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(54) **INBRED MAIZE LINE PHE2E**

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(58) **Field of Classification Search** ..... None
See application file for complete search history.

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(57) **ABSTRACT**

A novel inbred maize variety designated PHE2E and seed, plants and plant parts thereof. Methods for producing a maize plant that comprise crossing inbred maize variety PHE2E with another maize plant. Methods for producing a maize plant containing in its genetic material one or more traits introgressed into PHE2E through backcross conversion and/or transformation, and to the maize seed, plant and plant part produced thereby. Hybrid maize seed, plant or plant part produced by crossing the inbred variety PHE2E or a trait conversion of PHE2E with another maize variety. Inbred maize varieties derived from inbred maize variety PHE2E, methods for producing other inbred maize varieties derived from inbred maize variety PHE2E and the inbred maize varieties and their parts derived by the use of those methods.

21 Claims, No Drawings

Inari Exhibit 1066
Inari v. Pioneer

INBRED MAIZE LINE PHE2E

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. §119(e) to provisional application Ser. No. 60/870,134 filed Dec. 15, 2006, herein incorporated by refernece in its entirety.

FIELD OF THE INVENTION

This invention relates generally to the field of maize breeding, specifically relating to an inbred maize variety designated PHE2E.

BACKGROUND OF THE INVENTION

The goal of plant breeding is to combine, in a single variety or hybrid, various desirable traits. For field crops, these traits may include resistance to diseases and insects, resistance to heat and drought, reducing the time to crop maturity, greater yield, and better agronomic quality. With mechanical harvesting of many crops, uniformity of plant characteristics such as germination, stand establishment, growth rate, maturity, plant height and ear height, is important. Traditional plant breeding is an important tool in developing new and improved commercial crops.

SUMMARY OF THE INVENTION

According to the invention, there is provided a novel inbred maize variety, designated PHE2E and processes for making PHE2E. This invention relates to seed of inbred maize variety PHE2E, to the plants of inbred maize variety PHE2E, to plant parts of inbred maize variety PHE2E, and to processes for making a maize plant that comprise crossing inbred maize variety PHE2E with another maize plant. This invention also relates to processes for making a maize plant containing in its genetic material one or more traits introgressed into PHE2E through backcross conversion and/or transformation, and to the maize seed, plant and plant part produced by such introgression. This invention further relates to a hybrid maize seed, plant or plant part produced by crossing the inbred variety PHE2E or an introgressed trait conversion of PHE2E with another maize variety. This invention also relates to inbred maize varieties derived from inbred maize variety PHE2E to processes for making other inbred maize varieties derived from inbred maize variety PHE2E and to the inbred maize varieties and their parts derived by the use of those processes.

DEFINITIONS

Inbred Definitions

Certain definitions used in the specification are provided below. Also in the examples that follow, a number of terms are used herein. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided. NOTE: ABS is in absolute terms and % MN is percent of the mean for the experiments in which the inbred or hybrid was grown. PCT designates that the trait is calculated as a percentage. % NOT designates the percentage of plants that did not exhibit a trait. For example, STKLDG % NOT is the percentage of plants in a plot that were not stalk lodged. These designators will follow the descriptors to denote how the values are to be interpreted. Below are the descriptors used in the data tables included herein.

ABIOTIC STRESS TOLERANCE: resistance to non-biological sources of stress conferred by traits such as nitrogen utilization efficiency, altered nitrogen responsiveness, drought resistance cold, and salt resistance

ABTSTK=ARTIFICIAL BRITTLE STALK. A count of the number of "snapped" plants per plot following machine snapping. A snapped plant has its stalk completely snapped at a node between the base of the plant and the node above the ear. Expressed as percent of plants that did not snap.

ALEURONE: A thin layer of cells just beneath the pericarp of the seed.

ALLELE. Any of one or more alternative forms of a genetic sequence. In a diploid cell or organism, the two alleles of a given sequence typically occupy corresponding loci on a pair of homologous chromosomes.

ALTER. The utilization of up-regulation, down-regulation, or gene silencing.

ANTHESIS. The time of a flower's opening.

ANTHOCYANIN OF BRACE ROOTS: The degree of red coloration of the brace roots after exposure to sunlight taken at flowering. Brace root anthocyanin is scored 1-5 where 1=no red color, 2=pink, 3=red, 4=dark red, and 5=purple.

ANTIOXIDANT. A chemical compound or substance that inhibits oxidation, including but not limited to tocopherol or tocotrienols.

ANT ROT=ANTHRACNOSE STALK ROT (*Colletotrichum graminicola*). A 1 to 9 visual rating indicating the resistance to Anthracnose Stalk Rot. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

BACKCROSSING. Process in which a breeder crosses a hybrid progeny variety back to one of the parental genotypes one or more times.

BACKCROSS PROGENY. Progeny plants produced by crossing PHF3P plant parts with plant parts of another maize line that comprise a desired trait or locus, selecting F1 progeny plants that comprise the desired trait or locus, and crossing the selected F1 progeny plants with the PHF3P plants 1 or more times to produce backcross progeny plants that comprise said trait or locus.

BAR GLUMES: (glume band) The presence or absence of horizontal lines at the base of the glumes on tassel florets.

BARPLT=BARREN PLANTS. The percent of plants per plot that were not barren (lack ears).

BORBMN=ARTIFICIAL BRITTLE STALK MEAN. The mean percent of plants not "snapped" in a plot following artificial selection pressure. A snapped plant has its stalk completely snapped at a node between the base of the plant and the node above the ear. Expressed as percent of plants that did not snap. A high number is good and indicates tolerance to brittle snapping.

BRANCH ANGLE FROM CENTRAL SPIKE: The adaxial angle measured in degrees with a protractor on the top primary lateral tassel branch at flowering.

BRENGMN=BRITTLE STALK ENERGY MEAN. The mean amount of energy per unit area needed to artificially brittle snap a corn stalk. A high number is good and indicates tolerance to brittle snapping.

BREEDING. The genetic manipulation of living organisms.

BREEDING CROSS. A cross to introduce new genetic material into a plant for the development of a new variety. For example, one could cross plant A with plant B, wherein plant B would be genetically different from plant A. After the breeding cross, the resulting F1 plants could then be selfed or

sibbed for one, two, three or more times (F1, F2, F3, etc.) until a new inbred variety is developed. For clarification, such new inbred varieties would be within a pedigree distance of one breeding cross of plants A and B. The process described above would be referred to as one breeding cycle.

BRLPNE. Percent plants not root lodged following artificial selection pressure, preflowering. A high number is good and indicates tolerance to preflowering root lodging.

