ggaatcaatg 420
ttggtggagc tcacaacact tgaatacact tcacccaaat gaccaatttt attcttggca 480
ccttcatttt tttcaatgca atcaatgttg atagagctca caacacttga agtcagctcc 540
atgatctgct cagactttgt tccttttgtca tcaattgcat cctcagtagt tgtctctggc 600
atatcttcat aagtagagag tttgacagaa tcgctgaaag aaactctttt aatttttggc 660
gttattgggc tttctaactt agaaacatct gattcaacca ttgacataga aaatctttgt 720
atcggaccag gttggataaa aaaatttcta ccctttgacc aaatttttgtt agagtagtct 780
ttggttgtcc tccatctctt cagtttcgtg ctgccactgc tactttggct actggaagag 840
cctttaaagg tattaagttt caatttcatcc gtttcgctcg atgtggaatt tggagagacc 900
ctctcaagct ccagaacaga atttggagcc tgccttttttc ccccaagatc cttgggtgga 960
tgttgccccc aaagctatct cttactgaag gaa 993

<210> 153
<211> 435
<212> DNA
<213> Glycine max

<400> 153

aggcatcgga agatgagaag actgatgccc caaaagcaat tgagagtaca ccccagtcga 60

caccccagtc tacttctgga attgaggatt tatttaaaga ctcacctttа gttacaccaa 120
gttttaactcc agaaaaacca caaaaagatc taaaaaatga tatcatgagc ctctttgaga 180
aggtatgtgc cagtgcttca ataggtttgt ttaaggctga gttacttctt tgagtttata 240
tatatatata tggttagaaa tgcttttttaa aatatacaca ttctatattg ttgacatttc 300
ctccttgccc gatgtgagtt attatccaag acaccaaaac aagtgaattt agttgtcgat 360
cgatctctat ccttagatgg gttttttatgt tttggtatgt gaataagatt ttacctgacc 420
cagtaaattg gacat 435

<210> 154
<211> 362
<212> DNA
<213> Glycine max

<400> 154

aat acaat t a t t caat gaca at at gct ct a t t t at aaaag aaat t gagcc act acact ag 60
ccact aact c ct aggt gcct aggaaaacaa t at ccagcaa t aacat aat t t at t caaat a 120
ccccacat ca cct aat aaca at at caat aa cagaaact t a aaaccaat t a aat gacccac 180
gt cacct aac at t cct t ccc gt aaact gaa t gat caat at t cagt t t aaa caacat aagc 240
agt agaat at t at ct ct gaa act aat t at t caaaact gcc cacaccaagc aat t t t t gt a 300
gct t ct gaaa t acaggt gct t t gagaggt t t agt aagt at at cagcaact t gat ct t t ac 360
t t 362

<210> 155
<211> 652
<212> DNA
<213> Glycine max

<400> 155

at t gt gat t t t cact ggt t t gt gagagt gc aaaagaat t g t t cagt t gaa t gt gcaaaat 60
t gct t ggat c agt t gaaat g cacct at gaa t t t gt at t t t t ct t t t t t at gacaaagggc 120
at gt agaat a t gat t at at t t t gt t t gaat agt gt ggggg agcat t act g t t t t t t t t t t 180
t t t ggaaaaa aaaat ct gat gt ggt agt gg t gt ct gat t c acat gt ggaa aat t ct t at g 240
gat t gggaaa gaat at t gat t gt t t cct t t t ct cacagt g ct ggt ggt ga aagcagt gga 300
t t cct t gcat t cagagt t ca gggct gt gga t aat t t ggt t gt gt gcaat a ccaaccgt gt 360
cct t aaagct t t ccagaat g ct cgagt t gg at cccat gt a agcat t cccc t t gat t t at a 420
t aacct t t at gcaaat gt ac at t t aat at g at gct caat g ct caagggt t caaggct aat 480
aaact t gt t a act gt t t t ga t t gt aat t gg t agagat gt c ct t t aagcca t t gggct gat 540
ct t gat gcct t t at gt at t t t gacat t t t t accaaaaaca t aact aat at aggaacccaa 600
aaact t agga t t cgat t agg gagaacct aa ggct gcccat t aaaact t ga gc 652

<210> 156
<211> 1180
<212> DNA
<213> Glycine max

<400> 156

aaaat aaaat cggagt ggct aaccccagaa t t at ggt t gc cagt t t gagt ggct t t ggt a 60
gcct ggct gg ggt t agt gt t gct t caaaaa aaccat ct gg at at t t caac caaaat t t ag 120
t agcat gaca caaaagat gc t ct aacaaag gcaaaagt ga ggt agt gat a gt t acat gca 180
aat gccggag aaact aacca aacaagagcc aagt aagaag agccaat t t t aaaat agt t t 240
cccaaaat ga gaagt at aag ccat t gaaag gat ccagct t t at agagcca t ct t t cagcc 300
t ccat t t t ga caacagct gc t t t aat aat g ggggt caact gcct t ccct t t gat agt gt a 360
t t cgaaagat at t t t t gaag t agaagaaaa ccaaaat gt t gaccagt caa t gct ccgaga 420
aaagct ggt g caccaaat aa t ccaaccacc aacat t gggc t t gaaacat a t ggt act gga 480
gat gaagat a t caaaggt ag gagaaat gaa acaaggaagg agaaact t aa ggcaaagacc 540
cacat gagga gaacact caa acacgacaag gccaat gaag ct gcagt gac t caaggacaa 600
aaacat t at g t t aggt gct t gacaaacact t caat gcagt t caact aat c at aat at aat 660
at caat aat c aat gaagagg ggt t at at ct t t t t ct caat aact caat cc at caat at at 720
aat gat ct t t ct aaaccact gt t cat caac t cccat at ca t cagcgcgt c accaaat cat 780
at gat aagaa aaggt t t t ac t gct gt caac cat t cat at g at aagaaaag ggt t t t act g 840
ct gccaacca t act gt t ggt t gcggt t acc acccat cat g t t t gat ccac gcccagct gc 900
cgat ccacca t aaggagcac ct t gaggat a at t t ggagct ccaact ccat agccgct t cc 960
acccccacca cgaggaccac cact gggccc accgggcat a ccact t gacc cat aaggt gc 1020
accccgccct t gaggaggat at ggcccact t ccat aacca ct t cct cct c ct t gacct gc 1080
acgat t cggg t gat t gt at c ccccaccaga gt t cccacca gaaggat at c t t cct ggccc 1140
accagaagga cct cgaggct t t ccat aat g at ggct aggt 1180

<210> 157
<211> 628
<212> DNA
<213> Glycine max

<400> 157

at gcct gcag t t aaccacac at t aaagacc acgggagt t t cgat ggt t gt at t t gt at at 60
acgggt ggga at t t t t ct ga t t gt ct t aat t t aagat t aa aat acaaaaa t acaaat gct 120
gaat t ct ct t gaaaaaaaaa t acaaat act gaat t gt agc aaat caaact t t t t t t t ct a 180
cat aaaaaaa aacat t t t t t t t cct aaaaa t gcct t t t gt ggt t gaagat ggt t aacaac 240
cat t t t at t t t cagt t at gt at t caaat ag t aaat agt aa t at t cat t t a acct aat at t 300
at t cat at aa t caaaact t t acacaagat a ct agat t aaa at ct agt gt g at cat t gt ac 360
at aaaaagaa t aat cgaagc at t acact at t t t ct gt caa aaaagaaaac aat t gaaccg 420
t t t cgagcaa at caaat cat caacat cat a t caagt t t at aat caaagt a gat ct t t t ct 480

cgtatcatgt gattttttta tgtgtaaaaa tatgtcaaat taagacaatt ttttttaaga 540

ccctaaatca ataaaaaaaa ttatcgaatc gtgttgggtc aaatttattt attaggaaaa 600

aattcaattt aacttaaatt acccaaat 628

<210> 158
<211> 774
<212> DNA
<213> Glycine max

<400> 158

ggaaaaactt tgagacaaaa actaaaacac ttatgaaatt agacaaaaga atgcaatatt 60

aacagaatgc tacaacattt caagaggacc caaacgtaga ttatgaggag aataatgaat 120

cctcctattt aaaacagaaa gaaactccta tcctatctaa aacagaaaga acccaatgag 180

ccaaagtggc tcaaaaatgc aataaagtat tccaatattt tcgcatacaa atgattgatt 240

ctttgaagca gccattaacc aagaaccatc atagagacaa tcctatccta tgacgactgt 300

aaagggaaag aggtgctctt gaaaatacac gcatttcatt acaaccaaat gcactactag 360

ataactacat atactgcaca atgcgataaa atttaacact ctttgttcct ttcaaaacct 420

ttaaggcatg taaagagaaa agctccaacc tatgattgga gaaactcatt gttggctagg 480

aaccccaaaa caattcagca ggtgtaccac aaaagtggcc tacctatagt attatcagct 540

tattttagca tgtttatacc tagatgtctc tatttctttа tgaacttcaa tagttcaact 600

accatttgat gaatgtgtcc atgatcatat catAACTTAT atcacgcaaa cttcagaggt 660

tattatcttt tttgttttct cattgtattct acaccaatga ggtaaaacaa gcgagcccca 720

aacgcatgat gaaacataat catccattgt tgcttacttgt cagatcacct cttg 774

<210> 159
<211> 637
<212> DNA
<213> Glycine max

<400> 159

acaaagtgct tgcttgaact ttatggacta aaggtaaaat ttattctgga atcttcaatt 60
cttagtgagc tatgtctaac ttcaatgctt atattgcaag cctcgtctaa ctttcacaaa 120
ttgattgcta aattgtttac agtataagta tgacaaaatt gctttctgtt tatgagatac 180
gtccccccc ccccccccct actcatttatt ataatgaagg gaacagctga aaataattta 240
tagtaaggaa attagttgat ttttttttttt acatttgttt gttgtcgact gcaaccgaga 300
aatgacaata attgtgtcct tgttggcaag gacttctttt ctggcagctg gcagagttgc 360
agatgaaggt tcggtctgat gtgagttctg aatactggct caatgctaag tgtgcatatc 420
ctgacaggca attgtttgat tggggcatga tgaggttgcg ccgtccattg tatggtgttg 480
gagatccatt tgccatggat gctgatgatc aatttaaagaa gaaacgggag gctgaggtaa 540
ctttctttttc ttcttcagta atatgtattc ccccctctccc cttttgtggg tttgaacttg 600

gttttccatat catggatatc atagactata gttacat 637

<210> 160
<211> 1040
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1)..(1040)
<223> unsure at all n locations; n = a, t, c, or g

<400> 160

aacctccatc accatctggc tctttctcat agtgtagatt tgctgtagca aaagccacat 60
cctcaatcct ctttgcattc tcttcagcct tttcctggtc caaagttcca tacttctgtg 120
tgaaaatcga tttagtagtc agattgttgg tcatcctctc cacaagggtc tgcctagtgt 180
tctgactagg aggccataat ttgattgaaa atggtctcgg ctgtgaattc agctccatgg 240
caatgaaacc tacaagaact gcaagtgcaa gtatataaat ggaatatttt aggatacata 300
acaagagtaa aaaatagttc aagcagactt gttagagaaa acaattgtaa ggcaatgtca 360
ttcatagatg catgtcctca atatggtatc agcccttgtc agacagaata aaacatttta 420
caagcccttа acacaaattt gagttttgaa tggataaaaa aaaatgtttt acaaaacagg 480
ttagttaata ggagcagaag taaaagaaat cccatccaag aaataattgc tatаacatat 540
aaacatatat atacacccag gcccnnnnnc ncaanncanc acacacacac acacacacac 600
acacatatat atatatacac acacacgtaa agtggattgc aataataaag taggggcatg 660
ttcctttcca tttcaatcat atcatgttaa tgaaactaat aaaaacttca aagcatgatg 720
aaaaaatgaa aagggttagg gagtttataa aggaaacttt gcaaaacata ccatgaatgt 780
acgtacgagg ttgttttcctc tgaagagaag agaacactca caaaaccgtc gacagtaata 840
aataaccgac aatcaacttа gttttggttca cccacaaatc aaacccatcc taataaaaat 900
cttagctttа agctcgaatg caacagatcc gagactgcgc aaagatacaa acttttaaaca 960
cgaatttgaa aatctttgga gaaaggggaa ggaactggga acagggtaga ctgaaataaa 1020
gagagacaag tttgacaacc 1040

<210> 161
<211> 845
<212> DNA
<213> Glycine max

<400> 161

tgcatgcctg cagcttgctg ccaaactttg ctacatttgg tatgattcag acagaagaga 60
atcatgttag cttctgtact atgtagaatt gtatggttat tagtgggttt tgtcaagagt 120
taacagtgaa ctgcaaaatg gagtgtttag agggatgcat tgtatataat attttacgtaa 180
caagtggtgc ttcccagttt tcagccatca tgatatcagc ttaagtgaca taggcgcaaa 240
acaatactga tttcatgcta atgatcagat tttcctcgtg cagtggacaa tgctaaaaag 300

act gat ccca aagct caggc ct t gaagact gct at ggct g t gat t gt gaa at caggat gc 360
caagt gt t t a agaaaaaaac t aaat ggacc aggacat t ac t gt gacat cg at t acat t t g 420
gcaggccaaa gacat t gct g t aaat t t gaa act gt t t ggg at at t gct gt aaat t t t gga 480
ct gat at t ga acgt t t gat t ct gaaact gt t t t ggacaga t at t gct gt a aat t t cggcc 540
t t t gaggaaa aat gt t t t gt t gct gcaact gt t t t t t gat t ct gaaat at t gt t gat at t 600
gct gt aaat t ct t aaact gt gt t gt ggct t gt t t acgt t g t gt at t gat c aggt t t gaga 660
aaaaaacat a at gaat caaa gaaat t t gt c aat acat gcc aaaaacat t t gcgaat gcag 720
t aagt ct ggg t aaat cat gg t t t cat aacc accacgt t ag t aact gt gt a aat ggcaggg 780
act agaacac act aaat t t g t t t t gt acaa ggat t aaaaa ct t acaaggg gt caaaaat t 840
ct aaa 845

