

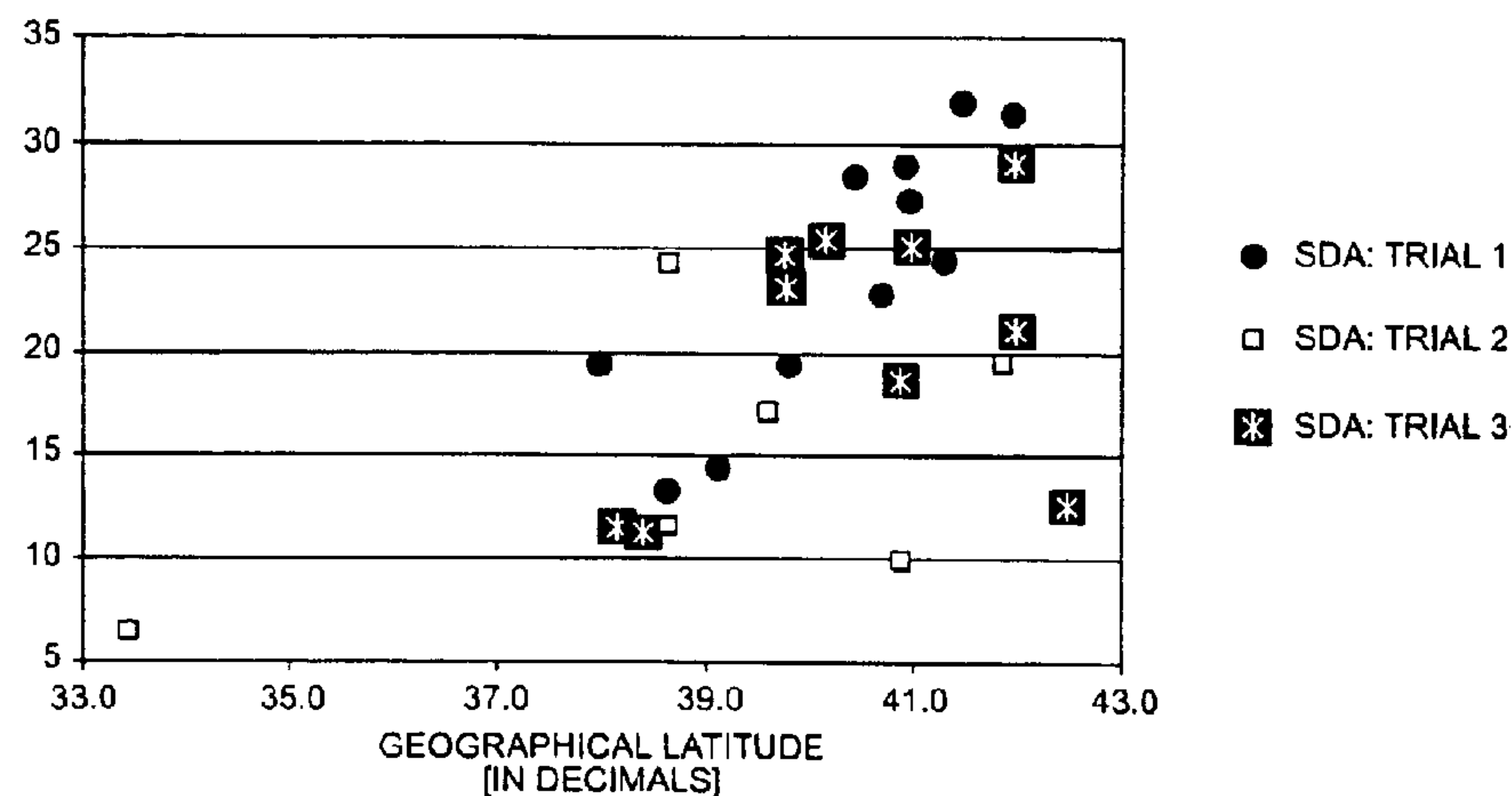


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MATURITE DE PLANTES DE SOJA
(54) Title: UTILITY OF SNP MARKERS ASSOCIATED WITH MAJOR SOYBEAN PLANT MATURITY AND GROWTH
HABIT GENOMIC REGIONS

% OF TOTAL FATTY ACIDS



(57) **Abrégé/Abstract:**

The invention includes methods and compositions of genomic regions for screening and selecting plants and seeds from the genus *Glycine* associated with soybean plant maturity and growth habit. The invention also includes methods and compositions 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.