BRLPNL. Percent plants not root lodged following artificial selection pressure, during grain filling period. A high number is good and indicates tolerance to late season root lodging.

BRTSTK=BRITTLE STALKS. This is a measure of the stalk breakage near the time of pollination, and is an indication of whether a hybrid or inbred would snap or break near the time of flowering under severe winds. Data are presented as percentage of plants that did not snap. Data are collected only when sufficient selection pressure exists in the experiment measured.

CARBOHYDRATE. Organic compounds comprising carbon, oxygen and hydrogen, including sugars, starches and cellulose.

CELL. Cell as used herein includes a plant cell, whether isolated, in tissue culture or incorporated in a plant or plant part.

CLDTST=COLD TEST. The percent of plants that germinate under cold test conditions.

CLN=CORN LETHAL NECROSIS. Synergistic interaction of maize chlorotic mottle virus (MCMV) in combination with either maize dwarf mosaic virus (MDMV-A or MDMV-B) or wheat streak mosaic virus (WSMV). A 1 to 9 visual rating indicating the resistance to Corn Lethal Necrosis. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

COMRST=COMMON RUST (*Puccinia sorghi*). A 1 to 9 visual rating indicating the resistance to Common Rust. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

COMMON SMUT (*Ustilago maydis*): A 1 to 9 visual rating indicating the resistance to Common Smut. A higher score indicates a higher resistance. Data is collected only when sufficient selection pressure exists in the experiment measured.

CROSS POLLINATION. A plant is cross pollinated if the pollen comes from a flower on a different plant from a different family or variety. Cross pollination excludes sib and self pollination.

CROSSING. The combination of genetic material by traditional methods such as a breeding cross or backcross, but also including protoplast fusion and other molecular biology methods of combining genetic material from two source

D/D=DRYDOWN. This represents the relative rate at which a hybrid will reach acceptable harvest moisture compared to other hybrids on a 1 to 9 rating scale. A high score indicates a hybrid that dries relatively fast while a low score indicates a hybrid that dries slowly.

DIPERS=*DIPLODIA* EAR MOLD SCORES (*Diplodia maydis* and *Diplodia macrospora*). A 1 to 9 visual rating indicating the resistance to *Diplodia* Ear Mold. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

DIPLOID PLANT PART. Refers to a plant part or cell that has the same diploid genotype as PHF3P.

DIPROT=*DIPLODIA* STALK ROT SCORE. Score of stalk rot severity due to *Diplodia* (*Diplodia maydis*). Expressed as a 1 to 9 score with 9 being highly resistant. Data are collected only when sufficient selection pressure exists in the experiment measured.

DRPEAR=DROPPED EARS. A measure of the number of dropped ears per plot and represents the percentage of plants that did not drop ears prior to harvest. Data are collected only when sufficient selection pressure exists in the experiment measured.

D/T=DROUGHT TOLERANCE. This represents a 1 to 9 rating for drought tolerance, and is based on data obtained under stress conditions. A high score indicates good drought tolerance and a low score indicates poor drought tolerance. Data are collected only when sufficient selection pressure exists in the experiment measured.

EARHT=EAR HEIGHT. The ear height is a measure from the ground to the highest placed developed ear node attachment and is measured in centimeters.

EARMLD=GENERAL EAR MOLD. Visual rating (1 to 9 score) where a 1 is very susceptible and a 9 is very resistant. This is based on overall rating for ear mold of mature ears without determining the specific mold organism, and may not be predictive for a specific ear mold. Data are collected only when sufficient selection pressure exists in the experiment measured.

EAR NODE: The node on the main stem that bears the top or primary ear.

EAR POSITION: The orientation of the primary ear 65 days after 50% silk. Ear position is scored as 1=upright, 2=horizontal, and 3=pendant (downward or drooping).

EAR SHANK LENGTH: The measurement of the structure from the butt of the primary ear to the ear node on the main stem.

EARSZ=EAR SIZE. A 1 to 9 visual rating of ear size. The higher the rating the larger the ear size.

EBTSTK=EARLY BRITTLE STALK. A count of the number of "snapped" plants per plot following severe winds when the corn plant is experiencing very rapid vegetative growth in the V5-V8 stage. Expressed as percent of plants that did not snap. Data are collected only when sufficient selection pressure exists in the experiment measured.

ECB1LF=EUROPEAN CORN BORER FIRST GENERATION LEAF FEEDING (*Ostrinia nubilalis*). A 1 to 9 visual rating indicating the resistance to preflowering leaf feeding by first generation European Corn Borer. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

ECB2IT=EUROPEAN CORN BORER SECOND GENERATION INCHES OF TUNNELING (*Ostrinia nubilalis*). Average inches of tunneling per plant in the stalk. Data are collected only when sufficient selection pressure exists in the experiment measured.

ECB2SC=EUROPEAN CORN BORER SECOND GENERATION (*Ostrinia nubilalis*). A 1 to 9 visual rating indicating post flowering degree of stalk breakage and other evidence of feeding by second generation European Corn Borer. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

ECBDPE=EUROPEAN CORN BORER DROPPED EARS (*Ostrinia nubilalis*). Dropped ears due to European Corn Borer. Percentage of plants that did not drop ears under second generation European Corn Borer infestation. Data are collected only when sufficient selection pressure exists in the experiment measured.

ECBLSI=EUROPEAN CORN BORER LATE SEASON INTACT (*Ostrinia nubilalis*). A 1 to 9 visual rating indicating late season intactness of the corn plant given damage (stalk breakage above and below the top ear) caused primarily by 2nd and/or 3rd generation ECB larval feeding before harvest. A higher score is good and indicates more intact plants. Data are collected only when sufficient selection pressure exists in the experiment measured.

EGRWTH=EARLY GROWTH. This is a measure of the relative height and size of a corn seedling at the 2-4 leaf stage of growth. This is a visual rating (1 to 9), with 1 being weak or slow growth, 5 being average growth and 9 being strong growth. Taller plants, wider leaves, more green mass and darker color constitute higher score. Data are collected only when sufficient selection pressure exists in the experiment measured.

ELITE INBRED. An inbred that contributed desirable qualities when used to produce commercial hybrids. An elite inbred may also be used in further breeding for the purpose of developing further improved varieties.

ENDOSPERM: The nutritive tissue (starch) within the seed that surrounds the embryo.

ERTLDG=EARLY ROOT LODGING. The percentage of plants that do not root lodge prior to or around anthesis; plants that lean from the vertical axis at an approximately 30 degree angle or greater would be counted as root lodged. Data are collected only when sufficient selection pressure exists in the experiment measured.