<210> 162
<211> 631
<212> DNA
<213> Glycine max

<400> 162

t t gcct gcag t t ct gcacat t gt aagct t c t ggat t agaa ct gt t t gt t g gaagt gat ag 60
t t gt t t at t a agggt aat ga gagt t cgaga t gt t agt gt t at t gt t gt t g t t aaaat gag 120
t t t t t t at aa ct t aaaat ga gt ct t aaaat gaat t t t t gc at aagt t aaa aat ct t t t aa 180
aaat ct at ga gagt t t t t at aaat t at t t t at t t agct t a t ct t cat t t a at t t t t t t t c 240
t ct t aaaagt gt t t t agaat aaat t cat t c aaat aagt aa t t at t at t gt t gt cgat at t 300
gt t at t gt t a t t at cat at t t t gt t t t t t t t t t gggaag t t gaat at ca t aaact gat t 360
t aaaaagaga ggcct t ggt t gt aaaaaacc at aaact t ac gt cat aggt g t gcgaat at g 420
at aact aaaa aact t t cgag gagt gact t t t gacggt gaa at t gggaaag aaaacaacat 480
act agagaaa t t cat caaca t act t t at ct t at t t at aat t t cact t t gt t acaat acat 540
t ggggt t t t t t t at aat t t t t aat t t t t t t t t at cgaat c t t t caat t t t at gt gccct t 600
t act gt t t ac cat aaaaaat at ccccct ac t 631

<210> 163
<211> 439
<212> DNA
<213> Glycine max

<400> 163

aaccaaactc ctttttgtgt tttacttagg cagccaaatg cttgggatat cttagatttga 60
aaagaagagg aatttgtaac ataattacag tcaacaaaaa taccaatggg tgctatctaa 120
tcactaggta aaaaaatttta gaaaaaaaaa ctgataaaaa cagcaaaggg acacaatttca 180
attgaaatat ggaaactgta acacatttatt taagttcata cttaatttagc aagtttgaca 240
aattgaatat ggagagctag catagaaatg atatcatttca ttaaaatagga aataaataaa 300
taaatagcaa ggacaagttg atcttaaatt tttaaacagt acaacaataa gcactaagta 360
gaccaagaca ccatgatagc gataatatca ccagttcaga attagagtat cagtcatttga 420
atatgaaaaa tgaatgtca 439

<210> 164
<211> 543
<212> DNA
<213> Glycine max

<400> 164

acgaagaggc aaagaagaaa gctcgacttg ctaggtttgc acctgcttcc aaagttgatc 60
ctcaagaaga agataagagg aaagcaaggg cacttaggtg ggttcatcat tcctctcata 120
attttgtttct cccaattcat attgtttaca agaatcaagc atgcatggtg tcttattagt 180
tattaggtct ttctgttttg ggttcccagg tttgcgaatc cgtcgtcaac ttctatagct 240
aatgttaatg gcgaggcaaa gattgagccg gtaagaccct tttggtcact ttcaatgctt 300
tgcgtcatac aaagatgaaa aaaaaatgta ttttttgtgtt gactgttgtt ctgttgtgtt 360
tcaaactaga aggctgctat tgcaggcaat gctggaggag ggacctgaat gacaggtcgc 420
gtctttaattt tgtaggaattt tttcttgtaa gtcaattatc ttttgctctt gcttattacc 480
ctttgctttg catattgcat atctgatttg tgatgttatt ctctttttttt cccctcaact 540
ttt 543

<210> 165
<211> 369
<212> DNA
<213> Glycine max

<400> 165

ggctt att ga ctt gat cagc t gaaagat ga act t t gcaag gagaat t t ac agct t gcagg 60

t at t t aat t t ct t t t at t t a at ggt cggcc t at aat t aaa t t gt agt aga gct t ct caaa 120

ct at t gcct t t act acagag gaaaat ct t c aaaaggaacc t cgt at cat g gaact t agga 180

at caagt aag aat acaat cc t at gat t agt at gct t t t t t ct t t t caat t t at t gct gac 240

t act gact t t t t ct t ct t cc t cccat ggaa acagt gt aga at aat t cgga caact gagt t 300

agct gct gct aaggagaaac t aaat gagct t gagaagcag aaagaagaca t gt t gaaat t 360

gaat t ccgc 369

<210> 166
<211> 821
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1)..(821)
<223> unsure at all n locations; n = a, t, c, or g

<400> 166

acat gaaacg cat t t aaccg agt at gt t ac cagt at t cat t cat t ct gt c ct t at acgac 60

t t gct gcgaa t cct t t gt t c ct t t at aaaa t gaat cgt ca t t t aat t gaa at at t ggggc 120

ct aat gct aa at t t t t aggg t t t t at aat c cacat t ct t c gggt t cgggc aagaagagag 180

agaagacgca at t t t gaccc t caat t t cac agacct t t aa t cat t cacgc gat t ct t ct t 240

ggt aact ccg cct t cct caa t ccat aat ct gct t t t at aa t t t at t t at t t agt t t t t at 300

t t t gat t t t g gct t gct gca agct aat t t a cgct ct t cag t t caat at t c cccgt t cat t 360

t gt t gcagaa at ct ggt t t t ggggcaat ct ccgt at t t cg at at t ct ggg t at gt at caa 420

aact gcacct t t t t ccct t g t at at t gt t t t gaaat gct t ct t agt t t t a at gact at ac 480

t gagct t t t a ct t cagt t t t t t ct gt t t t t ct gcacgcct t t t at gt t at t t t t cacct t 540

t gaggt ct ct t t gaaat t t a t gt t t at gt c gat t t gt gca at gat t at t g gcaaaaaat c 600

aaaaacaaaa at gact t caa t t cct cat gt t t cagcct gt gct t at t aga gagagt agga 660

aaggt gaaga ggggct gaaa at ggaat gca t ggaat gaat t t t cat t gag at ggagt at g 720

gaacanagca t t at gct t t c ct ct t act t g ggaggaat ga acat t at t t t t gggaaact c 780

at at t agaat aacct gcccc t aat t t acac t t t t t t ggga g 821

<210> 167
<211> 848
<212> DNA
<213> Glycine max

<400> 167

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tgtcaactgt aaagtagaaa ggagctcacc agtcaggcct tctccaattc ttgtatgaat 180
ttgtccctgc aaactctgta tgcctgatta tgatattagc atgatgacta tgatatacta 240
gtcatagctt aacaattaga aattaatatt taagtattat aactaatgct tcatttcttt 300
taatatttac acaagcatgt tggaccagct tgttatttc ctaatttctc ctggtatcct 360
taatttccact atgacatacc cttgcatacc gtggaggact taacatcttt tggacatctt 420
tattatttga tgtctgtatt tctttgtgaa attatttggt ttaattaatt ttttgaagtt 480
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atgccgtttt caacgaagaa tggagttgat cccatgggtc gaaatgtgga gaaacctaga 600
actgtggaag atggaataga taaagctaaa ccatggcagc tgtctgaaat tgtggatgct 660
gtccaatgtc ggttagttac aacgcctgac agtacagatt cttccagcaa ggtttgttga 720
ttttatgaaa ttgagattgc cattttctat tgtaaactgt gtactgtgaa ctgctttaac 780
tctaaagtca tacatagggt tgttcgactt ttatatacaa actctggtgc tggtcttttg 840
gcacttgg 848

<210> 168
<211> 825
<212> DNA
<213> Glycine max

<400> 168

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ttctccattt ttccaatttt aattatttttg catattcaat accttatgtt atttttctg 180
agtttttctc acaaatattg actgcaagtg ttttgtagtt tggttgggaa tatttttttt 240
tcattgacct agttttgttt ggtgcagaga gattggtcta atattgaatt ttttttattg 300
gtaatttttgt attgttatta aactattcag agattttatt gtgtaaaatt gtatgttgtt 360
cttatcattt ggttgaagtt tacttattag tagtttctta tgttataaac tacaggttct 420
gtaaatggag gaaattacaa agaattggca gcatgaccag caaatagatc atcattggta 480
attaatcatg ttgatgggta ctatatatga actttttttgg gactcaccaa attttgtct 540
acaggtaaat tgatctatca taaaaaagat ttgcaggtaa gagtctacgc atcttccgtt 600
tggtccttga gagagacatg gtttcatcct ccttgaaata tatttagacc cttaatttta 660
tgttaatttg cgttttttttg tatgctacct attttactc atttgtctcc attttactga 720
ttaactaata attttttttt cttattcaag gtacacttttt attatttat gatagattag 780
acaatttaaa ctagtctaat gcctaacatt ggctgcaggt cgact 825

<210> 169

<211> 953
<212> DNA
<213> Glycine max

<400> 169

atatgaaaa gaaagaaccc ggctggtggt tagttgcatg cacactcttc agtttaatca 60
ttttcagttt cattgtcttt gtcaaaaaat aagttttagc ttcttgagtg ttggttttgat 120
taaatttcga gcatccttaa tccttatgat tctatttttt actttggcag gttcagtggg 180
gatttaggac aactgagatg tactaaaatg gataaacaat tatttggaca ctaatgaaat 240
cagtatttca acacgtgtct taggagatgg tggactagtt catacgaaga aactcttatc 300
atacaatatg gtttgaaaat tttcttttag aaaaaaaatt gcagggactg tctgtactgc 360
taaatacata ttcttatatg ggaacaaatt ctaagaactg agtatctttt cctagacttg 420
tttctttgtt tgttatgaaa ttaatacttt cctggagctc tacaacatta ggaagttgat 480
cctcgttaat gtataataat atgattgatg aaatattttg aatgttgaag ttcaggaata 540
gaaaaacaaa atcaggaaaa tatatttaaa ttttcaatgg atttaatatt caagacaact 600
agatattta aatttaaaat taatttaaaat atagatgtaa ctttgttttc ggcctaactc 660
aaccgtaata aggcaaaaaa aattggtcgt attttggcac caaaaccact tggacccgcc 720
tgatttcaacc cataatctgc aacaaccgac ccgctgaaat tgacggtcaa ttctgtcata 780
aatgggccta aaaataaaaa ggatgtggat tggtatatca agagcttggg ctcggagatg 840
gaaaatattg gttacaacat gagagcctat gctatttgta gcttccaata acccctgggg 900

aactgcttgg gcacccagca gttttccaaa ataacatatt agctttttttc ttt 953

<210> 170
<211> 598
<212> DNA
<213> Glycine max

<400> 170

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acataatgtt ttgtaactat catacttaag agttttggat tcgaattatg aggtattcca 120
caagttttaga ttcctttaaa tcagttgaaa ctaatttagt ttgaaatttta atcttacata 180
aaaaaaatta tcctatccaa gacataatta aattatatta aaatgagtta tttatgacac 240
atagacattg gtttaatgaat taaaaatgac tttctttaag gaaaaataat tttttttttat 300
tattattata aagtaccaca aatttatttc cttcgtaatt tttaaagtat cttattgtat 360
ttttttaataa aataaaatat ttattacttc cttgacatag aactctaatg gctgattagc 420
atgacccatg gtttattaca cttcaagtct tatttttatt taaacataac ttccttttac 480
atacaatttc tataccatta tttattgaaa ataacaaaga taaataaatg tcctttcctt 540
aaaaagaaca agtggtgtaa taaatcctaa cgctttgttt ggctgagatg acagtctta 598

<210> 171
<211> 724
<212> DNA
<213> Glycine max

<400> 171

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ccccctcccc cgtttttttct atttagtgtg gttttattct cttgtacatt cttcagtgta 120
ctagcctaca acatttttagt tttgaaatttt aagttcaact tgcaaatttt tgtggtccgt 180
tcaaaaatta taatgaattt tgctgattta tgtttattag actggtgcaa tttcttaatg 240
gatttctctt gtctactgtt tcagctatga agcttgggtc atttataatt ttctgtcact 300
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gaagccatca ttttgtctga tgacttgttg ctttcctcct ataccgctgg atgggtgggt 420
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tcccctgatt tttctctatg gaggttttttt ttaatttacct aacttttttgt tagttgaaag 540
tactaggatg atacatttgc cacacaatat ggagatttat ttttatggat tattggaaaa 600
cgacctagac atcctggaga tgcaatggat tttagtagac ttctaacatg gtggcatgac 660
attatatcat aacttatatt cttctctcat ttctagaact tctatttcag gcgtttcata 720
cgta 724

<210> 172
<211> 698
<212> DNA
<213> Glycine max

<400> 172

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tttgg cattg ggcaa tcaaa aaaat gaaaa taaag ctatt aatac agca gtgtg tggtc 120
ttatt tccag agtta ataaa aacccaatgc atttc attaa atgtg tcatt gaagaaacaa 180
cttct ggaac tcctc catt t ataaa tacat caaag cagtt acacg acatc aaatt ggtct 240
ttgaa ggaaa atgaa tgcca caaat tatca tcaaa gcacc aacct ttgga ggaccaatct 300
aacct tgcaa atatc tttaa ggatc aaaat ggatg atatt ttatagatga taatg aaata 360
tataa catcg tggag atttg atgtt gtaag ggatg agcta gcaga tgaat tgcaa tcgac 420
caaaa tgaat tcatg aaaac attag ttgga acctt cagta gttca aggga aaaaa tcagt 480
gacac ctgtg ctcag ttaat tgatt ttatt atgca ttcta aattc atatg cacat taaga 540
aacat agcca cttaa ccaat gaact agcta tcctagttcg gaagt atta tacttcaatg 600
gcaac caact ccttc acatc acata actaa aaaat aatac tcatg taacc aaaaa tagt 660
tgcaa atcag gaata aaaaa tgtct caaag gcaat aac 698