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

% OF TOTAL FATTY ACIDS

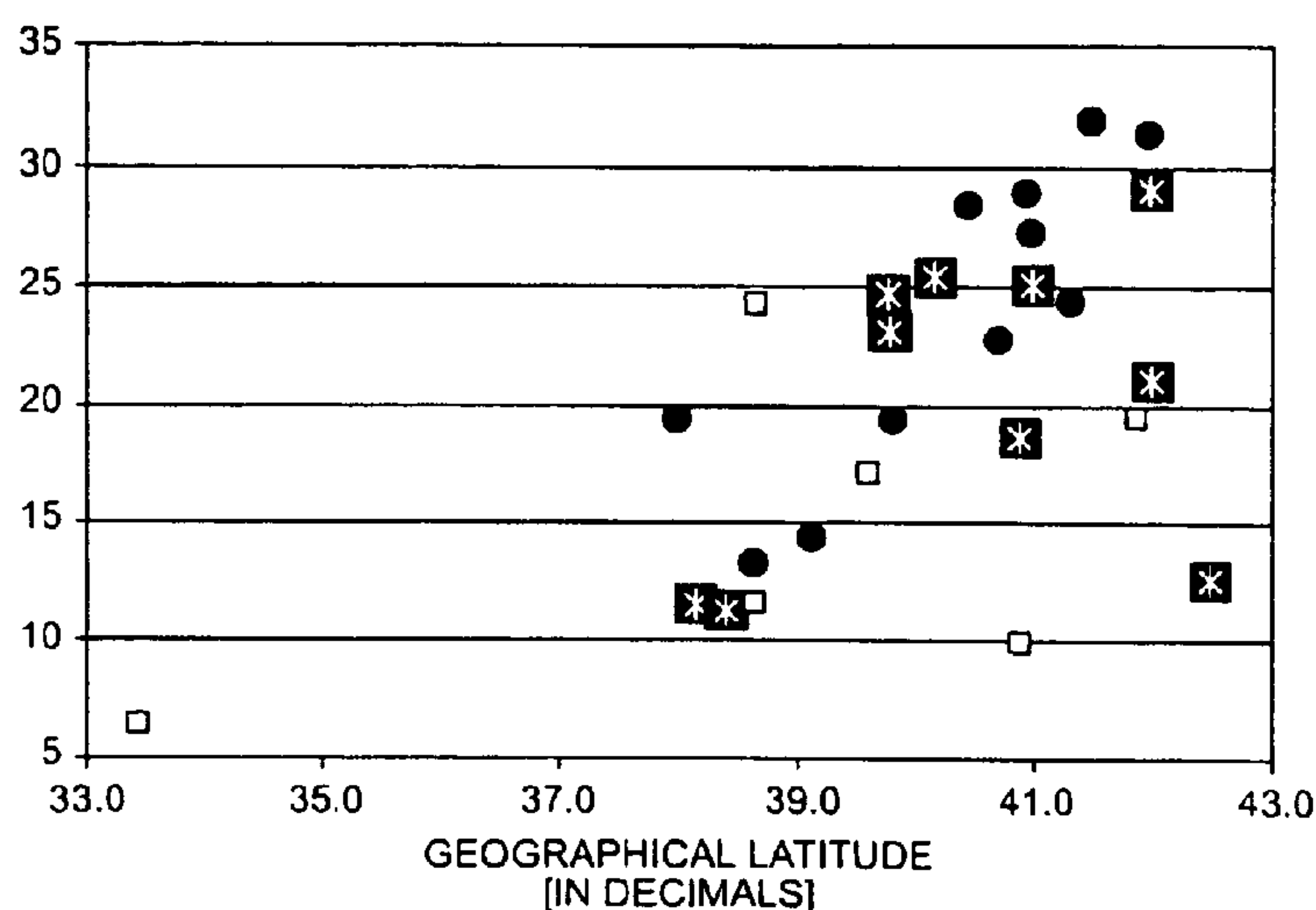


FIG. 3

(57) Abstract: The invention includes methods and compositions of genomic regions for screening and selecting plants and seeds from the genus *Glycine* associated with soybean plant maturity and growth habit. The invention also includes methods and compositions 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.

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Utility of SNP Markers Associated with Major Soybean Plant Maturity and Growth Habit Genomic Regions

Field of the Invention

5 The invention includes methods and compositions of genomic regions for screening and selecting plants and seeds from the genus *Glycine* associated with soybean plant maturity and growth habit. The invention also includes methods and compositions 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

10 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.

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.

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 trait 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.

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.

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.

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

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

The present invention 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 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 another aspect, the present invention 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 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.

The present invention also includes 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.

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.

An aspect of the present invention includes a method of 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 an aspect of the present invention, a 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.

An aspect of the present invention 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 any 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.

Another aspect 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 determining the desired geography for the progeny soybean plant growth, and a method for determining the non-maturity phenotype.

In one aspect the present invention includes 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.

In another aspect the present invention includes a method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent
5 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
10 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.

An aspect of the present invention includes a method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants
15 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.

Another aspect of the present invention includes a method of screening soybean
20 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 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 seed.

25 One aspect of the present invention 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.

Another aspect of the present invention includes a method of distributing a soybean plant based on maturity group by obtaining DNA from a soybean plant; determining if an
30 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.

Another aspect of the present invention includes a method to isolate indeterminate-
5 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.

An aspect of the present invention includes a method of determining if a soybean
10 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.

Another aspect 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
15 comprising determining if an 11-basepair insertion within the nucleic acid sequence of SEQ ID NO: 149 exists in the soybean seed.

An aspect of the present invention 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
20 region 2 is homozygous or heterozygous; and assigning a maturity group value for the soybean plant between 0.0-III.9.

One aspect of the present invention 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
25 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.

Another aspect of the present invention includes a method of introducing a desired
30 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.

5 A further aspect of the present invention 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
10 NOs: 143-174.

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:
15 143-213; and selecting a soybean seed with a desired maturity group.

An aspect 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. Another aspect 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.
20 Another aspect 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. Another aspect 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. Another aspect of the present invention includes a method of detecting maturity genomic
25 region 8 by detecting an allele using a marker selected from any of SEQ ID NO: 204-213.

A further aspect of the present invention 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.

30 Brief Description of Nucleic Acid Sequences

SEQ ID NO: 1 is a forward PCR primer for the amplification of SEQ ID NO: 143.

- SEQ ID NO: 2 is a reverse PCR primer for the amplification of SEQ ID NO: 143.
SEQ ID NO: 3 is a forward PCR primer for the amplification of SEQ ID NO: 144.
SEQ ID NO: 4 is a reverse PCR primer for the amplification of SEQ ID NO: 144.
SEQ ID NO: 5 is a forward PCR primer for the amplification of SEQ ID NO: 145.
5 SEQ ID NO: 6 is a reverse PCR primer for the amplification of SEQ ID NO: 145.
SEQ ID NO: 7 is a forward PCR primer for the amplification of SEQ ID NO: 146.
SEQ ID NO: 8 is a reverse PCR primer for the amplification of SEQ ID NO: 146.
SEQ ID NO: 9 is a forward PCR primer for the amplification of SEQ ID NO: 147.
SEQ ID NO: 10 is a reverse PCR primer for the amplification of SEQ ID NO: 147.
10 SEQ ID NO: 11 is a forward PCR primer for the amplification of SEQ ID NO: 148.
SEQ ID NO: 12 is a reverse PCR primer for the amplification of SEQ ID NO: 148.
SEQ ID NO: 13 is a forward PCR primer for the amplification of SEQ ID NO: 149.
SEQ ID NO: 14 is a reverse PCR primer for the amplification of SEQ ID NO: 149.
SEQ ID NO: 15 is a forward PCR primer for the amplification of SEQ ID NO: 150.
15 SEQ ID NO: 16 is a reverse PCR primer for the amplification of SEQ ID NO: 150.
SEQ ID NO: 17 is a forward PCR primer for the amplification of SEQ ID NO: 151.
SEQ ID NO: 18 is a reverse PCR primer for the amplification of SEQ ID NO: 151.
SEQ ID NO: 19 is a forward PCR primer for the amplification of SEQ ID NO: 152.
SEQ ID NO: 20 is a reverse PCR primer for the amplification of SEQ ID NO: 152.
20 SEQ ID NO: 21 is a forward PCR primer for the amplification of SEQ ID NO: 153.
SEQ ID NO: 22 is a reverse PCR primer for the amplification of SEQ ID NO: 153.
SEQ ID NO: 23 is a forward PCR primer for the amplification of SEQ ID NO: 154.
SEQ ID NO: 24 is a reverse PCR primer for the amplification of SEQ ID NO: 154.
SEQ ID NO: 25 is a forward PCR primer for the amplification of SEQ ID NO: 155.
25 SEQ ID NO: 26 is a reverse PCR primer for the amplification of SEQ ID NO: 155.
SEQ ID NO: 27 is a forward PCR primer for the amplification of SEQ ID NO: 156.
SEQ ID NO: 28 is a reverse PCR primer for the amplification of SEQ ID NO: 156.
SEQ ID NO: 29 is a forward PCR primer for the amplification of SEQ ID NO: 157.
SEQ ID NO: 30 is a reverse PCR primer for the amplification of SEQ ID NO: 157.
30 SEQ ID NO: 31 is a forward PCR primer for the amplification of SEQ ID NO: 158.
SEQ ID NO: 32 is a reverse PCR primer for the amplification of SEQ ID NO: 158.