ERTLPN=EARLY ROOT LODGING. An estimate of the percentage of plants that do not root lodge prior to or around anthesis; plants that lean from the vertical axis at an approximately 30 degree angle or greater would be considered as root lodged. Data are collected only when sufficient selection pressure exists in the experiment measured.

ERTLSC=EARLY ROOT LODGING SCORE. Score for severity of plants that lean from a vertical axis at an approximate 30 degree angle or greater which typically results from strong winds prior to or around flowering recorded within 2 weeks of a wind event. Expressed as a 1 to 9 score with 9 being no lodging. Data are collected only when sufficient selection pressure exists in the experiment measured.

ESSENTIAL AMINO ACIDS. Amino acids that cannot be synthesized de novo by an organism and therefore must be supplied in the diet.

ESTCNT=EARLY STAND COUNT. This is a measure of the stand establishment in the spring and represents the number of plants that emerge on per plot basis for the inbred or hybrid.

EYESPT=EYE SPOT (*Kabatiella zeae* or *Aureobasidium zeae*). A 1 to 9 visual rating indicating the resistance to Eye Spot. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

EXPRESSING. Having the genetic potential such that under the right conditions, the phenotypic trait is present.

FATTY ACID. A carboxylic acid (or organic acid), often with a long aliphatic tail (long chains), either saturated or unsaturated.

F1 PROGENY. Progeny plants produced by crossing plant parts of maize variety PHF3P with plant parts of another maize line.

FUSERS=*FUSARIUM* EAR ROT SCORE (*Fusarium moniliforme* or *Fusarium subglutinans*). A 1 to 9 visual rating indicating the resistance to *Fusarium* Ear Rot. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

GDU=GROWING DEGREE UNITS. Using the Barger Heat Unit Theory, which assumes that maize growth occurs in the temperature range 50 degrees F.-86 degrees F. and that temperatures outside this range slow down growth; the maximum daily heat unit accumulation is 36 and the minimum daily heat unit accumulation is 0. The seasonal accumulation of GDU is a major factor in determining maturity zones.

GDUSHD=GDU TO SHED. The number of growing degree units (GDUs) or heat units required for an inbred variety or hybrid to have approximately 50 percent of the plants shedding pollen and is measured from the time of planting. Growing degree units are calculated by the Barger Method, where the heat units for a 24-hour period are:

$$GDU = \frac{(\text{Max. temp.} + \text{Min. temp.})}{2} - 50$$

The highest maximum temperature used is 86 degrees F. and the lowest minimum temperature used is 50 degrees F. For each inbred or hybrid it takes a certain number of GDUs to reach various stages of plant development.

GDUSLK=GDU TO SILK. The number of growing degree units required for an inbred variety or hybrid to have approximately 50 percent of the plants with silk emergence from time of planting. Growing degree units are calculated by the Barger Method as given in GDU SHD definition.

GENE SILENCING. The interruption or suppression of the expression of a gene at the level of transcription or translation.

GENOTYPE. Refers to the genetic constitution of a cell or organism.

GIBERS=*GIBBERELLA* EAR ROT (PINK MOLD) (*Gibberella zeae*). A 1 to 9 visual rating indicating the resistance to *Gibberella* Ear Rot. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

GIBROT=*GIBBERELLA* STALK ROT SCORE. Score of stalk rot severity due to *Gibberella* (*Gibberella zeae*). Expressed as a 1 to 9 score with 9 being highly resistant. Data are collected only when sufficient selection pressure exists in the experiment measured.

GLFSPT=GRAY LEAF SPOT (*Cercospora zeae-maydis*). A 1 to 9 visual rating indicating the resistance to Gray Leaf Spot. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

GOSWLT=GOSS' WILT (*Corynebacterium nebraskense*). A 1 to 9 visual rating indicating the resistance to Goss' Wilt. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

GRNAPP=GRAIN APPEARANCE. This is a 1 to 9 rating for the general appearance of the shelled grain as it is harvested based on such factors as the color of harvested grain, any mold on the grain, and any cracked grain. High scores indicate good grain visual quality.

HAPLOID PLANT PART. Refers to a plant part or cell that has the same haploid genotype as PHF3P.

HCBLT=*HELMINTHOSPORIUM CARBONUM* LEAF BLIGHT (*Helminthosporium carbonum*). A 1 to 9 visual rating indicating the resistance to *Helminthosporium* infection. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

HD SMT=HEAD SMUT (*Sphacelotheca reiliana*). This score indicates the percentage of plants not infected. Data are collected only when sufficient selection pressure exists in the experiment measured.

HSKCVR=HUSK COVER. A 1 to 9 score based on performance relative to key checks, with a score of 1 indicating very short husks, tip of ear and kernels showing; 5 is intermediate coverage of the ear under most conditions, sometimes with thin husk; and a 9 has husks extending and closed beyond the tip of the ear. Scoring can best be done near physiological maturity stage or any time during dry down until harvested.

HUSK EXTENSION: The distance the husk extends past the end of the primary ear at harvest.

HUSK TIGHTNESS: The tightness of the husk 65 days after 50% silking on a scale from 1 (very loose) to 9 (very tight).

INBRED. A variety developed through inbreeding or doubled haploidy that preferably comprises homozygous alleles at about 95% or more of its loci.

INC D/A=GROSS INCOME (DOLLARS PER ACRE). Relative income per acre assuming drying costs of two cents per point above 15.5 percent harvest moisture and current market price per bushel.

INCOME/ACRE. Income advantage of hybrid to be patented over other hybrid on per acre basis.

INC ADV=GROSS INCOME ADVANTAGE. Gross income advantage of variety #1 over variety #2.

INTERNODE: The structure between two nodes on the main stem.

INTROGRESSION. The process of transferring genetic material from one genotype to another.

KERUNT=KERNELS PER UNIT AREA (Acres or Hectares).

KERPOP=KERNEL POP SCORE. The visual 1-9 rating of the amount of rupturing of the kernel pericarp at an early stage in grain fill. A higher score is good and indicates no popped (ruptured) kernels.

KER_WT=KERNEL NUMBER PER UNIT WEIGHT (Pounds or Kilograms). The number of kernels in a specific measured weight; determined after removal of extremely small and large kernels.

KSZDCD=KERNEL SIZE DISCARD. The percent of discard seed; calculated as the sum of discarded tip kernels and extra large kernels.

LEAF ANGLE: The adaxial angle measured in degrees with a protractor on the second leaf above the top ear at flowering.

LEAF SHEATH PUBESCENCE: The density of pubescence on the face of the leaf sheath at flowering. Leaf Sheath Pubescence is scored on a 1-9 scale where 1=no pubescence (smooth) and 9=high level of pubescence (like peach fuzz).