<210> 173
<211> 673
<212> DNA
<213> Glycine max

<400> 173

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aaaga aaatg gtatt gttga acgta tggag aatgg gggaa aaaat agcat tcaac acttt 180
ctttt tgttt ggatg agaga gaaag agaaa aaaat taatt tttct ttttc t agact tatct 240
ttcct ccct a ctttt attt t cattatctct tcaac aatta agaga aatttc ccaat ttttt a 300
agatg ttctt ccgta actat tttct ttctc ccgat ccaaa aatag ggcta aagaa gtacg 360
aagaa gagca attca tataa aaaag catttt gatat agcaa acaga atatc ttcct tgata 420
cctgg taata tgcac attag aagta gtaaa tacac tctac atacc ttctg acggc tctgg 480
tttat atctg gcagt tctat acttc tgaaa tttaa aaaat a atgtg aaaag cattagatta 540
aataa aattg acata caccc a taagc attt aagag gatga taaat cacag atgta cctgc 600
aagtg gcttt ttaca tgata gatag taagg ccctc aactt tcatt agatt caaca caccc 660
tttgg agtag cct 673

<210> 174
<211> 868
<212> DNA
<213> Glycine max

<400> 174

aaacg ctagt gttct tgcat tcttacacta cgaga acaat cctcc catac ttcac cataa 60

cct t aaat ct gcct gcat ct t cct agat ga t gact at t ct gt caagat t g caggat t t gg 120
t ct gat caac t ccaat t t t t act at ggt t c t cact t acac aagaact at g aagcat t t ga 180
cat ct gcaaa aat gat gt t t acgat at ggg t gt gt t gct t ct t gagat t a t ct caggct c 240
aaat cagt t g gat t caccaa ct t t ggct t t acagcat gt a agggct ggaa aat t t gaaga 300
aat t t t ggac ccat t t ct t t gct at gat ga acaaccacat t accgccaag agcaaat gca 360
aat aat t gca gat ct agct a caaggt gcct gt t at t t ggg gt agat ggaa ggct aggaat 420
gat agat gt t gt gagggagt t agt acacat gact aaagaa agt ct t gat g gaggaat t at 480
gaaaggacct gcact ggagg agacat t ct c aaat t caagc ct t ct t caga t gat at caat 540
gt ct cct gat t ct at gagt g t ccct t gaat ct t t at gt cc cagt cagt t t agt t t gt cag 600
t ccct t caaa agat gat aaa caaccacaat t gt at gt gt g cact at aagt ccccagccac 660
t gt acat t gg ggaat gcat c caat at t ct g gt t ct gacat act t cact aa ggt acaaagc 720
aagt gt at t t ggt agct act t ct t aat aaa t t t aat caac t gct at t gt t aat gt gt ggg 780
aat cat t t t c aat acagagg t t t t t t t at g ggt at at at a t agt t gat ga aaat ct t cgc 840
gaaaat t gt a at gt t t aat t t at t gcat 868

<210> 175
<211> 564
<212> DNA
<213> Glycine max

<400> 175

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aaat caacca gcaacct caa ccagacat aa aagt aat gcc t gaat cacaa gcaaaagt ac 120
t caagat caa cct gat act c agcaaat t ca act gccagt t cct t gaacgc t t t gt ct gct 180
ggt t gaagt a act t at gggc t t cct gaaat t cgacaagaa t gggat t t ca t ggaagaat a 240
t gcaaaaact at cagcacca agt agaacaa at aaaacaat at t agat gaa t cat ccacaa 300
cat at t at gc agat gaat at t t t acat at t t gct aat at a aat caaat gt caaat at t ac 360
at ct at gaaa gt t ggt at cc t t t ccat t t t cat cact aga t acaat ggga ct t gcaaat a 420
t t t ggaat ga at ct cat ccc at gt caccat ct at caaggt t gagct t at a acaaggaaat 480
gacat aaat a acaat t gat a t at t t t ct at t aaaaagaaa agaat caaca at t caacaac 540
caaat t gaga caaat acct t t t ca 564

<210> 176
<211> 780
<212> DNA
<213> Glycine max

<400> 176

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cctccaacta aattggtagc aagatttca ttgaataaaa aaagctctcg gttgttctta 120

agcatgctat caatcgaagg atatgcaata ggttcaattt catttccatc tgatcttcca 180

gacaaacaaa ctgacttgtc tatcttacag agcatgtatg tacatttttc taggccatcc 240

aatgcagcct cacgaaccca agaacctaca tcacctctat tatcaacaga ataatcatca 300

agagctttaa ataaacttat catcacctca ttctttatca gaataaacag ggaaaaatca 360

tcctcaacaa aagaggtagc agtatcttct cttccattaa ttaatgtttc acacactaat 420

gtgagccctt tgacagcatt tactcgtgct tcagcatctc tgtcttcagg gttttcctgc 480

acatgggaaa acattgtgta acacaatcat tgaacctaag attgtataat atatagcatt 540

tgcaatgtgg agcacctcaa ttttacaaga gccacaaagc ttcaaaagca catttctcca 600

ttgactggct aataactcat atggcaaaac acctatttgcc aatgcagatc ctctccttac 660

agctacattt ggatcagtca acatactgga agtacctttg cttgtcacca tcacttttatt 720

acctttatta ttcttgaaag ccatggccaa taattgccac ccggattaaa agtggttttc 780

<210> 177
<211> 1536
<212> DNA
<213> Glycine max

<400> 177

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gttggaaaat tcttcctgtt tcatacatct gtttggatca tgtgaaaagt ttgtgtggaa  120
ctacataatg aagcactagt agcatcctga gatattcttt ggatatagta attagaaata  180
taataataag aaatgctagc tacacacttt cagaaatgct cttttcaagt cacactcttt  240
actattgggt gcattgtttt gtgggtactg ctccctttct agtgggtcat gcataaattt  300
cacccaataa caaaaggtgt gttgctactt gctagccgtt ctcatacata atatatggcc  360
ataaattatg atttcctcat tcacacaact tgtgctactt atatttgatt tcatgaacat  420
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<210> 178
<211> 727
<212> DNA
<213> Glycine max

<400> 178

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tatctatttca ctatctactc tgctgaccaa ttttatgcca cgcaggtttg ggatgttaac 180
ataattgaga cagcagaaga aagattctat gactccaaca tagacgagtt caccaatgcc 240
attcaagaga atattacggt attttatgca gtagctttct attatcccca atccatggaa 300
ttacttcaaa gttagagatg cttactccaa attttctgaa acagaaaaca tggtccgatc 360
aagtactagg atgggaaacc tgcgattcta aggagactgc atgccctgat atgtatgtcc 420
ctttagttct ttatttatgc aaaagtttat tccttcatca ctgaaatata tgctgttgaa 480
atattggaac ctgattcatt agttgattta catatgttgt tgaaatataa ttgtttaaca 540
aacttgggat tttttttcaga tacgcgtctg aaggagttca agcagcctgt caatgggcat 600
ataaaggtgc tcccgaaggt tcagtgctag aaggtaagat aaaatgattc tgagaagtta 660
aagagtttca gtcacttttc agattttctg acaatatcat gaaataatac tctgcaggca 720
tgcaaga 727

<210> 179
<211> 535
<212> DNA
<213> Glycine max

<400> 179

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aatcatcctg tcgattattc tattgtacta atttgaaaat tccaactctt gttaactgac 180
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tctgattgta cgactataat taggatatgc tatttatttcc tttcttagtt acaacagtta 360
tagggatttt ggttcctgat ttttagctct aaattagtgt acaaaatcag tcttgtaacc 420

ctatttatac acaccattgc acctttttca aacaatagaa aaatacagtt cattttctta 480
tatggtatca gagctcgatc tgatacttcc ctgaacccag tgccgggcct acaat 535

<210> 180
<211> 1201
<212> DNA
<213> Glycine max

<400> 180

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<210> 181
<211> 681
<212> DNA
<213> Glycine max

<400> 181

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ctacagtgac gactgttacg aacagaggac aaagctagct atgctaaact acactaatgg 180
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acaaaagat a at at at ggca t t ccaaat gg ccat aacaga aaggaaaat a t cct aat aac 300
agagt gagat gaagt t t gt t at aacagaaa ggt at t t t gg ggcaat aaca gaat t agt gg 360
agt gagt ggt ggaat at cct gaagt t ggt g cccat gct gt t t at cct aca ct t gagt cat 420
agcagcgt t g ct at caacga cgcagagaga aaggggct t t gaat t aat ac t t at t cct gg 480
t cat gaagag gaacgcaaaa agt at gcgaa acacaggt ac t aat t ccagc t t ct ct t aac 540
aat aaaaaca t at gt t t t ga at gt cct t at t gt ccacagg t ggat t t aga gt ccat t aaa 600
agt t ggt t cc caacacat ga t gggagaaca ccct at aat t cat aaagat a ct accat t ag 660
ggagt gat t t t t gaaagaaa a 681

<210> 182
<211> 802
<212> DNA
<213> Glycine max

<400> 182

ccaaaagaat at ccat acat ct cact gat c cat cct t t cc cat agat gt c accagt t at g 60
t t t gt cgccc agt gagccct at ct t cccgt act t ct t cgg t t t t t gaaag ccacaagggg 120
gcaaaaact c gcaggt cat c t at at gaaag gccaaaagcc caccaact t t gt cacat agt 180
t ct gggt gt t t cgt gt gcaa t t t agccaaa ct gt t gt cac aacct at t aa gt acct ggag 240
aaat aat at a gaat at at ag caagt t t caa t ggt gagcca aggaaagaaa cact aat at g 300
aaat acaaga t at aagt act cct t t aagag at t t aat caa gt t t cat aac t t caagaaaa 360
gct ct ct agc t t gt gcat t a aaaaaaacct at t ccct gat t cat at cgt c gagt gaat gc 420
at t at gacca at gt aaat gt agaaaaaggg ct aaggcat c cagaat t t cc at at t gt t at 480
aaat t gt t aa t agct aaat g t aagct gt at t agt ccat t a gcct cct t cc aaaat at ct g 540
aaat ggaagt gat gggt aaa t gt ct agcgg ct t acact ac at cact aaaa gaaaaggt gt 600
gaaaaagaaa caagt aaaaa at t agt gaat acccat aat a t gct gcaaca ggt ct t cct t 660
t ct ct gcacc aagt t cccaa agt at aat t g gccct cggat t at cat gt ct gcat ccagaa 720
t gacaaccca at caacat t t t t t gcct t ct t act at gt t t aagcccagt g t acaacccca 780
gcagggt t t g t t t at t ggca gg 802

<210> 183
<211> 744
<212> DNA
<213> Glycine max

<400> 183

agaaaactt c tct ccgt t ca t ct t ct t t ct act caat ggc at cct ct t at caacaaagcc 60
ct t ccat gaa gcaacaagat gct t ccacca acact gat ag gagcacccaa at cccagcat 120
ct acagt gac gact gt t acg aacagaggac aaagct agct at gct aaact acact aat gg 180
t t acct t cgt aat t ct t cct t cct t ct t at t t cat t act g ccat at t t at aat gat t t ca 240

acaaaagat a at at at ggca t t ccaaat gg ccat aacaga aaggaaaat a t cct aat aac 300
agagt gagat gaagt t t gt t at aacagaaa ggt at t t t gg ggcaat aaca gaat t agt gg 360
agt gagt ggt ggaat at cct gaagt t ggt g cccat gct gt t t at cct aca ct t gagt cat 420
agcagcgt t g ct at caacga cgcaaagaga aaggggct t t gaat t aat ac t t at t cct gg 480
t cat gaagag gaacgcaaaa agt at gcgaa acacaggt ac t aat t ccagc t t ct ct t aac 540
aat aaaaaca t at gt t t t ga at gt cct t at t gt ccacagg t ggat t t aga gt ccat t aaa 600
agt t ggt t cc caacacat ga t ggagaacac cct at aat t c at aaagat ac t accat t agg 660
agt gat t t t t t gaaagaaaa aagt gggat t t t agaact ct t ccccccaaaa aagaaagaat 720
ggt aaaact t t ggaacccaa aaag 744

<210> 184
<211> 905
<212> DNA
<213> Glycine max

<400> 184

gat cgacct g caggt at gag t ggt gggat t gct t at gt t c t t gat gt gga t ggaaaat t c 60
caat ct cgat gcaact t gga act t gt agat ct agat aagg t t gaagagga agaggacat t 120
ct t acact t a gaat gt t gat t cagcagcat caacgt caca caaat agt ct gct cgccaaa 180
gaagt gct t g at gat t t t ga gaat ct t ct t cct aaat t t a t caaggt gt t ccct agggag 240
t at aaacgt g t t ct t gcaag t at gaagt ct gaggaaacct ccaaagat gc agt ggt gcat 300
gct gct aaac at gagcaaga t gat gaagca caagcagt gg agaaggat gc t t t t gaagag 360
ct t aagaaac t ggcgact gc at cat t gaat gagaaaccga gt caggt t ag t t t t t t aaat 420
t t t t at t at a t t ct t t t t at ggt act t gt a cct t t gat gt t caaaaaaag cgat t t t t t t 480
aaaaacct gt agat t gggca t t cacact t c ct t aaagt ag t t at t gagct at t gct t t t t 540
caaat gaaat t caat gggcg gt gt t agat t gaat t gaggt gagt t t gaaa at ggagat ct 600
t ggt t aat t a cagggaagaa t gcct agaaa t t ct act t t g agaccgt t t c t cct t t at gt 660
gaagat ggaa agat ct t t t t agt aaggaaa gt t t t t t act t cct ct t t gc t gt aggt at c 720
ct at aaat gt t t t aaat t aa cct agt agat act gt gct gc at t t aat gga t gt t t aacga 780
t at ct t t t gg t ggggt gcaa gaat agt at a gt t t gt t t at t gcat aaat g t gaat aacat 840
acaggggaaa t aagcacct a gagaaat t t t t t cacagt t t at ct t t gt t g at gt ct t t cg 900
aat at 905