SEQ ID NO: 33 is a forward PCR primer for the amplification of SEQ ID NO: 159.
SEQ ID NO: 34 is a reverse PCR primer for the amplification of SEQ ID NO: 159.
SEQ ID NO: 35 is a forward PCR primer for the amplification of SEQ ID NO: 160.
SEQ ID NO: 36 is a reverse PCR primer for the amplification of SEQ ID NO: 160.
5 SEQ ID NO: 37 is a forward PCR primer for the amplification of SEQ ID NO: 161.
SEQ ID NO: 38 is a reverse PCR primer for the amplification of SEQ ID NO: 161.
SEQ ID NO: 39 is a forward PCR primer for the amplification of SEQ ID NO: 162.
SEQ ID NO: 40 is a reverse PCR primer for the amplification of SEQ ID NO: 162.
SEQ ID NO: 41 is a forward PCR primer for the amplification of SEQ ID NO: 163.
10 SEQ ID NO: 42 is a reverse PCR primer for the amplification of SEQ ID NO: 163.
SEQ ID NO: 43 is a forward PCR primer for the amplification of SEQ ID NO: 164.
SEQ ID NO: 44 is a reverse PCR primer for the amplification of SEQ ID NO: 164.
SEQ ID NO: 45 is a forward PCR primer for the amplification of SEQ ID NO: 165.
SEQ ID NO: 46 is a reverse PCR primer for the amplification of SEQ ID NO: 165.
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SEQ ID NO: 48 is a reverse PCR primer for the amplification of SEQ ID NO: 166.
SEQ ID NO: 49 is a forward PCR primer for the amplification of SEQ ID NO: 167.
SEQ ID NO: 50 is a reverse PCR primer for the amplification of SEQ ID NO: 167.
SEQ ID NO: 51 is a forward PCR primer for the amplification of SEQ ID NO: 168.
20 SEQ ID NO: 52 is a reverse PCR primer for the amplification of SEQ ID NO: 168.
SEQ ID NO: 53 is a forward PCR primer for the amplification of SEQ ID NO: 169.
SEQ ID NO: 54 is a reverse PCR primer for the amplification of SEQ ID NO: 169.
SEQ ID NO: 55 is a forward PCR primer for the amplification of SEQ ID NO: 170.
SEQ ID NO: 56 is a reverse PCR primer for the amplification of SEQ ID NO: 170.
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SEQ ID NO: 58 is a reverse PCR primer for the amplification of SEQ ID NO: 171.
SEQ ID NO: 59 is a forward PCR primer for the amplification of SEQ ID NO: 172.
SEQ ID NO: 60 is a reverse PCR primer for the amplification of SEQ ID NO: 172.
SEQ ID NO: 61 is a forward PCR primer for the amplification of SEQ ID NO: 173.
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SEQ ID NO: 63 is a forward PCR primer for the amplification of SEQ ID NO: 174.

SEQ ID NO: 64 is a reverse PCR primer for the amplification of SEQ ID NO: 174.
SEQ ID NO: 65 is a forward PCR primer for the amplification of SEQ ID NO: 175.
SEQ ID NO: 66 is a reverse PCR primer for the amplification of SEQ ID NO: 175.
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SEQ ID NO: 74 is a reverse PCR primer for the amplification of SEQ ID NO: 179.
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SEQ ID NO: 76 is a reverse PCR primer for the amplification of SEQ ID NO: 180.
SEQ ID NO: 77 is a forward PCR primer for the amplification of SEQ ID NO: 181.
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SEQ ID NO: 84 is a reverse PCR primer for the amplification of SEQ ID NO: 184.
SEQ ID NO: 85 is a forward PCR primer for the amplification of SEQ ID NO: 185.
SEQ ID NO: 86 is a reverse PCR primer for the amplification of SEQ ID NO: 185.
SEQ ID NO: 87 is a forward PCR primer for the amplification of SEQ ID NO: 186.
25 SEQ ID NO: 88 is a reverse PCR primer for the amplification of SEQ ID NO: 186.
SEQ ID NO: 89 is a forward PCR primer for the amplification of SEQ ID NO: 187.
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 25 197.
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 SEQ ID NO: 111 is a forward PCR primer for the amplification of SEQ ID NO:
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 30 SEQ ID NO: 112 is a reverse PCR primer for the amplification of SEQ ID NO:
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5 SEQ ID NO: 115 is a forward PCR primer for the amplification of SEQ ID NO:
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202.

15 SEQ ID NO: 120 is a reverse PCR primer for the amplification of SEQ ID NO:
202.

SEQ ID NO: 121 is a forward PCR primer for the amplification of SEQ ID NO:
203.

SEQ ID NO: 122 is a reverse PCR primer for the amplification of SEQ ID NO:
203.

20 SEQ ID NO: 123 is a forward PCR primer for the amplification of SEQ ID NO:
204.

SEQ ID NO: 124 is a reverse PCR primer for the amplification of SEQ ID NO:
204.

25 SEQ ID NO: 125 is a forward PCR primer for the amplification of SEQ ID NO:
205.

SEQ ID NO: 126 is a reverse PCR primer for the amplification of SEQ ID NO:
205.

30 SEQ ID NO: 127 is a forward PCR primer for the amplification of SEQ ID NO:
206.

SEQ ID NO: 128 is a reverse PCR primer for the amplification of SEQ ID NO:
206.
SEQ ID NO: 129 is a forward PCR primer for the amplification of SEQ ID NO:
207.
5 SEQ ID NO: 130 is a reverse PCR primer for the amplification of SEQ ID NO:
207.
SEQ ID NO: 131 is a forward PCR primer for the amplification of SEQ ID NO:
208.
SEQ ID NO: 132 is a reverse PCR primer for the amplification of SEQ ID NO:
10 208.
SEQ ID NO: 133 is a forward PCR primer for the amplification of SEQ ID NO:
209.
SEQ ID NO: 134 is a reverse PCR primer for the amplification of SEQ ID NO:
209.
15 SEQ ID NO: 135 is a forward PCR primer for the amplification of SEQ ID NO:
210.
SEQ ID NO: 136 is a reverse PCR primer for the amplification of SEQ ID NO:
210.
SEQ ID NO: 137 is a forward PCR primer for the amplification of SEQ ID NO:
20 211.
SEQ ID NO: 138 is a reverse PCR primer for the amplification of SEQ ID NO:
211.
SEQ ID NO: 139 is a forward PCR primer for the amplification of SEQ ID NO:
212.
25 SEQ ID NO: 140 is a reverse PCR primer for the amplification of SEQ ID NO:
212.
SEQ ID NO: 141 is a forward PCR primer for the amplification of SEQ ID NO:
213.
SEQ ID NO: 142 is a reverse PCR primer for the amplification of SEQ ID NO:
30 213.

SEQ ID NO: 143 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 144 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

5 SEQ ID NO: 145 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 146 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

10 SEQ ID NO: 147 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 148 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 149 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

15 SEQ ID NO: 150 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 151 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

20 SEQ ID NO: 152 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 153 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 154 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

25 SEQ ID NO: 155 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 1.

SEQ ID NO: 156 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 2.

30 SEQ ID NO: 157 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 2.

SEQ ID NO: 158 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 2.

SEQ ID NO: 159 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 2.

5 SEQ ID NO: 160 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 2.

SEQ ID NO: 161 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 2.