LINKAGE. Refers to a phenomenon wherein alleles on the same chromosome tend to segregate together more often than expected by chance if their transmission was independent.

LINKAGE DISEQUILIBRIUM. Refers to a phenomenon wherein alleles tend to remain together in linkage groups when segregating from parents to offspring, with a greater frequency than expected from their individual frequencies.

LOCUS. A specific location on a chromosome.

LOCUS CONVERSION. A locus conversion refers to plants within a variety that have been modified in a manner that retains the overall genetics of the variety and further comprises at least one locus with a specific desired trait, such as insect, disease or herbicide resistance.

L/POP=YIELD AT LOW DENSITY. Yield ability at relatively low plant densities on a 1 to 9 relative system with a higher number indicating the hybrid responds well to low plant densities for yield relative to other hybrids. A 1, 5, and 9 would represent very poor, average, and very good yield response, respectively, to low plant density.

LRTLDG=LATE ROOT LODGING. The percentage of plants that do not root lodge after anthesis through harvest; plants that lean from the vertical axis at an approximately 30 degree angle or greater would be counted as root lodged. Data are collected only when sufficient selection pressure exists in the experiment measured.

LRTLPN=LATE ROOT LODGING. An estimate of the percentage of plants that do not root lodge after anthesis through harvest; plants that lean from the vertical axis at an approximately 30 degree angle or greater would be considered as root lodged. Data are collected only when sufficient selection pressure exists in the experiment measured.

LRTLSC=LATE ROOT LODGING SCORE. Score for severity of plants that lean from a vertical axis at an approximate 30 degree angle or greater which typically results from strong winds after flowering. Recorded prior to harvest when a root-lodging event has occurred. This lodging results in plants that are leaned or "lodged" over at the base of the plant and do not straighten or "goose-neck" back to a vertical position. Expressed as a 1 to 9 score with 9 being no lodging. Data are collected only when sufficient selection pressure exists in the experiment measured.

MALE STERILITY. A male sterile plant is one which produces no viable pollen. Male sterility prevents self pollination and the pollination of neighboring plants. These male sterile plants are therefore useful in hybrid plant production.

MDMCPX=MAIZE DWARF MOSAIC COMPLEX (MDMV=Maize Dwarf Mosaic Virus and MCDV=Maize Chlorotic Dwarf Virus). A 1 to 9 visual rating indicating the resistance to Maize Dwarf Mosaic Complex. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

MST=HARVEST MOISTURE. The moisture is the actual percentage moisture of the grain at harvest.

MSTADV=MOISTURE ADVANTAGE. The moisture advantage of variety #1 over variety #2 as calculated by: MOISTURE of variety #2−MOISTURE of variety #1=MOISTURE ADVANTAGE of variety #1.

NEI DISTANCE. A quantitative measure of percent similarity between two varieties. Nei's distance between varieties A and B can be defined as 1-(2*number alleles in common/(number alleles in A+number alleles in B). For example, if varieties A and B are the same for 95 out of 100 alleles, the Nei distance would be 0.05. If varieties A and B are the same for 98 out of 100 alleles, the Nei distance would be 0.02. Free software for calculating Nei distance is available on the internet at multiple locations such as, for example, at: evolution.genetics.washington.edu/phylip.html. See Nei, Proc Natl Acad Sci, 76:5269-5273 (1979) which is incorporated by reference for this purpose.

NLFBLT=NORTHERN LEAF BLIGHT (*Helminthosporium turcicum* or *Exserohilum turcicum*). A 1 to 9 visual rating indicating the resistance to Northern Leaf Blight. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

OILT=GRAIN OIL. Absolute value of oil content of the kernel as predicted by Near-infrared Transmittance and expressed as a percent of dry matter.

PEDIGREE DISTANCE. Relationship among generations based on their ancestral links as evidenced in pedigrees. May be measured by the distance of the pedigree from a given starting point in the ancestry.

PEDUNCLE NODE: The node on the main stem that the tassel originates from.

PERCENT IDENTITY. Percent identity as used herein refers to the comparison of the homozygous alleles of two inbred varieties. Each inbred plant will have the same allele (and therefore be homozygous) at almost all of their loci. Percent identity is determined by comparing a statistically significant number of the homozygous alleles of two inbred varieties. For example, a percent identity of 90% between inbred PH8JV and other inbred variety means that the two inbred varieties have the same homozygous alleles at 90% of their loci.

PERCENT SIMILARITY. Percent similarity as used herein refers to the comparison of the homozygous alleles of an inbred plant with another plant. The homozygous alleles of PHF3P are compared with the alleles of a non-inbred plant, such as a hybrid, and if the allele of the inbred matches at least one of the corresponding alleles from the hybrid then they are scored as similar. Percent similarity is determined by comparing a statistically significant number of loci and recording the number of loci with similar alleles as a percentage. For example, a percent similarity of 90% between inbred PHF3P and a hybrid maize plant means that the inbred variety matches at least one of the hybrid alleles at 90% of the loci. In the case of a hybrid produced from PHF3P as the male or female parent, such hybrid will comprise two sets of alleles, one set of which will comprise substantially the same alleles as the homozygous alleles of inbred variety PHF3P.

PLANT. As used herein, the term "plant" includes reference to an immature or mature whole plant, including a plant that has been detasseled or from which seed or grain has been removed. Seed or embryo that will produce the plant is also considered to be the plant.

PLANT PARTS. As used herein, the term "plant parts" includes leaves, stems, roots, seed, grain, embryo, pollen, ovules, flowers, ears, cobs, husks, stalks, root tips, anthers, pericarp, silk, tissue, cells and the like.

PLTHT=PLANT HEIGHT. This is a measure of the height of the plant from the ground to the tip of the tassel in centimeters.

POLPRD=POLLEN PRODUCTION SCORE. The estimated total amount of pollen produced by tassels based on the number of tassel branches and the density of the spikelets.

POLSC=POLLEN SCORE. A 1 to 9 visual rating indicating the amount of pollen shed. The higher the score the more pollen shed.

POLWT=POLLEN WEIGHT. This is calculated by dry weight of tassels collected as shedding commences minus dry weight from similar tassels harvested after shedding is complete.

POP K/A=PLANT POPULATIONS. Measured as 1000's per acre.

POP ADV=PLANT POPULATION ADVANTAGE. The plant population advantage of variety #1 over variety #2 as calculated by PLANT POPULATION of variety #2−PLANT POPULATION of variety #1=PLANT POPULATION ADVANTAGE of variety #1.