<210> 185
<211> 863
<212> DNA
<213> Glycine max

<400> 185

tagcaaagag gaagcctttt ttgattccag gcctggttag actcagattg tgaagatgat 60
ttctatagtg tcaatggtgg taagcatttc cttcaactct ctcctttttt gtacttttt 120

tcttcttctg gtagagcatt taaatttgtt tacttgacca ttttgttata atatagttat 180
gacatggatg atattggtta gaggtgaggc tttgtggctg ataatatgtg atggtaaaca 240
ttgtcttacc attattgaca ttatttataa tatgacaatt tagtttgtca tggacaaatg 300
gatattgtat cataatcaga ctttatgtaa tgcaagttga tgaagaagga ataactcatt 360
ttagaaattt tggatatatt gttttacctt tcttatgtag tttctctttc aactatttc 420
attactctcc ccaaccacct tcagctgtat tgtctacttc attttatgca gactttacac 480
catctagagg gaccacacca gttcaccaca cttttgggac ccctttctagg aatagaattc 540
atggctctat ggctgaaaca tccccagaaa agaaaaagaa attgttagag cttttttcgcg 600
aaagtgtcaa agatgaccaa ggtgatgttc atggacacaa agaagtcaag ccaactatac 660
aagatgttat tatgcctaaa tctgcacatt gcactcctta tctctcagag gctaactctg 720
cctgtagtag tgaaaggacc atgagcatga gcgaggatcg ttcatccatt agagagaaat 780
cagtcaagtc tttgcagtgg tgcattccaa gcttgtcttc atgccgaagc tttcgcgaga 840
ggaggccaaa gacgagtcct gca 863

<210> 186
<211> 593
<212> DNA
<213> Glycine max

<400> 186

tcgacctcgc ggatttgctt aacaattgat attttttccca gtgctagata tgaaactatt 60
aagttgcaca gtgttttgga gtcttgttat gtttgtaatc taatcaggct atgttttttac 120
tagatatact acactaatac tggagcttga ttattattac tataataaaa gcacttggtt 180
aatttagaat attttacaaa atttgttctt cttttcttcc ttttttcccttt taatttctac 240
aaaacaacttt cactgaacct gcccaattgg agggtgctgc taatagtaag tagattatga 300
attgcttgta aaaaggcatg gatgtaacca tcaaacttgc tctacttttat tgcagtatgg 360
ttggtgaagg aagtgaatgc ggttttcaatt tgaacttttt ttggctgtag actggatcct 420
tctttcttca ttctgttttta tgtgactagt atttgttttc ctattgcattt tgtcaaaaaa 480
atcagttttt ctatgtttac cattattatg caggtgctat tgtcatgcag gagatattga 540
gcgtggtctt ccgagttttg agaaccacct aaggcaggac aggtctgttc ccc 593

<210> 187
<211> 791
<212> DNA
<213> Glycine max

<400> 187

tcccattcat atacctaggg atgcctatag gtgttaaccc tagaaggaag gtggtgtggg 60
agcctataat cagaaaattt gaagccaaat tgaacaaatg gaaccacaga agcatctcta 120
tggctggcag aattaccttа atcaatgctg tcttgacagc tttgcccttg ttttatatgt 180

ctttttcag ggcccctca gcagtcatca agaggctcac tactatccaa agacaatttc 240
tttggggtgg aaacttggaa ggaaaaaaga tagcttggat ctcatggcag caagtgtgtg 300
ctcctagaga aaagggaggg ttgggaatca aagatatcaa ggcttttaat agagctcttc 360
tcatcaagtg gaaatggttg atgttccagc aaccagatca tctatggagc agaatcctca 420
cttcaaagta caggggttgg agaggtttcg aagagggtcc tcctaagcag attttctcct 480
cttggtggtc tgacttaaga tcaattattc aacatagtag catggctgct gttaataagc 540
agttttcttg gaaactgggc aggggtgatc aaatttttatt ttgggaagac tcatgggtgg 600
gagatggaac tattcttaga gacaaatact cagaattata tcaaatatca tctcaaaaac 660
tacagacagt ggcaagcatg gggatttttg gagaaactgg ctgggagtgg aaattctcct 720
ggagaagata tctctttgac aatgaattgg ggggagcctc agcttttatt gacaagactg 780
caggcatgca g 791

<210> 188
<211> 907
<212> DNA
<213> Glycine max

<400> 188

aat t gcat ct at t gccaaat at gggcat at agcat cagca ccaaaaccaa caagggt gca 60
gaaat gat gc act t t gcgt g gct cagcaga t t caact at c aaggcaaccc t agt gcgct c 120
aagagt t t t a act agat gct gat gaacagc accaacagcc aggagggagc t cacagagat 180
gcgt t t ct t t gagaaggct a t cacagat ac aaat aaat t a gat ggat gt t cact gt aaaa 240
agt aact t t a accaat acaa gcaaaacat a gt gcaat acc t ct at cagac agcacaagag 300
t ggt gt agcc t t cat t aat t gcat cat gt g cct ct gcaca cat cct gt cc aaggct t cgt 360
ccaaccct ct ct t accacat t cct t t gaat aagt t at gt c t at aact t t g ct gcgccat c 420
ccct at aat t cat t t t t t t a at ggct t cca t t t ct t cagt ggat aaaagg ggacct t t t a 480
gt gaaaggcg gt gacat t gc t cct cagt ga t t t ct gt aag at cacct t ct ggaccaacca 540
t acat t gcat agaagt gact at t t t ct ct c t aat aggat c aat aggaggg t t t gt cact t 600
gagcaaacat t t gct t gaaa t act caaaag t gagt t t t t c t ct t t t agac at gacagcca 660
at ggagt at c at t t cccat t gacccaaggg ct t ct acacc at cct t ggcc at aggaagt a 720
at agcat t t c caat gat t ca act gt at at c t gcat gaat a aagcat aat a t aaaaat at t 780
t cct t cat aa at gcagcaga t aaaat t gag gaaat at t aa t gat ggt cat t gcat accca 840
aaagct t t ca gt ggaact aa t aaaccat ga at t cccat at t t t ccat at c t gcat cat ca 900
t t ggat a 907

<210> 189
<211> 568
<212> DNA
<213> Glycine max

<400> 189

act t t cact t cat ct t cagg cat at act cc acaccgccat cagt aaggt c at ccaaccag 60
cct t gaagat ct gat ccaat ct cct t ggt a at agat ggat cggat gct cg aaccacaaac 120
t t gcacagca t ggt t gt agt ct cat caccc aagt ccacat t t ct act cac t t cact t gca 180
ccaaat at ca t cat gcccaa gaagccacca t gccaagt t t t agcagcat a acacat ct ag 240
t ccggt aaag gggggagaaa aagt aaagaa t t agt aaat t cat t ct at gc aact agat gc 300
at at aacccc t at t gt agt c ct t gct t t t t agt t t t t at c ct at t t t aca at ggct aagt 360
t t at cgt t ct t t aggt acaa at t t act gct t ct gt ccaag t agaaacagt caggt aaat g 420
cat acaaggg acagat t gaa t agt accacc act agat t t t aat aaaacaa ggggat t ccg 480
ggaat gaaac at aacaact t agt gcat gt t t ggat t gcca gt agcggcag t ccaact t ac 540
gt t t t caaaa gcat caact t t gat act t 568

<210> 190
<211> 826
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1)..(826)
<223> unsure at all n locations; n = a, t, c, or g

<400> 190

aaat gaagt t gat ggt gaat at gaagggt c t cact caact ggt t aaggag aaat gt agt t 60
t agct t agaa aact t t gt ag t aagaaat cc cagt t ccat t ct t cct t gt t t t gt aat aat 120
t t t cagct aa cat gt t t t t g t aggt gt aaa t t gt cat t at t ct t t t at ct t t gt aagggg 180
t at cat agca aaat acagaa t acat agt gc t gct t gct t c t t ct t ct act t t t gat gagt 240
t cct gct t gc t ggt act ggc at t at t aaca t aaat ct agt gt t t ct t t t t t t t at t t t at 300
t t t at aacaa act acagagt aact t gact a t gaat t ct gc gt aagaagat t at gat gat a 360
cat aaact aa ct aaaagt ct gaaat aacaa aaat gaacca gt t gccat t g gat cat cacc 420
t ccaagcaca agaggt aat a agaact t gat t cat ccaacc aagacacaga gccccat ct c 480
t ct cct ct ag agt gt aat gt cct cggt agc t t cgct gaag at t t t t t at t gaacaagt aa 540
t aaacgagt t cagt ggat at ggt gcgaat c cagccat agt aaaacgcgat ct ccact t ct 600
t cagaagct c gt gacgt t cc act ct t t cct gccct t caca t gct at t aag t t gacaact t 660
ct cgagccaa acaat gct gc t ccacat t aa t cct t t ct t t gt gct ccct c ggcagagcaa 720
cat caat t ga t t canaaat a gccaagt agt agt t cat cgt ct caacgaaa cgggggat aa 780
t gggannngt gt ggt at gt g at t ct t gct c aact agt gt c acaat c 826

<210> 191
<211> 969
<212> DNA
<213> Glycine max

<400> 191

atctgctgct tatactatgg atgagcatcg gagaatt gct tgtgcagaaa ttgagcgttt 60
gaataaagat tctgagaagc agcaagagct gtttacacag aaggtatgcc attgttctgg 120
ttcatttgta aatatttttt ggctgatgga aattcatgtg attgtcatta aacttctttc 180
gacaattgac ccttagccat tactatgtat tggtgtt act tgcaatgaaa ttatcttgaa 240
tgttcatatt gtcttaaatt gttttttttg tagctgaagg agtctgaaga aaagattggg 300
ggcttaagca aagaaagaga gcaattaatc aggcagagag atgctgctat tcaggaagca 360
aatatgtggc gttctgaact ggcaaaagct agagagcatg atgtgatctt agaagcagct 420
gtagtaagag cagaagaaaa ggttagggtt gcagaagcaa atgctgaaac taggataagg 480
gaggctgttc agagagaatc cgcagcatta aaagagaagg aagagcttct tgcatatgtg 540
aatgtactaa aagcccaact tcaaaggtct agcgtcttat tttcttttttc ccttgctttt 600
tattttgtta aattagattt gttggctact tctgttttcc cacctaaaca taaagatgga 660
aaaaatatat atcaatacct agtgaaacag ggaaatggaa ggagacttt t gatggttt at 720
ttgtctttt t accagtttat tgagttt gaa tatgtatatc agctacgaaa tgtggagctt 780
cataaaacca aagttgacat agcagatatt tttctttt ca acaggcaaca cattgataca 840
actcaagttt ttgagaagac agagtcatgc tcagatacaa agcatgttga ccccactgaa 900
gaaaatgtta taaagcatgc ttgagtgttt ctagagccat ccccgtccct gcaggcatgc 960
aagctggcg 969

<210> 192
<211> 1269
<212> DNA
<213> Glycine max

<400> 192

aaaattttg gagaatatac agagagtaca gcatttgaaa gaccacttac tagtggtgtt 60
gcttatgctt tgaaagttct ccactctgat aggatgcatt ttgagaagca gcatgggtgg 120
acaattaaga aaatggaaac tgagaatgag gcattagtcc aagattgtat tcctgaaaaa 180
ttggatccag cacccatt ca agatgaatat gcaccagtga tatttgctca agaaacagtt 240
tcccatattg tatctattga catgatgtca gggaaggtgt gtcttgctta gcttgctgtc 300
accctagcat gatttacttt ttctaagcaa attgtggggc aatggcttaa actgaaaatt 360
ttacattcct gtcaatgttc ttaccatatt tgttctgcac aagtatgtat aagaaaacta 420
gtgtgaagtc atcagttaga aagacttttt tttctttgta ttttctttat gcaaggttta 480
ggtcatagca ttagatgctt ggagcttttg tatacatgga gtggaatatt agaactggag 540
atcactaaac agtatatatt ttactttgaa cagtgaaaat gtgaaagtta aatgtggggt 600
aaacagaatc aactacatac aagagttttta ctcatgaaca tcaataaaat gactctgagc 660
actggttaaa agaaataaga ctaggagtta ctattatcta ttgaatttatt tgttaaattt 720
ctcatttatct gtctggttaa aagaaaatat tttgttgcat tgttgcacag gaggaccatg 780

agaatattt gagagcaagg gcatctggaa aggggttct gacatcccct tttaaactac 840
taaagtccaa tcacctgggt gttgtactta catttgctgt ctataacact aatcttcctt 900
tagatgctac accggagcag cgtaccgaag ctactgtggg gtaatcctac atttaactat 960
ctactggtta aaatatgcat ttcatttgtg ctctgatcca cctcccctaa gaagaaaaca 1020
attacaaagt gtaatgtgag tgttgttacc tatttattgg caggtatctg ggtgcatctt 1080
atgatgttcc atcactggtg gacaagcttc tgcaccaact tgccagtaaa caaaccattg 1140
ttgtaaatgt ttatgacaca actaatgcat ctgcaccaat cacaatgtat ggtacagatg 1200
ttgctgacac tggcctacta cacataagca gcctagattt tggggatccg ctacgaaaac 1260
atagatgca 1269