10 SEQ ID NO: 162 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 163 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 164 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

15 SEQ ID NO: 165 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 166 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

20 SEQ ID NO: 167 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 168 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 169 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

25 SEQ ID NO: 170 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 171 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

30 SEQ ID NO: 172 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 173 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

SEQ ID NO: 174 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 3.

5 SEQ ID NO: 175 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 4.

SEQ ID NO: 176 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 4.

10 SEQ ID NO: 177 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 4.

SEQ ID NO: 178 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 4.

SEQ ID NO: 179 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 4.

15 SEQ ID NO: 180 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 4.

SEQ ID NO: 181 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

20 SEQ ID NO: 182 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

SEQ ID NO: 183 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

SEQ ID NO: 184 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

25 SEQ ID NO: 185 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

SEQ ID NO: 186 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

30 SEQ ID NO: 187 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

SEQ ID NO: 188 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

SEQ ID NO: 189 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 5.

5 SEQ ID NO: 190 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 6.

SEQ ID NO: 191 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 6.

10 SEQ ID NO: 192 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 6.

SEQ ID NO: 193 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 6.

SEQ ID NO: 194 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 6.

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SEQ ID NO: 196 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 6.

20 SEQ ID NO: 197 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 7.

SEQ ID NO: 198 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 7.

SEQ ID NO: 199 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 7.

25 SEQ ID NO: 200 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 7.

SEQ ID NO: 201 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 7.

30 SEQ ID NO: 202 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 7.

SEQ ID NO: 203 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 7.

SEQ ID NO: 204 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

5 SEQ ID NO: 205 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

SEQ ID NO: 206 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

10 SEQ ID NO: 207 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

SEQ ID NO: 208 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

SEQ ID NO: 209 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

15 SEQ ID NO: 210 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

SEQ ID NO: 211 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

20 SEQ ID NO: 212 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

SEQ ID NO: 213 is a genomic sequence derived from *Glycine max* corresponding to maturity locus 8.

SEQ ID NO: 214 is a probe for the detection of the SNP of SEQ ID NO: 143.

SEQ ID NO: 215 is a probe for the detection of the SNP of SEQ ID NO: 143.

25 SEQ ID NO: 216 is a probe for the detection of the SNP of SEQ ID NO: 144.

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SEQ ID NO: 220 is a probe for the detection of the SNP of SEQ ID NO: 146.

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5 SEQ ID NO: 351 is a probe for the detection of the SNP of SEQ ID NO: 211.
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SEQ ID NO: 354 is a probe for the detection of the SNP of SEQ ID NO: 213.
SEQ ID NO: 355 is a probe for the detection of the SNP of SEQ ID NO: 213.

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Definitions

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

15 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.

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

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

20 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.

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
25 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.

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
30 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.

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
5 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
10 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.

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

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
20 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
25 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
30 genetic background is a background where the plants are isogenic except for one or more markers of the present invention.

As used herein, a “cultivar” is a race or variety of a plant that has been created or selected intentionally and maintained through cultivation.

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
5 parts of a plant.

Detailed Description of the Invention

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
10 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
15 present invention can further be utilized to determine whether a plant is suitable for one, two, or more maturity belts or regions.

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
20 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,
25 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,
30 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 seed of the present invention can be sent to a geographic region that is desirable to optimize a trait, such as yield.

5 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.

10 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 15 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, etc.

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 20 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.

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 25 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 nucleic acid molecule of the present invention. Nucleic acids include deoxynucleic acids (DNA) and ribonucleic acids (RNA) and functionally equivalent analogues thereof.

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.

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 20060042527A1. 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.

In an aspect, the maturity genomic region associated with plant maturity and plant growth habit of the present invention 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 of the present invention is selected from an elite *Glycine max* line.

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
5 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.

Methods of the present invention include determining if a locus contains a
10 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
15 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.

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,
20 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
25 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 30 cM either side of SEQ ID NO: 149 or SEQ ID NO: 151.

An aspect 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
5 can be recessive or dominant. In another preferred aspect, the maturity of the plant is delayed where the marker is homozygous dominant.

Another aspect 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
10 SEQ ID NO: 149 exists in the soybean seed.

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
15 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-
20 161. 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.

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
25 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
30 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.

5 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
10 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 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.

15 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, NS0113878, NS0101863, NS0115066, NS0123168, NS0119165, NS0123724, NS0103446, and NS0099024. SNP marker DNA sequences for region 5
20 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
25 side of SEQ ID NO: 187. An aspect 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.

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
30 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
5 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 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.

The state of homozygosity or heterozygosity and dominance or recessivity of
10 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
15 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 present invention includes a method of detecting maturity genomic region 7 by detecting an allele using a
20 marker selected from any of SEQ ID NO: 197-203.

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,
25 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
30 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 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.

Nucleic acid molecules of the present invention 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 of the present invention contain any of SEQ ID NO: 143-213, complements thereof and fragments of any. In another aspect, the nucleic acid molecules of the present invention include nucleic acid molecules that hybridize, 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). 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.

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 nucleic-acid probes and primers

of the present invention 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.

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.

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 nucleotide sequences of the present invention 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.

As used herein, an agent, be it a naturally occurring molecule or otherwise may be
5 “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
10 solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the present invention 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
15 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.

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

The agents of the present invention 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).
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In an aspect, an agent of the present invention 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 of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth
30

in SEQ ID NO: 143 through SEQ ID NO: 213 or complements or fragments of either under high stringency conditions.

Agents of the present invention 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.

Agents of the present invention include fragment nucleic acid molecules of the present invention. 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 of the present invention. 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.

In one aspect of the present invention, a preferred marker nucleic acid molecule of the present invention 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 of the present invention, a preferred marker nucleic acid molecule of the present invention 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 of the present invention, a preferred marker nucleic acid molecule of the present invention 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 of the present invention, a preferred marker nucleic acid molecule of the present invention 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.

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
5 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.

The present invention further provides one or more single nucleotide polymorphism
10 (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.

15 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 No. 50,424; European Patent No. 84,796; European Patent No. 258,017; European Patent No. 237,362; European Patent No. 201,184; U.S. Patent No. 4,683,202; U.S. Patent No. 4,582,788; and U.S. No. Patent 4,683,194), using primer pairs that are capable of
20 hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

Alleles that associate with plant maturity can be determined based on linkage analysis of plants and nucleic acid molecules of the present invention. A number of molecular genetic maps of *Glycine* have been reported (Mansur *et al.*, *Crop Sci.* 36: 1327-
25 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
30 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.

5 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
10 genomic region 8 is located on LG M.

 In an aspect, the present invention can be used to identify additional markers associated with maturity genomic regions 1-8. The present invention includes 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
15 molecules of the present invention 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
20 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
25 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 of the present invention can be used for the selection or introgression of the region associated with maturity and/or plant growth habit.

30 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 of the present invention, 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.

5 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
10 variety and IV.9 is a late group IV.

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
15 31st 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
20 maturity groups have corresponding maturity belts.

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.

25 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
30 and separately elucidate other traits, such as those associated with yield.

The present invention 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 alleles at a locus within maturity genomic region 1 are homozygous or heterozygous; 5 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 10 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.