PRM=PREDICTED RELATIVE MATURITY. This trait, predicted relative maturity, is based on the harvest moisture of the grain. The relative maturity rating is based on a known set of checks and utilizes standard linear regression analyses and is also referred to as the Comparative Relative Maturity Rating System that is similar to the Minnesota Relative Maturity Rating System.

PRMSHD=A relative measure of the growing degree units (GDU) required to reach 50% pollen shed. Relative values are predicted values from the linear regression of observed GDU's on relative maturity of commercial checks.

PRIMARY LATERAL TASSEL BRANCH: A branch that originates off the main axis of the tassel with more than 2 florets.

PROT=GRAIN PROTEIN. Absolute value of protein content of the kernel as predicted by Near-infrared Transmittance and expressed as a percent of dry matter.

RESISTANCE. Synonymous with tolerance. The ability of a plant to withstand exposure to an insect, disease, herbicide or other condition. A resistant plant variety will have a level of resistance higher than a comparable wild-type variety.

RTLDG=ROOT LODGING. Root lodging is the percentage of plants that do not root lodge; plants that lean from the vertical axis at an approximately 30 degree angle or greater would be counted as root lodged. Data are collected only when sufficient selection pressure exists in the experiment measured.

RTLADV=ROOT LODGING ADVANTAGE. The root lodging advantage of variety #1 over variety #2. Data are collected only when sufficient selection pressure exists in the experiment measured.

SCTGRN=SCATTER GRAIN. A 1 to 9 visual rating indicating the amount of scatter grain (lack of pollination or kernel abortion) on the ear. The higher the score the less scatter grain.

SDGVGR=SEEDLING VIGOR. This is the visual rating (1 to 9) of the amount of vegetative growth after emergence at the seedling stage (approximately five leaves). A higher score indicates better vigor.

SEED. Fertilized and ripened ovule, consisting of the plant embryo, varying amounts of stored food material, and a protective outer seed coat. Synonymous with grain.

SEL IND=SELECTION INDEX. The selection index gives a single measure of the hybrid's worth based on information for up to five traits. A maize breeder may utilize his or her own set of traits for the selection index. One of the traits that is almost always included is yield. The selection index data presented in the tables represent the mean value averaged across testing stations.

SELF POLLINATION. A plant is self-pollinated if pollen from one flower is transferred to the same or another flower of the same plant.

SIB POLLINATION. A plant is sib-pollinated when individuals within the same family or variety are used for pollination.

SINGLE LOCUS CONVERSION TRAIT. A trait that can be introgressed into a corn variety through introgression and/or transformation of a single locus. Examples of such single locus traits include mutant genes, transgenes and native traits finely mapped to a single locus. One or more single locus conversion traits may be introduced into a single corn variety.

SITE SPECIFIC INTEGRATION: Genes that create a site for site specific DNA integration. This includes the introduction of FRT sites that may be used in the FLP/FRT system and/or Lox sites that may be used in the Cre/Loxp system. For example, see Lyznik, et al., Site-Specific Recombination for Genetic Engineering in Plants, Plant Cell Rep (2003) 21:925-932 and WO 99/25821.

SLFBLT=SOUTHERN LEAF BLIGHT (*Helminthosporium maydis* or *Bipolaris maydis*). A 1 to 9 visual rating indicating the resistance to Southern Leaf Blight. A higher

score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

SOURST=SOUTHERN RUST (*Puccinia polysora*). A 1 to 9 visual rating indicating the resistance to Southern Rust. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

SPKDSC=SPIKLET DENSITY SCORE. The visual 1-9 rating of how dense spikelets are on the middle tassel branches. A higher score indicates higher spikelet density.

STAGRN=STAY GREEN. Stay green is the measure of plant health near the time of black layer formation (physiological maturity). A high score indicates better late-season plant health.

STDADV=STALK STANDING ADVANTAGE. The advantage of variety #1 over variety #2 for the trait STKCNT.

STKCNT=NUMBER OF PLANTS. This is the final stand or number of plants per plot.

STKLDG=STALK LODGING REGULAR. This is the percentage of plants that did not stalk lodge (stalk breakage) at regular harvest (when grain moisture is between about 20 and 30%) as measured by either natural lodging or pushing the stalks and determining the percentage of plants that break below the ear. Data are collected only when sufficient selection pressure exists in the experiment measured.

STKLDS=STALK LODGING SCORE. A plant is considered as stalk lodged if the stalk is broken or crimped between the ear and the ground. This can be caused by any or a combination of the following: strong winds late in the season, disease pressure within the stalks, ECB damage or genetically weak stalks. This trait should be taken just prior to or at harvest. Expressed on a 1 to 9 scale with 9 being no lodging. Data are collected only when sufficient selection pressure exists in the experiment measured.

STLLPN=LATE STALK LODGING. This is the percent of plants that did not stalk lodge (stalk breakage or crimping) at or around late season harvest (when grain moisture is below 20%) as measured by either natural lodging or pushing the stalks and determining the percentage of plants that break or crimp below the ear. Data are collected only when sufficient selection pressure exists in the experiment measured.

STLPCN=STALK LODGING REGULAR. This is an estimate of the percentage of plants that did not stalk lodge (stalk breakage) at regular harvest (when grain moisture is between about 20 and 30%) as measured by either natural lodging or pushing the stalks and determining the percentage of plants that break below the ear. Data are collected only when sufficient selection pressure exists in the experiment measured.

STLTIP=STERILE TIPS SCORE. The visual 1 to 9 rating of the relative lack of glumes on the tassel central spike and branches. A higher score indicates less incidence of sterile tips or lack of glumes on the tassel.

STRT=GRAIN STARCH. Absolute value of starch content of the kernel as predicted by Near-infrared Transmittance and expressed as a percent of dry matter.

STWWLT=Stewart's Wilt (*Erwinia stewartii*). A 1 to 9 visual rating indicating the resistance to Stewart's Wilt. A higher score indicates a higher resistance. Data are collected only when sufficient selection pressure exists in the experiment measured.

SSRs. Genetic markers based on polymorphisms in repeated nucleotide sequences, such as microsatellites. A marker system based on SSRs can be highly informative in linkage analysis relative to other marker systems in that multiple alleles may be present.

TASBLS=TASSEL BLAST. A 1 to 9 visual rating was used to measure the degree of blasting (necrosis due to heat stress) of the tassel at the time of flowering. A 1 would indicate a very high level of blasting at time of flowering, while a 9 would have no tassel blasting. Data are collected only when sufficient selection pressure exists in the experiment measured.