<210> 193
<211> 1246
<212> DNA
<213> Glycine max

<400> 193

aacttcctac acatggaagg ccaatggtgc tccatgagag tgaaggtggg cacactgtcc 60
gttcaaattt tcaaaatcat atgaaatact gtgatgtcgt attcgatcca atgctcaaac 120
tatttgttgg ggttttgattc caataaaaac aatgaggtat ctatttcttc ttttttatttt 180
aaaaagacat aaataaaagg aaattatcca aacaccaaac ctagtttcaa gggtaaattg 240
ttactgtgcc taggttagga aaatttggta gcatttgaac catttgataa aatttttaaat 300
ggaatccagt tgttaaagaa gcttgtgagg aatctgtttt tatatgacc gaaggggtt 360
aaagaactac ggttaaacaa tgaaactcct ttgtatcctg tgtgtataac atgcataaaa 420
cagtaaggaa atgtttgatt tgattatttt ttatttttcat ttttactgaa aacgaaaaat 480
ggtgataaaa atgtgtttgg ttgaatttct gaaaatattt tcagtgaaaa taaaaacaga 540
aaataatcag aaaatgataa cagaaacctc atttcggata aaataaaatt acggtaacaa 600
tgaatgtaat tttaaacaaa tctaaaaata caaaaagaca agaagttaat atatcataca 660
ttttcagtat ttttatttca tgaaaacaaa aaacaagaag ttaaaccaaa catgttttca 720
gaattctttc ttttgaaaat gaaaacaatt ttcaaaaaat aaaaaaaaaa tgaaaataca 780
aattaaacac acctaatatt ttcgacattt ttactagtac agtagtacat gtaccagtct 840
gatttatttg tttctatttg gaaaatagtt attgcaggaa atttataaaa taaaataaaa 900
aaatcccgag gaaaggaatg tgtggattga attacaaaga taggactcaa attcggttgt 960
acagttttatt gataactgaa accaatgttt acaaggtttg accagagaaa gctagctcta 1020
tctgtggaag cactaactca tgtcatcatc ttacacaaag caccaccaga gacaactact 1080
tctccactat gaagaacctt tttcttattc tccacaagga acgctccacc tggccaaact 1140
attcacaaga caacattctt ctacaacaac cttgtcatac catactgaac aggtccaacc 1200
tttctatgag cagtggtact aatcccacca tattatgagc cttgac 1246

<210> 194
<211> 671
<212> DNA
<213> Glycine max

<400> 194

atgctttaat attacaacag atggaagttg atgaggttca gaagcctgaa aatgtaactg 60
gaaacatgat atatctttct aagattgaga atcaagaaaa ggaaaaaggc tacgactcta 120
aatcctctat ggtaaaatgca cttcaagatg ccaataatag tgaaaaagtg gagcctagaa 180
ctagtggcaa gaaagggatt gtatgcggag ttgaagtagc aatgtctaaa gaaactattg 240
aatgtcagaa ggaagataaa acgaaggtat tcttctaatg ttattgttaa tttttttttct 300
tgatgtttgta ttattgttct taacttgtga attgtgatca cgttaagctt catttttatt 360
tcatttacttt caatttttctt agtatgtacc accaatgatg aattaaagat tttgatccaa 420
tgatgatcct tttgatatat ttagttttagt aagttcaaat attttaggct agcattgcaa 480
tgttttacac agttacccac cctttcccgt aaccaataaa aaaaagtgtg atcacattgt 540
tgtacttgtg tatgtctata tccaaagtct ttatatggac accttaatta tgtggggttc 600
catattgtgg agtgactgtg taatgatttt aagactagtt acattggttc ttttgctaaa 660
ttttgatcat c 671

<210> 195
<211> 1137
<212> DNA
<213> Glycine max

<400> 195

aactgcttcg gcatgaggaa cgtgacgagg atgttttttct ttcttgtctc ccctgagctg 60

tttcagacca tgcttaagtg ccggcaataa agcttccata cactcggcaa cagcattagg 120

gttttccaggc atgttaatga tctgaatttg aacaaatcaa gggccataac ttagccagta 180

agtacaagtc tagaagaaag acagattaga tgtctggatc cagggtgtac tagtagttac 240

agcaataaat gcaagatttt ccttaactac tcatgataca gctccatttt gaagccaagg 300

gcacttgtat accaaatgta aatggatgaa actaaagtaa ctagtaataa acacagatta 360

tcatataaaa aagcttcaga atctagattt gagtttcctg aaaatagtaa ctgtttaact 420

aaaacaacct tactgtaacg gtgaagattg aaaacaatag gtaccttaaa actcaaataa 480

ttaaaatcta acaacagtac aagacatgga cgctttatcc ctcctaatat tctttttaat 540

aaaccagcag ggttttattc atactaactg tgttggtcat ttataatcaa ttttcttatt 600

ttcttataat ttctaaaacg acacttgtta tttcttgtca tcaccctcgt ttaattaatt 660

taagattaaa agggctttct ggctgttta acaaaccatt ttttctgcat tgaataacag 720

ttaatttactt tctcacttgt tactgatagg atattgtaca agtgagagaa taagatattt 780

tcctagaaca gcccataaaa agaaaaagag aaccatgcaa aaccaacaaa gaacatttta 840

aaaataaagt caaccattat tgagatgaaa tattctttta caaattaata agtcatttga 900

gagttgagac actaaattca cactcagtaa ttctatttttt ttttagataa caagaggaag 960

agaagattga catatttaca ttcttacatg aaatacttac attgttctat aaagaaattt 1020

tctaagatgc ataaaaagct atagtcacaa agcaattcca attataacac taaaatgagt 1080

tttaaagtag atattaatta gcatttttgc cttaccaagg ttgatcctct gattcca 1137

<210> 196
<211> 694
<212> DNA
<213> Glycine max

<400> 196

aagctccttc tttgggagaa gaaactcttt aacgaagtta aggtatggat cttaaatcac 60
caatctcatt cattccattg ctttcagttt tttccacttt taatttttaa tctctgtgag 120
gcaatttaat cctgctgcat tcacatcagt tcttgtatat tctattgtaa ccaacctgtg 180
ctgataatt t gaaagaaacc aactgatcag aagtctttta tgccataagt aaaacattgt 240
taaccagtgt ttacaggttt ccacattttt ttttttccaac gtttcatttgt ttgcaggcag 300
aggaaaagat gcgtgttatg catgatagga agtgtcgcaa gctgaagcgt ttggatgata 360
ggggtgctga ttttcataaa gttgattcaa ctcgaacttt ggttaggaat ctgtccacaa 420
aaattagaat ggcaattcag gtggttgata agatttctat gactataaac aagataaggg 480
atgaagaact gtggccacag ctgaaggaat taatccaggg gtatgtgatg ttaaaaacta 540
accattcttg ttatttgttc aagtcctaaa tgtctctctg ttaatgatgg gcaacactgt 600
atgtaaggat ggatggaaaa ataattccca tatctatgct ccataatcca atccttcaat 660
tccccccaat ccattgaata ttgaattttg aaaa 694

<210> 197
<211> 693
<212> DNA
<213> Glycine max

<400> 197

cgctgcagca gctggaaacc aataaccata taccatactt ggtaagagaa taagtgcgag 60
gtggaaatct agaaaaccaa tgggtgttac tttgagtttt catcatttca tggaaactca 120
ttattcaaaa atagaatcat cgttaatgtg ggttggttga cttggttcaa ttggtagcct 180
taactaaatg gtttccaagt acaaaaccct ggcagaggcc tgtggcatgc attgagcttg 240
cttggaatgg agtaacctct cctcccccaa acttctctca caaaaaaatt aaagaaatta 300
gaatcttcag gagttctagg acaaccctc cat cat gct a aaaaactatt ttttgaagta 360
ttgttcaaaa tagtatacca aataccccat gaagctactc aggacagttg taaaagtaat 420
ctaattaaca tgttggaatg cagataaagt cagagaggtg ctgaagcttg atctggagat 480
gaaggatcta gcaaagcagt tgattgctga gcagtctctt cttgtctttg ggagaggata 540
caactatgca acttgctctt gagggagctt tgaaagtaaa ggaagtggct ctaatgcata 600
gtgaagggat acttgctggt gagatgaaac atggtccttt ggcattagtg gatgaaaatc 660

ttccgaatgt tgatctagct acccgtgatg cct 693

<210> 198
<211> 738
<212> DNA
<213> Glycine max

<400> 198

aagaaaacat aaagtatatc ggttttgagca tcacttttt gtagaatgcc cacaataaca 60
gtaaatttcag atcaaagtaa aaggctgcac aagactcatc agccagagca aatttctgatt 120
tgaatttcaac ttttacatga ggagtcagag ccaatgcccg tttatagact gagttgcata 180
cagttacagc acctatgact acttttattgt ttaaaatttt agtctcctct agctcaacct 240
aaataatatc ctcaatataa agatgacatt gacagtaaat acaaaaagag accaaacaga 300
aaagtcaaga ttgcatacgt gatatactct aaaaaggttg acaacggttc tgtggcttgg 360
catagcatgt tcttgtaatc atcaaccagc ttaagagtac acttctccac aatcgtggtg 420
gtatgcaacg gagaaggctc tgcaataggt aacttactca tcagccatca gcataagacca 480
ataatcttaa ttagatcttg tcaacgagta aacaccattg tactaatttgt actaatacaa 540
aagcaacaga aatttcttgta aaccttcaat caaattcaat tcaacagaca gagttaaaca 600
aaacccagac taacaaacaa cagttcactt tcaataatag ttaacattca gacagatata 660
acatggaaat aaacaagata acacaccact ttttctttg tttcccacaa gtatcatcct 720
ttggaagaga caatcctа 738

<210> 199
<211> 610
<212> DNA
<213> Glycine max

<400> 199

tgcagacata ttgctcatgc catcaaggtt tgagccatgt ggattgaacc aactctatgc 60
catgaactat ggaacagttc ctgttgtgca tgctgttggt ggactgagag atactgtgca 120
gcctttttgat cctttttaatg agtcaggcct tgggtggaca tttgatagtg cagattaagg 180
taagttatca catgcattag ggaattgctt aaggacctat agggagtata agaagagcag 240
ggaagggctt caaaggagag gaatgacaca agatcttagt tgggacaatg ctgctcagca 300
gtatgaggag gtgcttcttg ctgccaaata ccaatggtga acttttggca tttattccat 360
ctaagaagac ttgtaaaatg gagctgctaa ttcatgttga atacttccag tgtactgatt 420
gttgtgttag ggaaaagaac tgtgcaagtt gttttaaattt tatatggtta cagttagagcc 480
ttttttatgg gaagtgggaa ggccaaatтt tggtgctgga ttatgtaact gtaatatagt 540
tgacccttcg tgtcaatgta ttaggatcat accaagtgtt caaccacttc aataatactt 600
tgccataata 610

<210> 200
<211> 915
<212> DNA
<213> Glycine max

<400> 200

tgatt atggt tttcacacag gactgataat ttttt ctggt ctaaagagga agttacccga 60
tgactcgagc aaaagtgatg atatggattc caatgacatg attttttcaa actgtaaaag 120
aagtcgagct cacgatgcag aggatttgga ggacaatcca ccagggaata cagcatatga 180
ttgtatggaa accagtagac aaaatagtcc attgtgttca tctatgtccc catgtgcagt 240
tgaaggttgt ctgtctaagg ggtttgcagg actactcaac ttgttcctat gtgtagtttg 300
gtagggagag aagggcttcc ttttgatgaa gctcccctct tatagttaaa gaaatacata 360
gaaggttctt ttgctagttg atatctgttg atgtattcat tttgaatggg ctacaattac 420
atgatcctag tttctcatta atattattcg tggcgttgta attttaaca tcatcctggt 480
gagtgttaaa taactatcca ttgccttga taaaatgaat agaaatgttg tgttttgctt 540
ctatgggaaa tttgatccat aattcccatt gtttcaatat gtatacttga aattgaaaac 600
taaggacata tggtgaacca gtatattaaa ttttagaact ttgattgaat tttaaaaaaa 660
attattcccg ggtttacctt atgaaaaaga aaaaatggaa aaactgtaaa tggatttat 720
ttattggtat ttatttattt tactgggctc tttctaacaa caacttttag ggacataaat 780
ctaagtacca aattaccttc cttatttttt ttaaggccct gaacaacctc tgaataaata 840
aaagaaattt ttttgccca aatttttga accctcatta aaaaaaaaaa tgtaaatgag 900
actggaaaaa taaaa 915

<210> 201
<211> 668
<212> DNA
<213> Glycine max

<400> 201

actttgtac aagctcatca atgtatatca tagttttga aatcggtaat gaaccaatgc 60
aaaaaatggt ttaaacccgt atttctttag gagattatag gtgaattgga tgattaagga 120
aaaatggaag gaaaaaatat cacaagttta attcctgcta ataaaattaa tattttaaca 180
actaacattt gctcatataa aaaacccaa tatttttaa aatttaatct aaagcatttt 240
taagttaact aaaaacatat ttaataagaa ttaaaatagt tgtaaattat tttattaatt 300
attattaatt actcttataa aacatataat ttaatcatta tatcaatttg caatttttta 360
tatcttgatt tcacataatc ttatattaac ttcttgtttt cttttttatt ctagatgtaa 420
acttgttatg aagtgatttt actgggtttt gaccagtttt gattcttcgc caattccttg 480
aacgattttg tagtttattt atatcaaaca ctaaatcaat tcatcagttt tctgggtcaa 540
accaacaaat ttgatctggc atcttataac acaattgttt atggaaaaca catctaatgt 600
gattaaacaa ggacatcacg caacttggca gttaccactt ctttgccttt gctccaatat 660
ttttattt 668