In another aspect, the present invention 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; 15 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 20 the alleles within maturity genomic regions 1, 2, 3 and 4; and assigning a maturity group value to the soybean plant or soybean seed.

The present invention also includes 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.

25 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 30 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.

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
5 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
10 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
15 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.

An aspect of the present invention includes a method of establishing where a
20 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
25 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
30 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 - I.0 and the mid-maturity parent soybean plant is between III.0-IV.9

5 An aspect of the present invention 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
10 maturity genomic region 1, homozygous dominant within maturity genomic region 2 and is grown under the same environmental conditions.

Another aspect of the present invention 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
15 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
20 maturity genomic region 1 and heterozygous dominant at maturity genomic region 2 and has a maturity group between I.5 - II.9.

The present invention includes 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
25 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.

In an alternate aspect, if the maturity group of a plant is between III and V, the
30 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.

In another aspect, the maturity group of the parent plants is known. In an aspect,
5 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
10 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.

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
15 correlates with a delay in maturity.

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
20 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.

In an aspect, a progeny plant has a maturity group earlier than one parent by 5, 10, 25 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.

In an aspect, an early parent of maturity group 0.1 is crossed with a later maturity
30 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.

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 F₁, F₂, F₃, F₄ 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).

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.

In another aspect of the present invention, 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.

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 of the present invention 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.

Another aspect of the present invention includes a method 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.

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.

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.

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.

5 One aspect of the present invention 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
10 maturity growth value to the soybean plant; and shipping the soybean plant to a preferred geographic region.

 A plant of the invention 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
15 Nos. 7,154,021.

 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
20 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.

 In another aspect, a transgene may be employed that alters plant carbohydrate
25 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
30 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

5 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

10 gene encoding the LEAFY protein in its genome.

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

15 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, $\Delta 9$, 12) is produced from oleic acid (18:1, $\Delta 9$) by a $\Delta 12$ -desaturase (encoded by FAD2) while alpha linolenic acid (ALA) (18:3, $\Delta 9$, 12, 15) is produced from LA by a $\Delta 15$ -desaturase (encoded by FAD3). Moreover, stearidonic acid (SDA) (18:4, $\Delta 6$, 9, 12, 15) and gamma

20 linolenic acid (GLA) (18:3, $\Delta 6$, 9, 12) are polyunsaturated fatty acids (PUFAs) produced from LA and ALA by a $\Delta 6$ -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* $\Delta 15$ -desaturase of the '544 patent

25 resulted in accumulation of ALA. U.S. Pat. Publication 20060156435 describes the expression of fungal $\Delta 15$ -desaturases to increase omega-3 fatty acid profiles in plants. PCT Publication WO05/021761 discusses genetically engineered plants which produce both SDA and GLA as a result of expressing a $\Delta 6$ -desaturase and a $\Delta 15$ -desaturase. Long chain PUFAs such as EPA and

30 DHA can be produced in plants as disclosed in US Pat. Publication 20040172682.

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 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 20040006792 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.

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.

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

5 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
10 endo-1,4- β -glucanase.

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
15 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,
20 protoplasts, meristematic cells, pollen, leaves or anthers. In these ways, plants of the present invention or parts thereof 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 No. 4,992,375; U.S. Patent No. 5,015,580; U.S. Patent No. 5,024,944, and U.S. Patent No. 5,416,011. An
25 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,
30 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
 5 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
 10 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
 15 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,
 20 *Principles of Cultivar Development* Vol. 1, pp. 2-3 (1987)).

The present invention includes 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
 25 a soybean seed possessing a genotype for preferred maturity. The present invention also includes 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
 30 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
5 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 an aspect of the present invention, a method of soybean plant breeding includes crossing at least two different parent soybean plants; obtaining a progeny soybean plant
10 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
15 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
20 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.

25 In an aspect of the present invention, at least one or both parent soybean plant are an elite variety. In an aspect of the present invention, a progeny soybean plant is an exotic soybean plant or one or both parent soybean plants are exotic soybean plants.

An aspect of the present invention includes a method of selecting a soybean plant for germplasm improvement by determining a maturity group by crossing at least two
30 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
5 soybean plant or parts thereof for transformation, and use of soybean plants or parts thereof for mutagenesis.

Another aspect 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
10 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.

15 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,
20 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.

25 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.

30 In one aspect, plants of the present invention 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

5 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
10 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.*, F₁ hybrid cultivar, pureline cultivar, etc).

15 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 the present invention includes a method of soybean plant breeding by assaying a soybean plant for the presence of a marker sequences selected from the group
20 consisting of SEQ ID NO: 143 through SEQ ID NO: 213; and associating the soybean plant with a maturity group.

In another aspect the present invention includes 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
25 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
30 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.

An aspect of the present invention includes a method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants
5 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.

Another aspect of the present invention includes a method of screening soybean
10 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 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 seed.

15 One aspect of the present invention 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
20 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 of the present invention includes a method of introducing a desired
25 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
30 group. In a preferred aspect, the desired trait is transgenic.

A further aspect of the present invention 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
5 with the allele and a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-174.

Another aspect of the present invention 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
10 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 of the present invention 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
15 markers from SEQ ID NO: 143-213 or of the markers 143-162.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless expressly
20 specified.

Examples

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

Soybean is a short day plant, therefore flowering is initiated by short days due to a
25 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
30 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.

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 (Δd)	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
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
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Table 2: Estimated effect in days of maturity genomic regions

Region	Marker	SEQ ID NO:	Est. effect on plant maturity (Δ d)	Effect (Δ d)	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
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

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, where "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
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
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

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
5 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	TTCGAAGATT	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
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

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
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
5	NS0123724	189	93	94	306	G	307	A

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
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

SEQ ID				
Region	Marker	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
7	NS0102630	202	C	A
8	NS0102362	204	C	T

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.

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.

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.

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.

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.

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.

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.

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

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

The three populations segregate widely for maturity and are polymorphic at genomic regions 1 and 2. F₃ seed are obtained by selecting one pod per F₂ plant (modified single seed descent). The F₃ populations are planted in Guelph, ON and 1,214 F₃ 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 F₃ 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	Days to Maturity (D after August 31 st)			
	Region 1	Region 2	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

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 F₃ 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.

The three segregate widely for maturity and are polymorphic at genomic regions 1, 2, and 3. F₃ seed are obtained by selecting one seed per F₂ plant (single seed descent). 5,984 F₃ 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. F₃ 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
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

5

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

5

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

Plant growth habit is an important characteristic for late maturity group growing regions. To identify genomic regions associated with plant growth habit, three F₃ 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. F₃ seed are obtained by selecting one seed per F₂ plant (single seed descent). 5,984 F₃ individuals from all three population were phenotyped with the SNP NS0115535 (genomic region 3) and seeds with the same marker haplotype are bulked. F₃ 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.

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

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.

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 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

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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		42.78	12.00	
Non-Check				
Mean		42.60	12.38	
Check Mean		44.08	9.25	
# Locs		3	2	
# Reps		3	2	
CV		9.978	15.094	

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	
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)	Maturit y (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

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.

A BC₂F₁ 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 BC₂F₁ plants are screened with 106 SNP markers to evaluate the genetic similarity to the recurrent MG
5 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
10 based on adaptation to specific maturity group regions using the allelic combination for the genomic maturity regions.