TASBRN=TASSEL BRANCH NUMBER. The number of tassel branches, with anthers originating from the central spike.

TASSZ=TASSEL SIZE. A 1 to 9 visual rating was used to indicate the relative size of the tassel. The higher the rating the larger the tassel.

TAS WT=TASSEL WEIGHT. This is the average weight of a tassel (grams) just prior to pollen shed.

TEXEAR=EAR TEXTURE. A 1 to 9 visual rating was used to indicate the relative hardness (smoothness of crown) of mature grain. A 1 would be very soft (extreme dent) while a 9 would be very hard (flinty or very smooth crown).

TILLER=TILLERS. A count of the number of tillers per plot that could possibly shed pollen was taken. Data are given as a percentage of tillers: number of tillers per plot divided by number of plants per plot.

TSTWT=TEST WEIGHT (UNADJUSTED). The measure of the weight of the grain in pounds for a given volume (bushel).

TSWADV=TEST WEIGHT ADVANTAGE. The test weight advantage of variety #1 over variety #2.

TOP EAR: The highest and primary seed bearing structure of the corn plant.

VARIETY. A substantially homozygous inbred line and minor genetic modifications thereof that retain the overall genetics of the inbred line including but not limited to a locus conversion, a mutation, or a somoclonal variant.

WIN M %=PERCENT MOISTURE WINS.

WIN Y %=PERCENT YIELD WINS.

YIELD BU/A=YIELD (BUSHELS/ACRE). Yield of the grain at harvest by weight or volume (bushels) per unit area (acre) adjusted to 15% moisture.

YLDADV=YIELD ADVANTAGE. The yield advantage of variety #1 over variety #2 as calculated by: YIELD of variety #1−YIELD variety #2=YIELD ADVANTAGE of variety #1.

YLDSC=YIELD SCORE. A 1 to 9 visual rating was used to give a relative rating for yield based on plot ear piles. The higher the rating the greater visual yield appearance.

Definitions for Area of Adaptability

When referring to area of adaptability, such term is used to describe the location with the environmental conditions that would be well suited for this maize variety. Area of adaptability is based on a number of factors, for example: days to maturity, insect resistance, disease resistance, and drought resistance. Area of adaptability does not indicate that the maize variety will grow in every location within the area of adaptability or that it will not grow outside the area.

Central Corn Belt: Iowa, Illinois, Indiana

Drylands: non-irrigated areas of North Dakota, South Dakota, Nebraska, Kansas, Colorado, and Oklahoma

Eastern U.S.: Ohio, Pennsylvania, Delaware, Maryland, Virginia, and West Virginia

North central U.S.: Minnesota and Wisconsin

Northeast: Michigan, New York, Vermont, and Ontario and Quebec Canada

Northwest U.S.: North Dakota, South Dakota, Wyoming, Washington, Oregon, Montana, Utah, and Idaho

South central U.S.: Missouri, Tennessee, Kentucky, Arkansas

Southeast U.S.: North Carolina, South Carolina, Georgia, Florida, Alabama, Mississippi, and Louisiana

Southwest U.S.: Texas, Oklahoma, New Mexico, Arizona

Western U.S.: Nebraska, Kansas, Colorado, and California

Maritime Europe Northern France, Germany, Belgium, Netherlands and Austria

DETAILED DESCRIPTION OF THE INVENTION AND FURTHER EMBODIMENTS

All tables discussed in the Detailed Description of the Invention and Further Embodiments section can found at the end of the section.

Morphological and Physiological Characteristics of PHE2E

Inbred maize variety PHE2E is a maize inbred that may be used as either a male or female in the production of the first generation F1 maize hybrid.

The inbred has shown uniformity and stability within the limits of environmental influence for all the traits as described in the Variety Description Information (Table 1, found at the end of the section). The inbred has been self-pollinated and ear-rowed a sufficient number of generations with careful attention paid to uniformity of plant type to ensure the homozygosity and phenotypic stability necessary for use in commercial hybrid seed production. The variety has been increased both by hand and in isolated fields with continued observation for uniformity. No variant traits have been observed or are expected in PHE2E.

Inbred maize variety PHE2E, being substantially homozygous, can be reproduced by planting seeds of the variety, growing the resulting maize plants under self-pollinating or sib-pollinating conditions with adequate isolation, and harvesting the resulting seed using techniques familiar to the agricultural arts.

Genotypic Characteristics of PHE2E

In addition to phenotypic observations, a plant can also be identified by its genotype. The genotype of a plant can be characterized through a genetic marker profile, which can identify plants of the same variety or a related variety, or be used to determine or validate a pedigree. The SSR profile of Inbred PHE2E can be found in Table 2 at the end of this section.

As a result of inbreeding, PHE2E is substantially homozygous. This homozygosity has been characterized at the loci shown in the marker profile provided herein. An F1 hybrid made with PHE2E would substantially comprise the marker profile of PHE2E shown herein. This is because an F1 hybrid is the sum of its inbred parents, e.g., if one inbred parent is homozygous for allele x at a particular locus, and the other inbred parent is homozygous for allele y at that locus, the F1 hybrid will be x.y (heterozygous) at that locus. The profile can therefore be used to identify hybrids comprising PHE2E as a parent, since such hybrids will comprise two sets of alleles, one set of which will be from PHE2E. The determination of the male set of alleles and the female set of alleles may be made by profiling the hybrid and the pericarp of the hybrid seed, which is composed of maternal parent cells. One way to obtain the paternal parent profile is to subtract the pericarp profile from the hybrid profile.

Subsequent generations of progeny produced by selection and breeding are expected to be of genotype x (homozygous), y (homozygous), or x.y (heterozygous) for these locus positions. When the F1 plant is used to produce an inbred, the resulting inbred should be either x or y for that allele. In that regard, a unique allele or combination of alleles unique to that inbred can be used to identify progeny plants developed with PHE2E.

Therefore, in accordance with the above, an embodiment of this invention is a PHE2E progeny maize plant or plant part that is a first generation (F1) hybrid maize plant comprising two sets of alleles, wherein one set of the alleles is the same as PHE2E at substantially all of the SSR loci listed in Table 2. A maize cell wherein one set of the alleles is the same as PHE2E at substantially all of the SSR loci listed in Table 2 is also an embodiment of the invention. This maize cell may be a part of a hybrid seed, plant or plant part produced by crossing PHE2E with another inbred maize plant.