<210> 202
<211> 941

<212> DNA
<213> Glycine max

<400> 202

caagctt gtt gcctgcagaa aaagcacatg ggatagttgt taatagtttt gaagagttgg 60
aagcagaata tgttgaagag tgtcaaagat ttacggacca tagggtatgg tgtgttgggc 120
ctgtgtcgct gtcaaataag gatgacaagg acaaggctat gagaagtaag agaaactcaa 180
gtgatattga gagtgagtat gtgaagtggc ttgattcatg gcctccgagg tcagtgattt 240
atgtttgcct tggtagccta aaccgtgcaa cgccagagca gttgatagag ctcgggttag 300
gattggaagc gacaaaaagg ccattcattt gggtgcttag aggtgcatat ggaagagagg 360
agatggagaa gtggctgttg gaagatgggt ttgaagagag ggtgaaaggg agagggcttt 420
tgatcaaggg ttgggtgcca caagtgttga tcttatcaca tagagcaata ggagcgttca 480
tgacacattg cggatggaat tccacactcg aagggatttg tgctggcgtg ccgttggtaa 540
cttttcctct gtttgctgag cagttcatca atgagaaact tgtacaagtg gtgaagattg 600
gcgtgagtgt gggagctgaa tctgttgttc acttgggtga agaagataag tctcgggttc 660
aggtgaccag agaaaatgtt ctggattcta ttgaaaggta atgggagaat ggccaaaaaa 720
aaaaaaaata taggaaaggg ctttaaagta ttccgccatt ggcagggaaa gcaaaaaaaa 780
aagtgggttt ttttttctcac atggtcctac tcattgggcc atatacctt ggagggttaa 840
ccaagtttaa ccagggttct attttttgtt ttcaacacca attgcttttc tcaagggtca 900
accttaaacc caatttgtct tccgaaagaa ttttttttttt a 941

<210> 203
<211> 652
<212> DNA
<213> Glycine max

<400> 203

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ttggtcaaat attatcatcc ttttcattat ctcactaata aggtggattt ttttttgttg 120
acaaaatttc ttttttcaga ttggtcaaag ctaaagaaga tagaggagtt agatttatcc 180
ggcaacgaat ttaagggacc acttccctcg tcttttgtta acatgacatc tcttcgggag 240
ttggaaattt ctcataatca cttcattgga aatttcgatt ctaacattgc aagccttaca 300
tcacttgaat attttggttt tacagaaaac caatttgaag ttcctgtttc tttctcaaca 360
tttgccaatc atttcaaaga caagttgatc gacggtggag gaaacagatt catattggac 420
tcacaacata gtttaccaac ttggattcca aaatttcagt tacaagagct tagtgtgtct 480
tcaacaactg aaactaagtc tcttccactc cccaatttttc ttctatacca aaacagttta 540
atcagcctag acttcagtag ttggaagttg gaaggagact ttccttattg gttgttggaa 600

aacaacacaa aaatgactga agctctgttt agaaattgct ctttcactgg tg 652

<210> 204
<211> 699
<212> DNA
<213> Glycine max

<400> 204

tgcatgcctg cagcaatctc agctaaacaa gacaggtttc agcgaaaaac aaatttccat 60
tgctcacaac acacagttcg gcaaaaaagc ttcattaaac tcaaccatgc catcaccact 120
tcatttctgtg tagctttgtt ttttcattca tggaaatttct cagcatttca aaccccactc 180
tttgcctccc ccaaaccctc actttaaaat tcccaccaaa ccactccaaa cccacatccc 240
catttctcag aactccattt tcactctacc tatcacgctt cgccgtcata aagtttcaaa 300
cttgggcgca ttccgggcga cccagcaacc gccgcaactc cttttggaag aagctcctcc 360
gtgatcgcaa ggtaaactct aatcagattc ccaacgaccc tttctctgtt tcgggcaatg 420
gcgttgaaga gagtggtgtt ggtgatcagg gggttgacaa tgtggttgaa gttgaaaaac 480
caaagtctaa gcttttgcgt gagtctgttt tgtggaataa gttggagaat tgggctgacc 540
agtacaagag ggatgttgag tattggggtg taggatctgg tcctatattc actgtttatg 600
aagattccat tggaggtgtc aagagggtgg ttgtttatgt agaccagatt ctgaaaagaa 660
gcaaggtaaa catggctagg gagatggaga gtgggaata 699

<210> 205
<211> 578
<212> DNA
<213> Glycine max

<400> 205

aaacgtgttg aaatgaatat ttgggatctt aacaacttca ctaagatctg gaattccaaa 60
cctgtgagtc tttacttcaa ccctttactt tcatctctgc tatttaattgt taacttatct 120
tcctccagtt tacctttttgt tggtgcacat ttttttagtgc ttgatttttac aaatccttttt 180
aacctatgca gccaactaag gataacctcg gtatatttac acctacttgt ttcacatctg 240
ctacatttct tatgaaagat gaccatcgaa aatttgttgc tggcaccaac agccatcagg 300
taaatttaat tggtagattc ttctcatttct aaaataagtg aagaaatata atttttatat 360
ctaataatgc atggaatatt cctctttgat atccttgaaa aaacatgtgc tggagactat 420
tgagaaggat taataagttt ctcttaacct agaattacag agaaatggaa atgatatttt 480
tgagaatttt tttttgcaaa agaacactca agtacatgtc cttcaagtca catgagatct 540
ttcccatttt attaacaaat ataaaatgag taatatga 578

<210> 206
<211> 754

<212> DNA
<213> Glycine max

<400> 206

gagccagtat aagacatttg tggtgatcgc tctcgaccat gagaagcaga atgcaaagca 60
ttctttgaca aaaattcatc cacaagtgtt tgtaagtaat tgataacatc tttggtccaa 120
acatcagagc gagacagctg aatcttgtca gcagccccag aagaaatacc aacagaacca 180
ggtcgaacct gaaaaagcca atcataatct acaaatatta aaaaatataa agcaattcat 240
catAataggt aaatatacca acactgaagc atccctacct gattgaggta agtaaccttg 300
ataaaccagg tggccctaag caatggaaca ttattcctga taagaacctc taaaagtgat 360
gtccttttat aaccatgagg aacatgatca gccaaagagc gtaatcgctt gtgctgctga 420
gataaaccct gtaataaaat tttaactgag ttactaaaga tacattgaaa caccaagtaa 480
tgttcaaaaa gtagtattta aggatttac agccacaaca acctgtcagc atcaacaaca 540
aaaaacctaa ggccctattc ggggtggctg agttttctgt tttccgtttt aaaatgctat 600
ttcaaaatgg aaggtgttcg gctaaaatgg ttgcgagttg gatttttatc tgttttaaa 660
acagttgtca ccccatttta taaacaataa aaataggttt tatgttttat tattttaagg 720
ttactctat ccctacctca acgatctacg ctgc 754

<210> 207
<211> 798
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1)..(798)
<223> unsure at all n locations; n = a, t, c, or g

<400> 207

tctatctgga gagcagaaaa ttctctccag acatgctcac ctgtggagaa tatatttgcat 60
ttggagcccc ttgaggttct ctcaatatat atcatttaatt tgatttattga tttaagacat 120
ttatggagtg attaactgtg caagaaaata attgtatgtt taactgcctg catacatcgc 180
tatgctaatt ctgtccttca caaatctttt cacaacttgt ttgtgcatga ctctcggaaa 240
agacatgcta acatgcatat ggtgaagata agaaatttaaa agaaaatttgg aaaaggaaag 300
atgatatagc aatttaaata ttttttaaga tagatgtatg attgctatat cagaaaaggg 360
ttagtaaaac tagatttgatg tggttgtcct ggttctcttt gatagtaaaa ttttggtattt 420
tccttttgaca catatggtgt atctttgatg gtatgtagta ataccctgga attcagcctt 480
aaatttaaagc attttttttat tctctttgga aggtagatat cttccaagga gttaccctttc 540
cagatgctcc aagatttgga aaggggggtt ggggggcgcgg atgaatttgga caggtatgaa 600
ccctactggt ttttccttcc catattaaag cacacctccc ccatgccgag gggggccctt 660
ttatacctac gcttgcgtac gtggcaagtt tatttcttgta cgcccctggc cttgtagcac 720
tgtccaatcc tgggggacat tccagggttg tacagaacga attctcgtcg acgaancgtc 780
ccgtatccgg cctccacc 798

<210> 208
<211> 1102
<212> DNA
<213> Glycine max

<400> 208

gtttcgccag cttgcactgc ctgagatgaa gtaatt gctg ctgcggtgct gctccggcac 60
cgccttgtgc tggtgcccgg ccaccaggta gagcaaaaga tgtcactcac tctgttcatg 120
aaaaatgggc tcaaggtcaa tgtgcatgag agggatttga gaggggttat cacaagtatt 180
aaaaaggaaa gggaggaaga tgttgatttg agaagtaacg aaagttagtg tggtgttcaa 240
tagatgaagc agagggtgtt ggaggttttt gaatgtggag acaagttcaa atgagaaaaa 300
ttcagaccct ggggctttag cttatagaac aagagaacat aatttccttt taagaaaagg 360
gtatattcag agtatttata attcttatga taaattgtgg atggattctt tttccagggt 420
cgtgggatgg atgattgctt tctcaatcca tcgttccttg tagaatcctt gcaaatattc 480
attgtattct ttatttcttg tcggttttga tgtttctatt taatttt act ggtggtgaga 540
gctaaactca catttcacaa tgttgaatgt tgatgttcat aaaagaatgc cttacgtttt 600
atgaaagtat aatgatcgga tttgactctt ttgtcatata taatggatga tgcttaagtg 660
gtagtggtat actcaaaaac tgcaaaattt agctttacag ttcatctgca tttttt ggtg 720
aatattcatc tgtgattttta gattctgttt ccaggatcct tgcctatgac aatgaaattg 780
aaatgcacaa attgaaccag tagtaaaagt agatatactg atgtcttttg ttaggggaca 840
ttgaatcaga aaactgtgcg accaattttc tcagccatgt atgatgaaga agcagagttg 900
gccatataac atgtattttta actttaagca taagtatgct tgagttatat aagtggacat 960
tatccaccat ctatacagaa accatttaga tcatgggaca agacatttgc aaaaggtgcc 1020
tagttaatcc aagatttcta gataaaatgt aaaggctttc agctatttga tcaaaaactt 1080
tgatggttgc tctcttcgat tt 1102

<210> 209
<211> 697
<212> DNA
<213> Glycine max

<400> 209

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gaatataaaa aacaatt atc taatt catca agatcaataa aagtaatcat attagttaat 120
ttatcataaa ttttaatt at attccatgac tatccatgat tacttttcaa aagataattt 180
ttcaaccaat aagcttacct tgttttattg atagctcaat aaagacgcca cttttatggg 240
aaaatgaatg taatcattag ggataaaaaa taaatttagc aagaaaaaat tacctttgt 300
ttctgatata tgggatggaa gtggatggaa gtagtataat gatactcatg ccattggatt 360
atctatattg cacatgctaa tttcaagcta ttggaaaatg tggaaaagag atggaattat 420
aggcatgcaa ctttaatcaa ttactatttt ctagggtgac aatgtgttta gctctaaccc 480

gaatt gaaac tatt aaaaaa atagat cacg atgcat gaag atagaagata tatat at cat 540

ttgagt ctt t gtaat gcatg aatgct cata tttt att acc cattaaaaaa tatgggttga 600

gtggt at att gaatttt gat ttatttt gtc aatcagatta gattcgaacc aactatttag 660

tat aaaaaat actttt caaa gcatttcaaa tttt caa 697

<210> 210
<211> 934
<212> DNA
<213> Glycine max

<400> 210

ttttcactt t atctgtccct agtgtgttgt tgttattgat tggttt atgg tggtattgga 60

atgttgacca cttgtcttga cttgagtttt gactgtgtat aatggttaac tccggtctct 120

ctgttgaatg ttgttgagtt attccaagat ttgtgtgctg ctttttttt t ttttttttt t 180

ggagtggtta ggtgtaacct ttgtacttat ttttggatgc agacaaggag aaacttggct 240

aaactggagc tctaccgaaa gtttacaaac acgctcgcgg tgtctgtgtt gctgtccatt 300

gcgtggattg gctttgaggt agttcttgga aaaaatattt tgatgctcag aaatatgcaa 360

atttaggaga tttgctctat ctgtaggagt ttccaaacat tttcatttat gtatttttat 420

gcgagttgat gatgctcact aagcgttctt actgtgttca accagctata cttcaatgcc 480

actgatccat tgagtgaatt gtggcaaatt gcttggatta ttccagcttt ctggtgtctg 540

ctttcatatg ctctcttggt ggtgatatgc atcctttggg ctccatcacg gaaccctact 600

aggtacttgt tcttcccatg gtcttggggg gtgaatggta ttttttt aga gtttacctgg 660

tggttttatg cttatgtagt tagccctttt attgaaaggt ggttaatttt ttgaaattaa 720

actagttttg cattacaaag tgcttggggc tcatttgccg attttttcct tcatgcaact 780

ggattatgtc cgccacttag gggggggta ttttgcttgt aaatatacac agcaagtgtc 840

ttcctttaaa aaagaaaaac taaccccctt actcttcttt ttattgggta gagagagaaa 900

aaacataaac aattttatgg ggggtacatt gttt 934

<210> 211
<211> 835
<212> DNA
<212> DNA
<213> Glycine max

<400> 211

ttgcatgcct gcagacatcc tttgaaacac gctgtaaatt gagaattgta tactgattat 60
tgaatcacct ttgcagtctt acatcattgt caatgattgt accataacta tttcatttcc 120
catttacttgt aataaaagtg gctagttttat ttttgaacat atgtattaat aatagttgca 180
catgtgtgag atgatgatac atgtgcatcc tgaacttttg gaaaggtgct aaaatgagaa 240
actatctttt taaatcaggc tactttagtt ggttgaattc tgaataaagt cctctaattt 300
cttgttatga attgatatat cctctaagaa ataagaatat cgaatttaaaa gttgttttaga 360
gggaaaaaga ttccccagct tttaaatgga cccagttttgt tcaaatatcc catgcaacat 420

tttactctga ccatttcact tcaacccaag taacttaattg catcatagta gcatcaaata 480
cacaaacaaa aataagttaa aatcacttaa tagaatttaga agaaaaaaaa atcaaaatca 540
agatttctaga tatttcattgc caaataaaca acgaacttttg acagaagctg aaccagaaaa 600
gactaacaat aactgcttaa aataaaatca tgccagacac tgaatttatgt ggtcctattg 660
attaactgaa agctccttcc gcttatatcg gaccatcact ttcccctttca ctcccacaac 720
catggcattc caatcgatct ctggaaaagg tgacaccaac tccagctcaa aatttcctaag 780
cagatgagtc catattgcttt ttatctgcag gtcgactcta gagaggaccc gggtt 835