5

Table 13: Summary of heterozygosity 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			
Progeny:0093	79.7	x			x	

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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	
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	

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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			
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

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

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

10 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.

20 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

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
5 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
10 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,
15 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

20 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
25 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
30 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

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.

10 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.

15 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, 20 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

Fatty Acid	Latitude			Longitude		
	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

*significant at 0.05 level

5 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

10 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.

It is within the scope of this invention to utilize the methods and compositions for preferred trait integration for any trait, conventional or transgenic, affected or

15 influenced by latitude. It is contemplated by the inventors that the present invention will be useful for trait integration of one or more phenotypic traits that are influenced by latitude such that the methods and compositions provided herein will facilitate deployment of one or more traits into preferred germplasm based on maturity,

20 wherein the traits can be conventional or transgenic.

Having illustrated and described the principles of the present invention, it should be apparent to persons skilled in the art that the invention can be modified in

arrangement and detail without departing from such principles. The scope of the claims should not be limited by the preferred embodiments set forth herein, but should be given the broadest interpretation consistent with the description as a whole.

The embodiments of the present invention for which an exclusive property or privilege is claimed are defined as follows:

1. A method of establishing where a soybean plant or soybean seed should be grown based on its maturity group by determining the allelic combination of said soybean plant or soybean seed comprising
 - a. obtaining DNA from said soybean plant or soybean seed;
 - b. determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous;
 - c. determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous;
 - d. determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous;
 - e. determining the allelic combination of said alleles within said maturity genomic regions 1, 2, and 3, wherein said maturity genomic regions are genomic regions associated with soybean plant maturity, said maturity genomic region 1 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:143-155, said maturity genomic region 2 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:156-161, and said maturity genomic region 3 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:162-174; and
 - f. assigning a maturity group value to said soybean plant or soybean seed based on said allelic combination.
2. The method of claim 1, wherein said determining if alleles at a locus are homozygous or heterozygous comprises detecting a polymorphism with a nucleic acid molecule comprising a sequence selected from the group consisting of SEQ ID NOs: 143-174, or complements thereof.
3. The method of claim 1 further comprising selecting multiple soybean seeds.

4. The method of claim 3, wherein said multiple soybean seeds grow into soybean plants having indeterminate soybean plant habit.
5. The method of claim 1, wherein said alleles at a locus within maturity genomic region 1 comprise a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-149 and 154-155.
6. A method of establishing where a soybean plant or soybean seed should be grown based on its maturity group by determining the allelic combination of said soybean plant comprising
 - a. obtaining DNA from said soybean plant or soybean seed;
 - b. determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous;
 - c. determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous;
 - d. determining the allelic combination of said alleles within said maturity genomic regions 1 and 2, wherein said maturity genomic regions are genomic regions associated with soybean plant maturity, said maturity genomic region 1 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:143-155, and said maturity genomic region 2 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:156-161; and
 - e. assigning a maturity group value to said soybean plant or soybean seed based on said allelic combination.
7. The method of claim 6, wherein said determining if alleles at a locus are homozygous or heterozygous comprises detecting a polymorphism selected from the group consisting of SEQ ID NOs: 143-161.
8. The method of claim 6, wherein said 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.

9. The method of claim 8, wherein said early maturity group parent soybean plant has a maturity group value between 00.0 - 1.0 and said mid maturity parent soybean plant has a maturity group value between III.0 - IV.9.
10. A method of soybean plant breeding comprising
 - a. assaying a soybean plant for the presence of a marker sequence selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213; and
 - b. associating said soybean plant with a maturity group.
11. A method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent soybean plant, wherein said parent soybean plants differ in soybean plant maturity by over 10 days, comprising
 - a. crossing a parent soybean plant comprising a desired trait with a second parent soybean plant;
 - b. obtaining a progeny soybean seed from said cross;
 - c. screening a progeny soybean seed for said trait;
 - d. 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
 - e. selecting a progeny soybean seed containing said desired trait and desired soybean plant maturity.
12. The method of claim 11, where said desired trait is transgenic.
13. A method of soybean plant breeding comprising
 - a. crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 10 days;
 - b. obtaining a progeny soybean seed from said cross;

- c. genotyping a progeny soybean seed of said cross with a genetic marker, wherein said genetic marker is from a maturity genomic region selected from the group consisting of maturity genomic regions 1 to 8, said maturity genomic regions are genomic regions associated with soybean plant maturity, said maturity genomic region 1 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:143-155, said maturity genomic region 2 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:156-161, said maturity genomic region 3 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:162-174, said maturity genomic region 4 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:175-180, said maturity genomic region 5 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:181-189, said maturity genomic region 6 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:190-196, said maturity genomic region 7 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:197-203, and said maturity genomic region 8 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:204-213; and
- d. selecting a soybean seed possessing a genotype for preferred maturity.

14. A method to select a soybean seed based on indeterminate or determinate growth habit comprising determining if a molecular marker from maturity genomic region 3 is homozygous or heterozygous, wherein said maturity genomic region 3 is a genomic region associated with soybean plant maturity, and identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:162-174.

15. The method of claim 14, wherein said maturity genomic region 3 is characterized by a G at position 433 in marker SEQ ID NO: 169.

16. A method of distributing a soybean plant based on maturity group comprising

- a. obtaining DNA from a soybean plant;