Genetic marker profiles can be obtained by techniques such as Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) which are also referred to as Microsatellites, and Single Nucleotide Polymorphisms (SNPs). For example, see Berry, Don et al., "Assessing Probability of Ancestry Using Simple Sequence Repeat Profiles: Applications to Maize Hybrids and Inbreds", Genetics, 2002, 161:813-824, and Berry, Don et al., "Assessing Probability of Ancestry Using Simple Sequence Repeat Profiles: Applications to Maize Inbred Lines and Soybean Varieties", Genetics, 2003, 165: 331-342.

Particular markers used for these purposes are not limited to the set of markers disclosed herein, but may include any type of marker and marker profile which provides a means of distinguishing varieties. In addition to being used for identification of Inbred maize variety PHE2E, a hybrid produced through the use of PHE2E, and the identification or verification of pedigree for progeny plants produced through the use of PHE2E, the genetic marker profile is also useful in developing an introgressed trait conversion of PHE2E.

Means of performing genetic marker profiles using SSR polymorphisms are well known in the art. SSRs are genetic markers based on polymorphisms in repeated nucleotide sequences, such as microsatellites. A marker system based on SSRs can be highly informative in linkage analysis relative to other marker systems in that multiple alleles may be present. Another advantage of this type of marker is that, through use of flanking primers, detection of SSRs can be achieved, for example, by the polymerase chain reaction (PCR), thereby eliminating the need for labor-intensive Southern hybridization. The PCR detection is done by use of two oligonucleotide primers flanking the polymorphic segment of repetitive DNA. Repeated cycles of heat denaturation of the DNA followed by annealing of the primers to their complementary sequences at low temperatures, and extension of the annealed primers with DNA polymerase, comprise the major part of the methodology.

Following amplification, markers can be scored by electrophoresis of the amplification products. Scoring of marker genotype is based on the size of the amplified fragment, which may be measured by the number of base pairs of the fragment. While variation in the primer used or in laboratory

procedures can affect the reported fragment size, relative values should remain constant regardless of the specific primer or laboratory used. When comparing plants it is preferable if all SSR profiles are performed in the same lab. The SSR analyses reported herein were conducted in-house at Pioneer Hi-Bred. An SSR service is available to the public on a contractual basis by DNA Landmarks in Saint-Jean-sur-Richelieu, Quebec, Canada.

Primers used for the SSRs reported herein are publicly available and may be found in the Maize GDB on the World Wide Web at maizegdb.org (sponsored by the USDA Agricultural Research Service), in Sharopova et al. (Plant Mol. Biol. 48(5-6):463-481), Lee et al. (Plant Mol. Biol. 48(5-6); 453-461), or may be constructed from sequences if reported herein. Primers may be constructed from publicly available sequence information. Some marker information may also be available from DNA Landmarks.

Map information is provided by chromosome position and location. Bin numbers corresponding to these loci are reported in the Maize GDB for the IBM 2 and/or IBM 2 Neighbors maps. Map positions are also available on the Maize GDB for a variety of different mapping populations.

PHE2E and its plant parts can be identified through a molecular marker profile. An inbred corn plant cell having the SSR genetic marker profile shown in Table 2 is an embodiment of the invention. Such plant cell may be either diploid or haploid.

Also encompassed within the scope of the invention are plants and plant parts substantially benefiting from the use of PHE2E in their development, such as PHE2E comprising a introgressed trait through backcross conversion or transformation, and which may be identified by having an SSR molecular marker profile with a high percent identity to PHE2E, such as at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.5% identity. Likewise, percent similarity at these percentages may be used to identify plants produced by the use of PHE2E.

Comparing PHE2E to Other Inbreds

A breeder uses various methods to help determine which plants should be selected from segregating populations and ultimately which inbred varieties will be used to develop hybrids for commercialization. In addition to knowledge of the germplasm and plant genetics, a part of the selection process is dependent on experimental design coupled with the use of statistical analysis. Experimental design and statistical analysis are used to help determine which plants, which family of plants, and finally which inbred varieties and hybrid combinations are significantly better or different for one or more traits of interest. Experimental design methods are used to assess error so that differences between two inbred varieties or two hybrid varieties can be more accurately evaluated. Statistical analysis includes the calculation of mean values, determination of the statistical significance of the sources of variation, and the calculation of the appropriate variance components. Either a five or a one percent significance level is customarily used to determine whether a difference that occurs for a given trait is real or due to the environment or experimental error. One of ordinary skill in the art of plant breeding would know how to evaluate the traits of two plant varieties to determine if there is no significant difference between the two traits expressed by those varieties. For example, see Fehr, Walt, Principles of Cultivar Development, p. 261-286 (1987). Mean trait values may be used to determine whether trait differences are significant. Trait values should preferably be measured on plants grown under the same environmental conditions, and environmental conditions should be appropriate for the traits or traits being evaluated. Sufficient selection pressure should be present for optimum measurement of traits of interest such as herbicide, insect or disease resistance. A locus conversion of PHE2E for herbicide resistance should be compared with an isogenic counterpart in the absence of the converted trait. In addition, a locus conversion for insect or disease resistance should be compared to the isogenic counterpart, in the absence of disease pressure or insect pressure.

The results in Table 3A compare inbred PHE2E to inbred PH6CF. The results show inbred PHE2E has significantly different yield, tiller and plant height when compared to PH6CF.

The results in Table 3B compare inbred PHE2E to inbred PHC77. The results show inbred PHE2E differs significantly over multiple traits including moisture and resistance to Steward's Wilt when compared to inbred PHC77.

Development of Maize Hybrids using PHE2E

A single cross maize hybrid results from the cross of two inbred varieties, each of which has a genotype that complements the genotype of the other. A hybrid progeny of the first generation is designated F1. In the development of commercial hybrids in a maize plant breeding program, only the F1 hybrid plants are sought. F1 hybrids are more vigorous than their inbred parents. This hybrid vigor, or heterosis, can be manifested in many polygenic traits, including increased vegetative growth and increased yield.

PHE2E may be used to produce hybrid maize. One such embodiment is the method of crossing inbred maize variety PHE2E with another maize plant, such as a different maize inbred variety, to form a first generation F1 hybrid seed. The first generation F1 hybrid seed, plant and plant part produced by this method is an embodiment of the invention. The first generation F1 seed, plant and plant part will comprise an essentially complete set of the alleles of inbred variety PHE2E. One of ordinary skill in the art can utilize either breeder books or molecular methods to identify a particular F1 hybrid plant produced using inbred variety PHE2E. Further, one of ordinary skill in the art may also produce F1 hybrids with transgenic, male sterile and/or backcross conversions of inbred variety PHE2E

The development of a maize hybrid in a maize plant breeding program involves three steps: (1) the selection of plants from various germplasm pools for initial breeding crosses; (2) the selfing of the selected plants from the breeding crosses for several generations to produce a series of inbred varieties, such as PHE2E, which, although different from each other, breed true and are highly uniform; and (3) crossing the selected inbred varieties with different inbred varieties to produce the hybrids. During the inbreeding process in maize, the vigor of the varieties decreases, and so one would not be likely to use PHE2E directly to produce grain. However, vigor is restored when PHE2E is crossed to a different inbred variety to produce a commercial F1 hybrid. An important consequence of the homozygosity and homogeneity of the inbred variety is that the hybrid between a defined pair of inbreds may be reproduced indefinitely as long as the homogeneity of the inbred parents is maintained.