<210> 212
<211> 733
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1)..(733)
<223> unsure at all n locations; n = a, t, c, or g

<400> 212

agagat ct t t cat gt ct t ca acgcccaaag act cgcact g t cacagaaac agaaacagt g 60

aaacact at a aaat gct at a cat ct acagc aaat aat gaa ct at at ggaa at ct cct gt a 120

t t t t acat ct at at caaaca at acacat t g aaat agcaac aat gact at t t caaccat t t 180

t t t at aagaa aaaat t t t ac agat aaaagg gagaaaaaaa aaat t ggaaa ggacaaggt a 240

t t t cccaaac caaggggagg t gt gggat ac t gaat ct t ca gct t aagccc aat aat t gag 300

ct gaat agga t aaggat at g t t aagagt at t at aat aaag ggct t t agaa gt t agt t gt a 360

t gt acat t t a t aaaaat t t t t t t t cacaat ct t t t ct t t a t caaaaat t g agt gt gat ct 420

t t t cat t ct a aat gacagca t t act ggaat at t at t aat a t t t t t t t t gg aaaat agat t 480

t t gaaaaact t at at gggct t ggcccacat gcct t t at gt acat aacct a gt aat at aaa 540

t at gagagt c act acacat t ggagt ggagt ggat cccat t at agt t t at t gacacacct c 600

t t t at ct t t c t ct ct ct ct a ct ct acat gg t at caagagc caggt agggt t t ggt gccat 660

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Claims

1. A method of screening and selecting a soybean plant or soybean seed for maturity group association comprising:

   (a) assaying genomic nucleic acids of said soybean plant or soybean seed for the presence of a genomic maturity marker genetically linked to a genomic region, wherein said genomic region is associated with a plant maturity group, said genomic maturity marker is within 10 cM, or within 10,000 kilobases of any of SEQ ID NOs: 143-213;
   (b) determining whether said genomic maturity marker is homozygous or heterozygous;
   (c) and selecting said soybean plant or seed based on said determination.

2. The method of claim 1, wherein said genomic maturity marker is within 1 cM or 5 cM, or within 5 kilobases, 10 kilobases, 20 kilobases, 30 kilobases, 100 kilobases, 500 kilobases or 1,000 kilobases of any of SEQ ID NOs: 143-213.

3. The method of claim 1 or 2, wherein parents of said soybean plant or seed differ in soybean plant maturity by over 10 days.

4. The method of any one of Claims 1 to 3, wherein said genomic maturity marker is associated with maturity genomic region 1 located on linkage group C2 identifiable using SEQ ID NO: 143-155, or complements thereof.

5. The method of Claim 4, wherein said maturity genomic region 1 can be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or more markers of SEQ ID NO:143 through SEQ ID NO: 155, or complements thereof.

6. The method of any one of Claims 1 to 3, wherein said genomic maturity marker is associated with maturity genomic region 2 located on linkage group O identifiable using SEQ ID NO: 156-161, or complements thereof.

7. The method of Claim 6, wherein said maturity genomic region 2 can be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, or more markers of SEQ ID NO: 156 through SEQ ID NO: 161, or complements thereof.

8. The method of any one of Claims 1 to 3, wherein said genomic maturity marker is associated with maturity genomic region 3 located on linkage group L identifiable using SEQ ID NO: 162-174.

9. The method of Claim 8, wherein said maturity genomic region 3 can be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or more markers of SEQ ID NO:162 through SEQ ID NO: 174, or complements thereof.

10. The method of Claim 3, wherein said any of SEQ ID NOs: 143-213 is selected from SEQ ID NOs: 149, 151, 158, 169, 178, 187, 192, 202, 204, and complements thereof.

11. The method of any one of Claims 1 to 3, further comprising associating said soybean plant or said seed with an indeterminate or determinate growth habit if said genomic maturity marker is associated with maturity genomic

region 3 located on linkage group L identifiable using SEQ ID NO: 162 through SEQ ID NO: 174, or complements thereof.

12. The method of Claim 11, wherein said maturity genomic region 3 is **characterized by** a G at position 433 in marker SEQ ID NO: 169, or complements thereof.

13. The method of any one of Claims 1 to 12, further comprising obtaining DNA from said soybean plant or seed using a non-destructive method.

14. The method of Claim 1, wherein said maturity group is between 0.0-III.9 or between 00.0 - III.0.

15. The method of Claim 1, wherein said soybean plant reaches maturity at least 5 days before a soybean plant that is homozygous dominant within maturity genomic region 1 located on linkage group C2 identifiable using SEQ ID NO: 142-153, or complements thereof, homozygous dominant within maturity genomic region 2 located on linkage group O identifiable using SEQ ID NO: 156-161, or complements thereof, and is grown under the same environmental conditions.

16. The method of Claim 1, wherein

(i) said selected soybean plant or seed is homozygous recessive at maturity genomic region 1 located on linkage group C2 identifiable using SEQ ID NO: 142-153, or complements thereof, and homozygous recessive at maturity genomic region 2 located on linkage group O identifiable using SEQ ID NO: 156-161, or complements thereof, and said associated maturity group is between 0.5 - II.0; or
(ii) said selected soybean plant or seed is homozygous recessive at maturity genomic region 1 and heterozygous dominant at maturity genomic region 2 and said associated maturity group is between I.5 - II.9.

17. The method of Claim 5, wherein said allele is associated with SEQ ID NO:151, or complements thereof, and wherein said soybean plant or a soybean plant grown from said soybean seed has a maturity group of III-VI.

18. The method of Claim 7, wherein said allele is associated with SEQ ID NOs: 156 or 158, or complements thereof.

Patentansprüche

1. Verfahren zum Screening und Auswählen einer Sojapflanze oder eines Sojasamens für die Zuordnung zu einer Reifegruppe, umfassend:

(a) Testen genomischer Nucleinsäuren der Sojapflanze oder des Sojasamens auf die Anwesenheit eines genomischen Reifemarkers, der genetisch mit einem Genombereich verknüpft ist, wobei der Genombereich mit einer Pflanzenreifegruppe assoziiert ist, wobei sich der genomische Reifemarker innerhalb von 10 cM oder innerhalb von 10 000 Kilobasen von einer von SEQ ID Nr. 143-213 befindet;
(b) Bestimmen, ob der genomische Reifemarker homozygot oder heterozygot ist;
(c) und Auswählen der Sojapflanze oder des Sojasamens auf der Grundlage dieser Bestimmung.

2. Verfahren gemäß Anspruch 1, wobei sich der genomische Reifemarker innerhalb von 1 cM oder 5 cM oder innerhalb von 5 Kilobasen, 10 Kilobasen, 20 Kilobasen, 30 Kilobasen, 100 Kilobasen, 500 Kilobasen oder 1000 Kilobasen von einer von SEQ ID Nr. 143-213 befindet.

3. Verfahren gemäß Anspruch 1 oder 2, wobei sich Elternpflanzen der Sojapflanze oder des Sojasamens in der Sojapflanzenreife um über 10 Tage voneinander unterscheiden.

4. Verfahren gemäß einem der Ansprüche 1 bis 3, wobei der genomische Reifemarker mit Genomreifebereich 1 assoziiert ist, der sich auf der Kopplungsgruppe C2 befindet, die unter Verwendung von SEQ ID Nr. 143-155 oder Komplementen davon identifizierbar ist.

5. Verfahren gemäß Anspruch 4, wobei der Genomreifebereich 1 überwacht werden kann, indem man auf ein Allel von 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 oder mehr Markern von SEQ ID Nr. 143 bis SEQ ID Nr. 155 oder Komplementen davon testet.

6. Verfahren gemäß einem der Ansprüche 1 bis 3, wobei der genomische Reifemarker mit Genomreifebereich 2 assoziiert ist, der sich auf der Kopplungsgruppe O befindet, die unter Verwendung von SEQ ID Nr. 156-161 oder Komplementen davon identifizierbar ist.

7. Verfahren gemäß Anspruch 6, wobei der Genomreifebereich 2 überwacht werden kann, indem man auf ein Allel von 1, 2, 3, 4, 5, 6 oder mehr Markern von SEQ ID Nr. 156 bis SEQ ID Nr. 161 oder Komplementen davon testet.

8. Verfahren gemäß einem der Ansprüche 1 bis 3, wobei der genomische Reifemarker mit Genomreifebereich 3 assoziiert ist, der sich auf der Kopplungsgruppe L befindet, die unter Verwendung von SEQ ID Nr. 162-174 identifizierbar ist.

9. Verfahren gemäß Anspruch 8, wobei der Genomreifebereich 3 überwacht werden kann, indem man auf ein Allel von 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 oder mehr Markern von SEQ ID Nr. 162 bis SEQ ID Nr. 174 oder Komplementen davon testet.

10. Verfahren gemäß Anspruch 3, wobei die eine von SEQ ID Nr. 143-213 aus SEQ ID Nr. 149, 151, 158, 169, 178, 187, 192, 202, 204 und Komplementen davon ausgewählt ist.

11. Verfahren gemäß einem der Ansprüche 1 bis 3, weiterhin umfassend das Zuordnen der Sojapflanze oder des Sojasamens zu einer unbegrenzten oder begrenzten Wuchsform, wenn der genomische Reifemarker mit Genomreifebereich 3 assoziiert ist, der sich auf der Kopplungsgruppe L befindet, die unter Verwendung von SEQ ID Nr. 162 bis SEQ ID Nr. 174 oder Komplementen davon identifizierbar ist.

12. Verfahren gemäß Anspruch 11, wobei der Genomreifebereich 3 durch ein G auf Position 433 im Marker SEQ ID Nr. 169 oder Komplementen davon gekennzeichnet ist.

13. Verfahren gemäß einem der Ansprüche 1 bis 12, weiterhin umfassend das Gewinnen von DNA aus der Sojapflanze oder dem Sojasamen mit Hilfe eines zerstörungsfreien Verfahrens.

14. Verfahren gemäß Anspruch 1, wobei die Reifegruppe zwischen 0.0 und III.9 oder zwischen 00.0 und III.0 liegt.

15. Verfahren gemäß Anspruch 1, wobei die Sojapflanze ihre Reife wenigstens 5 Tage vor einer Sojapflanze erreicht, die innerhalb des Genomreifebereichs 1, der sich auf der Kopplungsgruppe C2 befindet, die unter Verwendung von SEQ ID Nr. 142-153 oder Komplementen davon identifizierbar ist, homozygot dominant ist, innerhalb des Genomreifebereichs 2, der sich auf der Kopplungsgruppe O befindet, die unter Verwendung von SEQ ID Nr. 156-161 oder Komplementen davon identifizierbar ist, homozygot dominant ist und unter denselben Umgebungsbedingungen gewachsen ist.

16. Verfahren gemäß Anspruch 1, wobei

(i) die ausgewählte Sojapflanze oder der ausgewählte Sojasamen im Genomreifebereich 1, der sich auf der Kopplungsgruppe C2 befindet, die unter Verwendung von SEQ ID Nr. 142-153 oder Komplementen davon identifizierbar ist, homozygot rezessiv ist und im Genomreifebereich 2, der sich auf der Kopplungsgruppe O befindet, die unter Verwendung von SEQ ID Nr. 156-161 oder Komplementen davon identifizierbar ist, homozygot rezessiv ist und die zugeordnete Reifegruppe zwischen 0.5 und II.0 liegt; oder
(ii) die ausgewählte Sojapflanze oder der ausgewählte Sojasamen im Genomreifebereich 1 homozygot rezessiv ist und im Genomreifebereich 2 heterozygot dominant ist und die zugeordnete Reifegruppe zwischen 1.5 und II.9 liegt.

17. Verfahren gemäß Anspruch 5, wobei das Allel mit SEQ ID Nr. 151 oder Komplementen davon assoziiert ist und wobei die Sojapflanze oder eine aus dem Sojasamen gewachsene Sojapflanze eine Reifegruppe von III-VI aufweist.

18. Verfahren gemäß Anspruch 7, wobei das Allel mit SEQ ID Nr. 156 oder 158 oder Komplementen davon assoziiert ist.

Revendications

1. Procédé de criblage et de sélection d'une plante de soja ou d'une graine de soja pour l'association du groupe de

maturité comprenant le fait :

(a) d'analyser des acides nucléiques génomiques de ladite plante de soja ou graine de soja pour détecter la présence d'un marqueur génomique de maturité génétiquement lié à une région génomique, où ladite région génomique est associée à un groupe de maturité de plante, ledit marqueur génomique de maturité se situe à environ 10 cM, ou à environ 10000 kilobases de l'une des séquences SEQ ID NOs: 143 à 213 ;
(b) de déterminer si ledit marqueur génomique de maturité est homozygote ou hétérozygote ;
(c) et de sélectionner ladite plante ou graine de soja sur la base de ladite détermination.