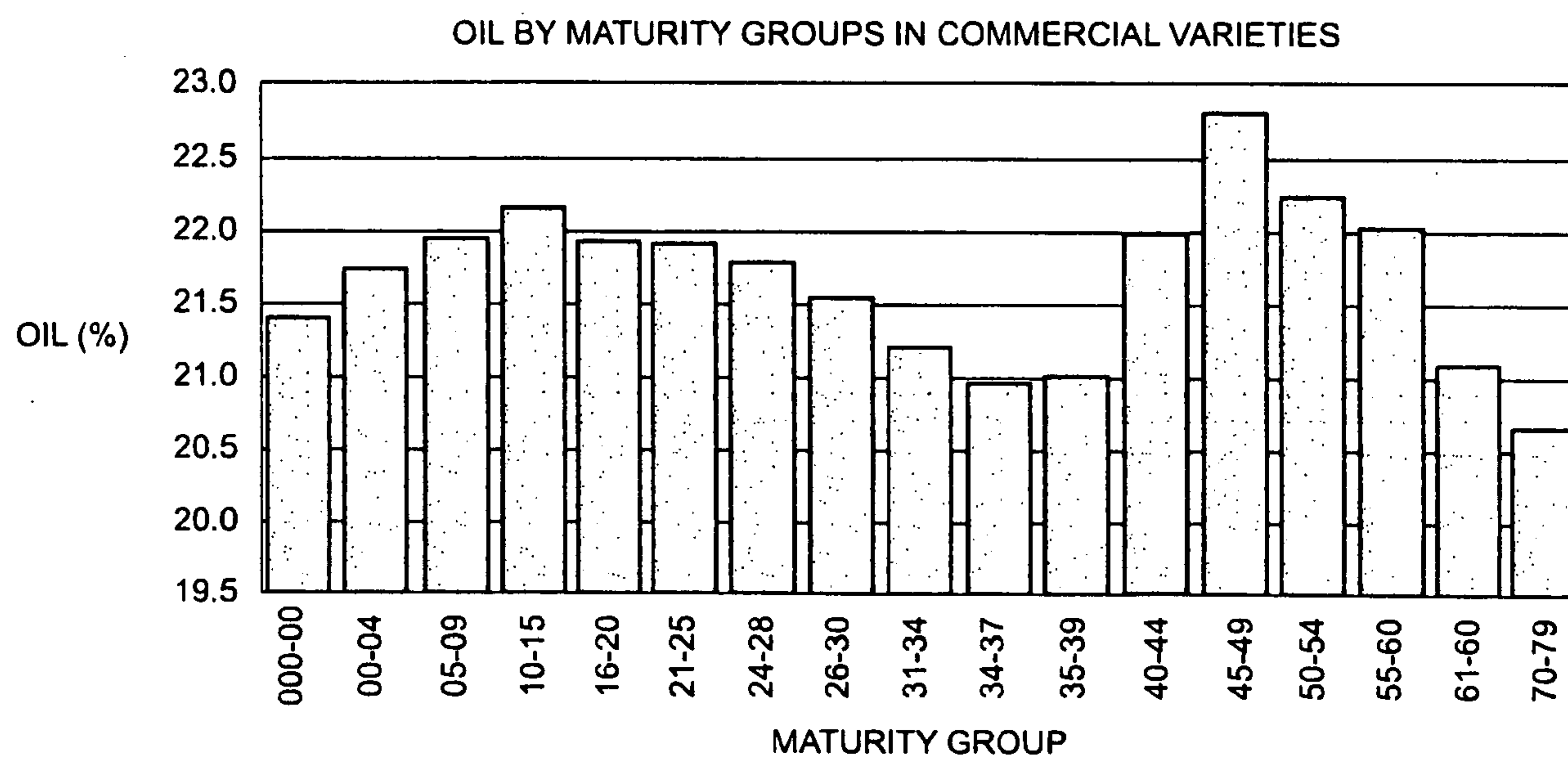
- b. determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous;
 - c. determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous;
 - d. determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous, wherein said maturity genomic regions are genomic regions associated with soybean plant maturity, said maturity genomic region 1 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:143-155, said maturity genomic region 2 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:156-161, and said maturity genomic region 3 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:162-174; and
 - e. assigning a maturity group value to said soybean plant based on results of said determination steps; and
 - f. shipping said soybean plant to a preferred geographic region.
17. A method to isolate an indeterminate-early maturity soybean seed comprising
- a. obtaining DNA from a soybean seed using a non-destructive method;
 - b. determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous;
 - c. determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous, wherein said maturity genomic regions are genomic regions associated with soybean plant maturity, said maturity genomic region 1 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:143-155, and said maturity genomic region 2 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:156-161; and
 - d. selecting said soybean seed based on results of said determination steps.
18. A method to determine if a soybean plant has a maturity group of 0.0- III.9 comprising
- a. obtaining DNA from said soybean seed using a non-destructive method;

- b. determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous;
 - c. determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous, wherein said maturity genomic regions are genomic regions associated with soybean plant maturity, said maturity genomic region 1 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:143-155, and said maturity genomic region 2 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:156-161; and
 - d. assigning a maturity group value for said soybean plant.
19. The method of claim 18, wherein maturity in said 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.
20. A method to determine if the maturity of a soybean plant is in a 00.0 - III.0 maturity group comprising
- a. determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous;
 - b. determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous, wherein said maturity genomic regions are genomic regions associated with soybean plant maturity, said maturity genomic region 1 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:143-155, and said maturity genomic region 2 is identifiable by a SNP marker selected from the group consisting of SEQ ID NOs:156-161; and
 - c. assigning a maturity group value for said soybean plant.
21. The method of 20, further comprising selecting a soybean seed that is homozygous recessive at maturity genomic region 1 and homozygous recessive at maturity genomic region 2 and has a maturity group value between 0.5 - II.0.

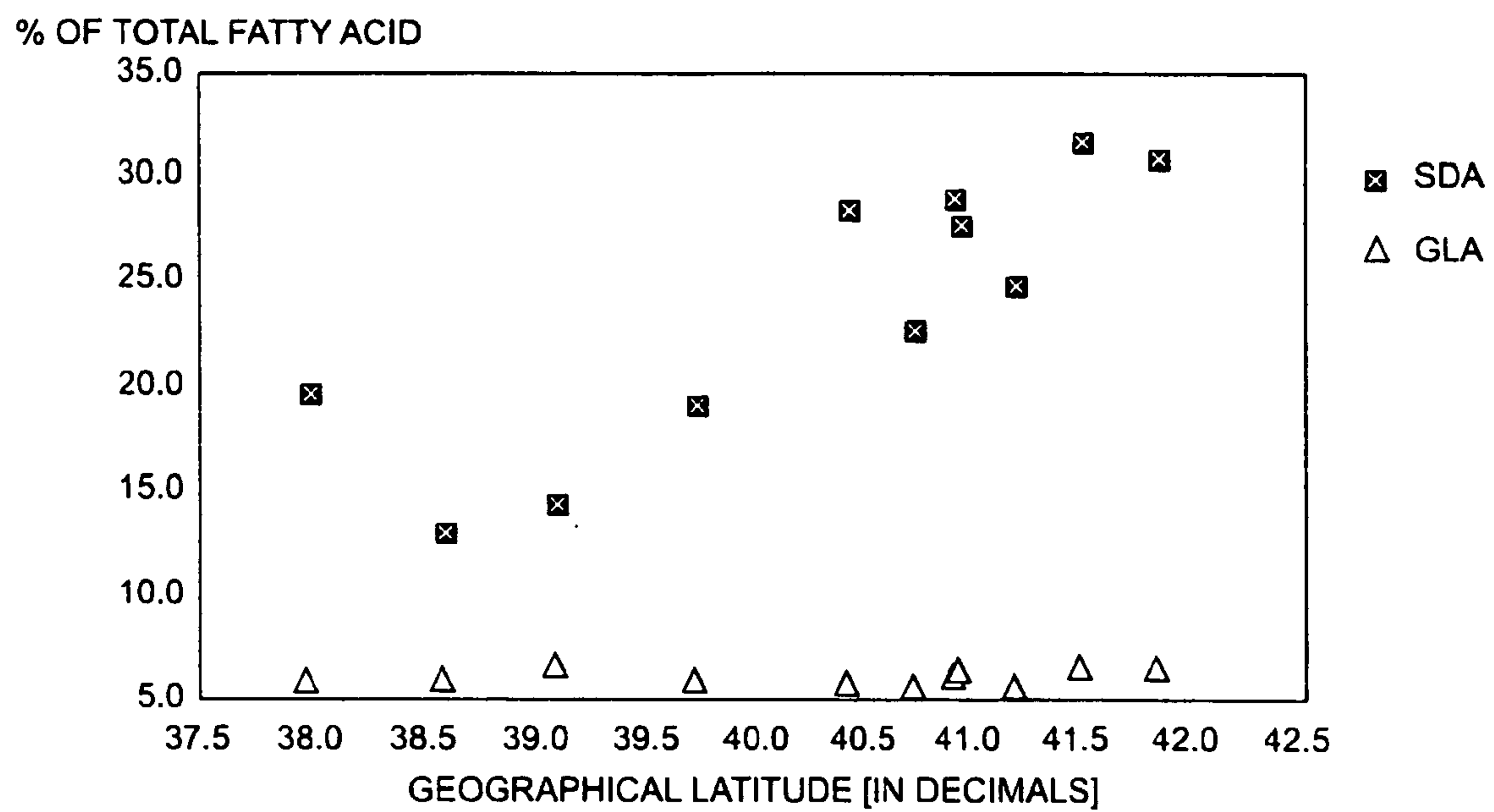
22. The method of 20, further comprising selecting a soybean seed that is homozygous recessive at maturity genomic region 1 and heterozygous dominant at maturity genomic region 2 and has a maturity group value between I.5 - II.9.
23. A method of screening and selecting a soybean plant or soybean seed 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 and comprises a sequence or fragment thereof selected from the group consisting of SEQ ID NOs:143-174, or complements thereof;
 - b. determining whether said genomic maturity marker is homozygous or heterozygous;
 - c. and selecting said soybean plant or seed based on said determination.
24. The method of claim 23, wherein parents of said soybean plant or seed differ in soybean plant maturity by over 10 days.
25. 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 two or more genomic maturity markers, each of which is from a maturity genomic region selected from the group consisting of maturity genomic regions 1 to 8, said genomic maturity marker is within 10 cM of any of SEQ ID NOs: 143-213;
 - b. determining whether said genomic maturity markers are homozygous or heterozygous; and
 - c. selecting said soybean plant or seed based on said determination.
26. The method of claim 25, wherein said genomic maturity marker is within 5 cM of any of SEQ ID NOs: 143-213.
27. The method of claim 25, wherein said genomic maturity marker is within 1 cM of any of SEQ ID NOs: 143-213.