2. Procédé de la revendication 1, dans lequel ledit marqueur génomique de maturité se situe à environ 1 cM ou 5 cM, ou à environ 5 kilobases, 10 kilobases, 20 kilobases, 30 kilobases, 100 kilobases, 500 kilobases ou 1000 kilobases de l'une des séquences SEQ ID NOs: 143 à 213.

3. Procédé de la revendication 1 ou 2, dans lequel les lignées parentales de ladite plante ou graine de soja diffèrent en terme de maturité de plante de soja de plus de 10 jours.

4. Procédé de l'une quelconque des revendications 1 à 3, dans lequel ledit marqueur génomique de maturité est associé à une région génomique de maturité 1 située sur un groupe de liaison C2 identifiable en utilisant les séquences SEQ ID NO: 143 à 155, ou leurs séquences complémentaires.

5. Procédé de la revendication 4, dans lequel ladite région génomique de maturité 1 peut être contrôlée par une analyse permettant de détecter un allèle de 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 marqueur (s) ou plus de la séquence SEQ ID NO: 143 jusqu'à la séquence SEQ ID NO: 155, ou de leurs séquences complémentaires.

6. Procédé de l'une quelconque des revendications 1 à 3, dans lequel ledit marqueur génomique de maturité est associé à une région génomique de maturité 2 située sur un groupe de liaison O identifiable en utilisant les séquences SEQ ID NO: 156 à 161, ou leurs séquences complémentaires.

7. Procédé de la revendication 6, dans lequel ladite région génomique de maturité 2 peut être contrôlée par une analyse permettant de détecter un allèle de 1, 2, 3, 4, 5, 6 marqueur(s) ou plus de la séquence SEQ ID NO: 156 jusqu'à la séquence SEQ ID NO: 161, ou de leurs séquences complémentaires.

8. Procédé de l'une quelconque des revendications 1 à 3, dans lequel ledit marqueur génomique de maturité est associé à une région génomique de maturité 3 située sur un groupe de liaison L identifiable en utilisant les séquences SEQ ID NO: 162 à 174.

9. Procédé de la revendication 8, dans lequel ladite région génomique de maturité 3 peut être contrôlée par une analyse permettant de détecter un allèle de 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 marqueur(s) ou plus de la séquence SEQ ID NO: 162 jusqu'à la SEQ ID NO: 174, ou de leurs séquences complémentaires.

10. Procédé de la revendication 3, dans lequel ladite l'une des séquences SEQ ID NOs: 143 à 213 est sélectionnée parmi les séquences SEQ ID NOs: 149, 151, 158, 169, 178, 187, 192, 202, 204, et leurs séquences complémentaires.

11. Procédé de l'une quelconque des revendications 1 à 3, comprenant en outre l'association de ladite plante de soja ou de ladite graine de soja à un port déterminé ou indéterminé si ledit marqueur génomique de maturité est associé à une région génomique de maturité 3 située sur un groupe de liaison L identifiable en utilisant les séquences allant de la SEQ ID NO: 162 à la SEQ ID NO : 174, ou leurs séquences complémentaires.

12. Procédé de la revendication 11, dans lequel ladite région génomique de maturité 3 est **caractérisée par** la présence de G à la position 433 dans la séquence SEQ ID NO: 169 du marqueur, ou ses séquences complémentaires.

13. Procédé de l'une quelconque des revendications 1 à 12, comprenant en outre le fait d'obtenir un ADN à partir de ladite plante ou graine de soja en utilisant un procédé non destructif.

14. Procédé de la revendication 1, dans lequel ledit groupe de maturité est compris entre 0.0 et III.9 ou entre 00.0 et III.O.

15. Procédé de la revendication 1, dans lequel ladite plante de soja atteint la maturité au moins 5 jours avant une plante de soja qui est homozygote dominante dans une région génomique de maturité 1 située sur un groupe de liaison

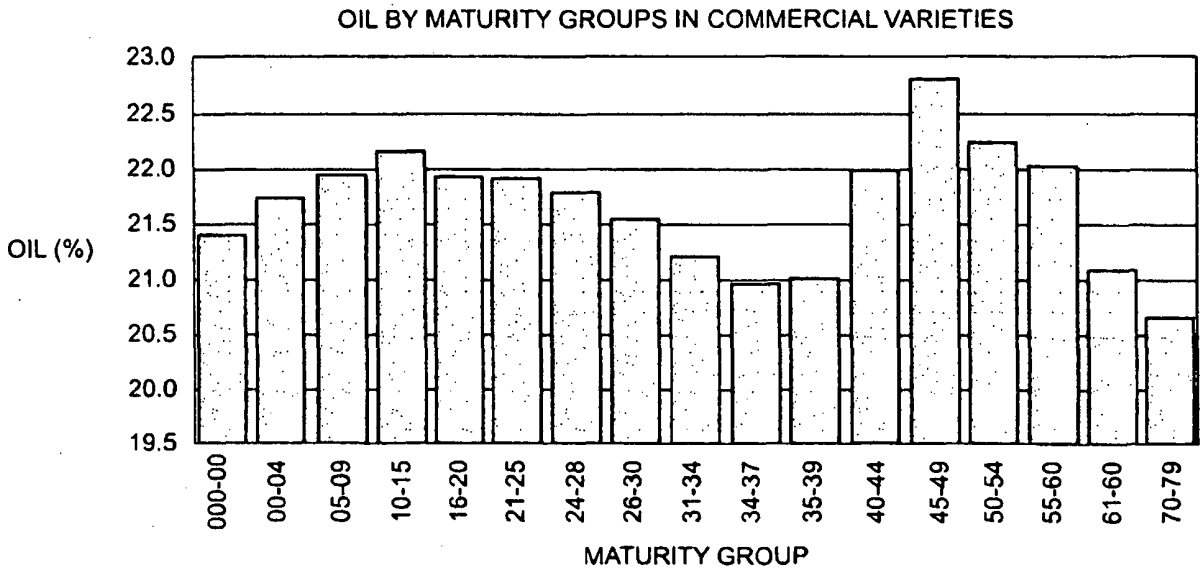
C2 identifiable en utilisant les séquences SEQ ID NO: 142 à 153, ou leurs séquences complémentaires, homozygote dominante dans une région génomique de maturité 2 située sur un groupe de liaison O identifiable en utilisant les séquences SEQ ID NO: 156 à 161, ou leurs séquences complémentaires, et qui est cultivée dans les mêmes conditions environnementales.

16. Procédé de la revendication 1, dans lequel

(i) ladite plante ou graine de soja sélectionnée est homozygote récessive au niveau d'une région génomique de maturité 1 située sur un groupe de liaison C2 identifiable en utilisant les séquences SEQ ID NO: 142 à 153, ou leurs séquences complémentaires, et homozygote récessive au niveau d'une région génomique de maturité 2 située sur un groupe de liaison O identifiable en utilisant les séquences SEQ ID NO: 156 à 161, ou leurs séquences complémentaires, et ledit groupe de maturité associé est compris entre 0.5 et II.0 ; ou
(ii) ladite plante ou graine de soja sélectionnée est homozygote récessive au niveau d'une région génomique de maturité 1 et hétérozygote dominante au niveau d'une région génomique de maturité 2 et ledit groupe de maturité associé est compris entre I.5 et II.9.

17. Procédé de la revendication 5, dans lequel ledit allèle est associé à la séquence SEQ ID NO: 151, ou à ses séquences complémentaires, et dans lequel ladite plante de soja ou une plante de soja cultivée à partir de ladite graine de soja a un groupe de maturité de III à VI.

18. Procédé de la revendication 7, dans lequel ledit allèle est associé aux séquences SEQ ID NO: 156 ou 158, ou à leurs séquences complémentaires.


OIL BY MATURITY GROUPS IN COMMERCIAL VARIETIES
OIL (%)
23.0
22.5
22.0
21.5
21.0
20.5
20.0
19.5
000-00
00-04
05-09
10-15
16-20
21-25
24-28
26-30
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35-39
40-44
45-49
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55-60
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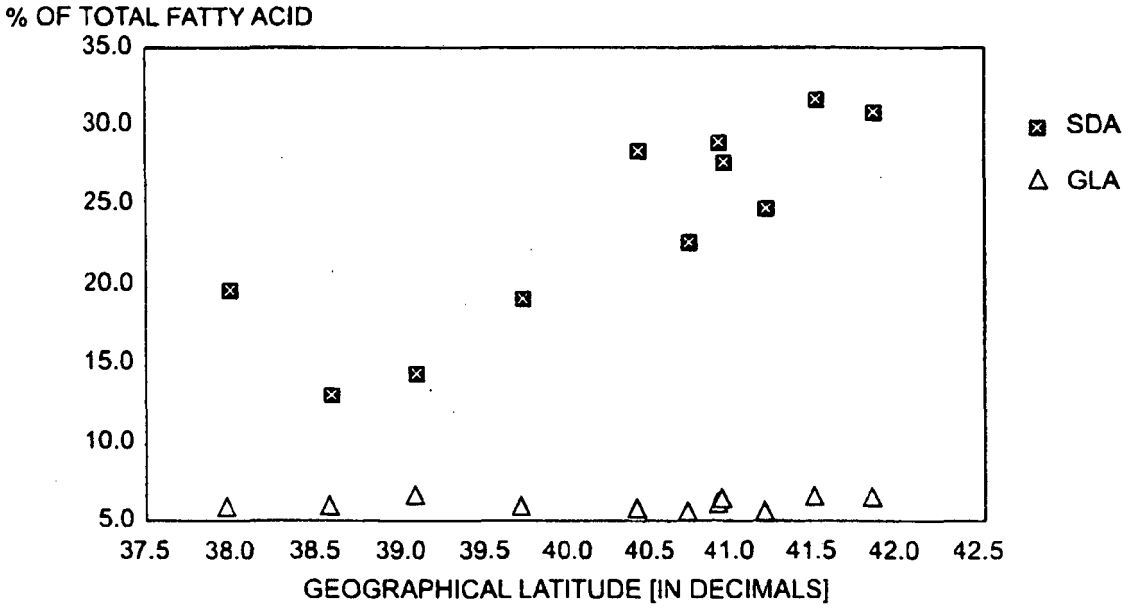
70-79
MATURITY GROUP

FIG. 1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30.0
25.0
20.0
15.0
10.0
5.0
37.5
38.0
38.5
39.0
39.5
40.0
40.5
41.0
41.5
42.0
42.5
GEOGRAPHICAL LATITUDE [IN DECIMALS]
SDA
GLA

FIG. 2

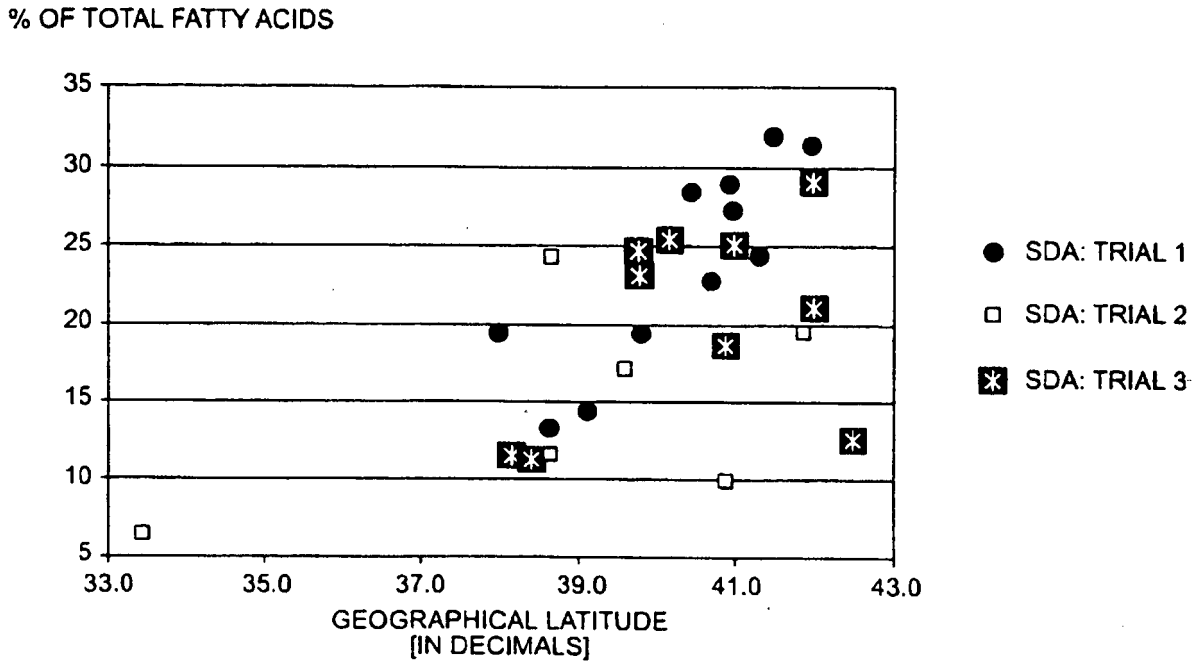
% OF TOTAL FATTY ACIDS
35
30
25
20
15
10
5
33.0
35.0
37.0
39.0
41.0
43.0
GEOGRAPHICAL LATITUDE
[IN DECIMALS]
SDA: TRIAL 1
SDA: TRIAL 2
SDA: TRIAL 3

FIG. 3

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