28. The method of claim 25, wherein said genomic maturity marker is within 1,000 kilobases of any of SEQ ID NOs: 143-213.
29. The method of claim 25, wherein said genomic maturity marker is within 500 kilobases of any of SEQ ID NOs: 143-213.
30. The method of claim 25, wherein said genomic maturity marker is within 100 kilobases of any of SEQ ID NOs: 143-213.
31. The method of claim 25, wherein said genomic maturity marker is within 30 kilobases of any of SEQ ID NOs: 143-213.
32. The method of claim 25, wherein said genomic maturity marker is within 20 kilobases of any of SEQ ID NOs: 143-213.
33. The method of claim 25, wherein said genomic maturity marker is within 10 kilobases of any of SEQ ID NOs: 143-213.
34. The method of claim 25, wherein said genomic maturity marker is within 5 kilobases of any of SEQ ID NOs: 143-213.
35. The method of claim 25, wherein said genomic maturity marker is selected from the group consisting of SEQ ID NOs: 143-213.

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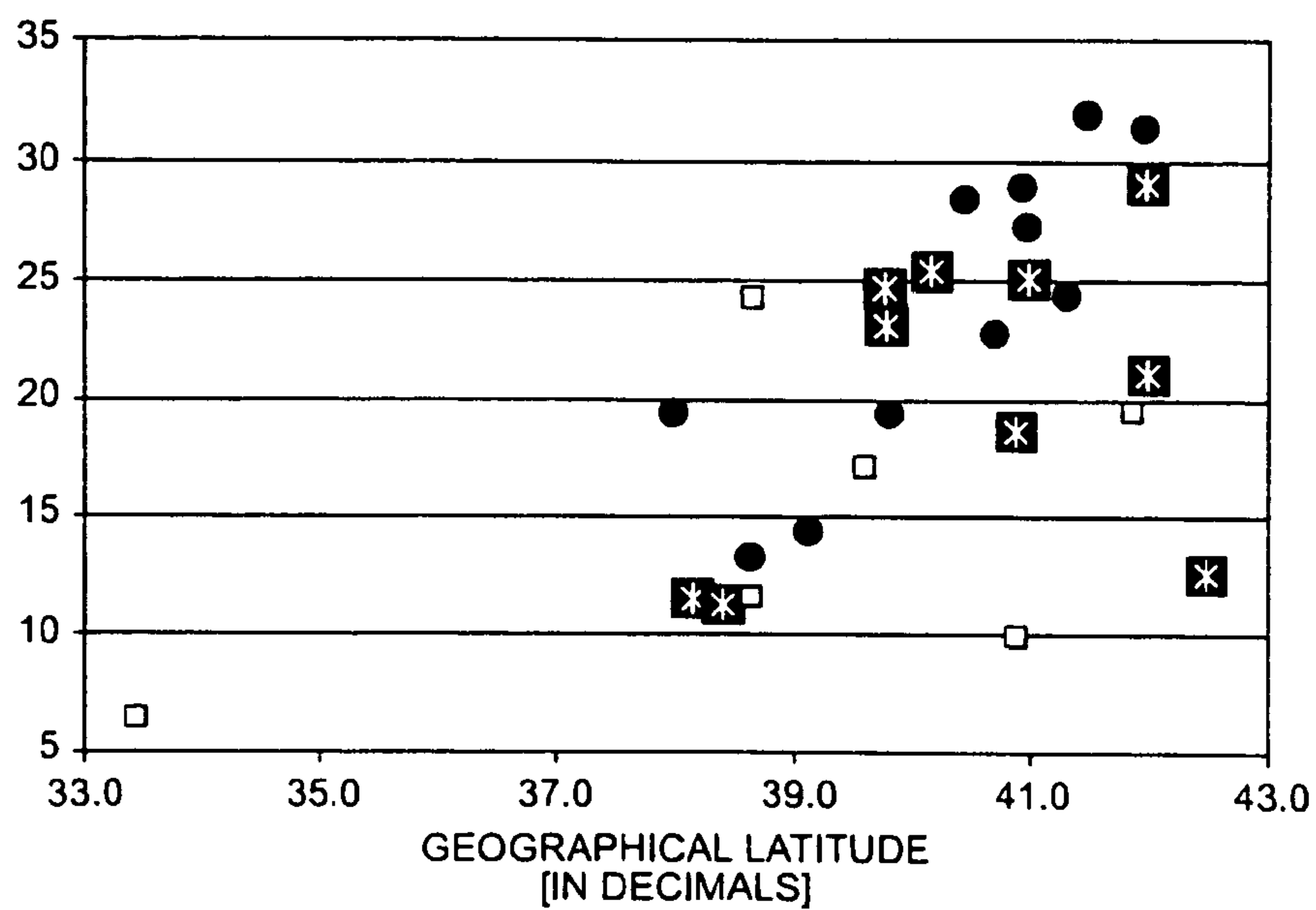
**FIG. 1**

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**FIG. 2**

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% OF TOTAL FATTY ACIDS

**FIG. 3**

% OF TOTAL FATTY ACIDS