PHE2E may be used to produce a single cross hybrid, a double cross hybrid, or a three-way hybrid. A single cross hybrid is produced when two inbred varieties are crossed to produce the F1 progeny. A double cross hybrid is produced from four inbred varieties crossed in pairs (A×B and C×D) and then the two F1 hybrids are crossed again (A×B)×(C×D). A three-way cross hybrid is produced from three inbred vari-

eties where two of the inbred varieties are crossed (A×B) and then the resulting F1 hybrid is crossed with the third inbred (A×B)×C. In each case, pericarp tissue from the female parent will be a part of and protect the hybrid seed.

Combining Ability of PHE2E

Combining ability of a variety, as well as the performance of the variety per se, is a factor in the selection of improved maize inbreds. Combining ability refers to a variety's contribution as a parent when crossed with other varieties to form hybrids. The hybrids formed for the purpose of selecting superior varieties may be referred to as test crosses, and include comparisons to other hybrid varieties grown in the same environment (same cross, location and time of planting). One way of measuring combining ability is by using values based in part on the overall mean of a number of test crosses weighted by number of experiment and location combinations in which the hybrid combinations occurs. The mean may be adjusted to remove environmental effects and known genetic relationships among the varieties.

General combining ability provides an overall score for the inbred over a large number of test crosses. Specific combining ability provides information on hybrid combinations formed by PHE2E and a specific inbred parent. A variety such as PHE2E which exhibits good general combining ability may be used in a large number of hybrid combinations.

A general combining ability report for inbred PHE2E is provided in Table 4. This data represents the overall mean value for these traits over hundreds of test crosses. Table 4 demonstrates that inbred PHE2E shows good general combining ability for hybrid production.

Introgression of a New Locus or Trait into PHE2E

PHE2E represents a new base genetic variety into which a new locus or trait may be introgressed. Direct transformation and backcrossing represent two important methods that can be used to accomplish such an introgression. The term locus conversion is used to designate the product of such an introgression.

Locus Conversions of PHE2E

A locus conversion of PHE2E will retain the genetic integrity of PHE2E. The molecular marker data provided in table # as well as the availability of the seed deposit for determining the genetic profile illustrates the genetic integrity of PHE2E. A locus conversion of PHE2E will comprise at least 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% of the base genetics of PHE2E. For example, a locus conversion of PHE2E can be developed when DNA sequences are introduced through backcrossing (Hallauer et al. in Corn and Corn Improvement, Sprague and Dudley, Third Ed. 1998), with PHE2E utilized as the recurrent parent. Both naturally occurring and transgenic DNA sequences may be introduced through backcrossing techniques. A backcross conversion may produce a plant with a trait or locus conversion in at least one or more backcrosses, including at least 2 crosses, at least 3 crosses, at least 4 crosses, at least 5 crosses and the like. Molecular marker assisted breeding or selection may be utilized to reduce the number of backcrosses necessary to achieve the backcross conversion. For example, see Openshaw, S. J. et al., Marker-assisted Selection in Backcross Breeding, In: Proceedings Symposium of the Analysis of Molecular Data, August 1994, Crop Science Society of America, Corvallis, Oreg., where it is demonstrated that a backcross conversion can be made in as few as two backcrosses.

The complexity of the backcross conversion method depends on the type of trait being transferred (single genes or closely linked genes as vs. unlinked genes), the level of expression of the trait, the type of inheritance (cytoplasmic or nuclear) and the types of parents included in the cross. It is understood by those of ordinary skill in the art that for single gene traits that are relatively easy to classify, the backcross method is effective and relatively easy to manage. (See Hallauer et al. in Corn and Corn Improvement, Sprague and Dudley, Third Ed. 1998). Desired traits that may be transferred through backcross conversion include, but are not limited to, waxy starch, sterility (nuclear and cytoplasmic), fertility restoration, grain color (white), nutritional enhancements, drought resistance, enhanced nitrogen utilization efficiency, altered nitrogen responsiveness, altered fatty acid profile, increased digestibility, low phytate, industrial enhancements, disease resistance (bacterial, fungal or viral), insect resistance, herbicide resistance and yield enhancements. In addition, an introgression site itself, such as an FRT site, Lox site or other site specific integration site, may be inserted by backcrossing and utilized for direct insertion of one or more genes of interest into a specific plant variety. In some embodiments of the invention, the number of loci that may be backcrossed into PHE2E is at least 1, 2, 3, 4, or 5 and/or no more than 10, 9, 8, 7, 6, 5, 4, 3, or 2. The seed industry commonly markets "triple stacks" of base genetics; which can be varieties comprising a locus conversion of at least 3 loci. Similarly, "quadruple stacks" would comprise the base genetics and could comprise a locus conversion of at least 4 loci. Stacking of traits is common to those of ordinary skill in the art of plant breeding and stacked traits account for a significant percentage of commercial corn hybrid sales. For example, figures from Purdue University show that biotech-trait corn accounted for 61% of all corn acres in 2006 and corn with two or more stacked traits accounted for 11.9 million acres. That's a significant portion of the approximately 80 million acres of corn grown in the U.S. In addition, for 2007 at least one company projects selling more triple-stack corn hybrids than single trait hybrids. (Wayne Wenzel, "Double, Triple, Quad", published Nov. 8, 2006, Agweb.com, accessed Dec. 4, 2006). A single locus may contain several transgenes, such as a transgene for disease resistance that, in the same expression vector, also contains a transgene for herbicide resistance. The gene for herbicide resistance may be used as a selectable marker and/or as a phenotypic trait. A locus conversion of a site specific integration system allows for the integration of multiple genes at the converted loci. Further, SSI and FRT technologies known to those of skill in the art may result in multiple gene introgressions at a single locus.

The locus conversion may result from either the transfer of a dominant allele or a recessive allele. Selection of progeny containing the trait of interest is accomplished by direct selection for a trait associated with a dominant allele. Transgenes transferred via backcrossing typically function as a dominant single gene trait and are relatively easy to classify. Selection of progeny for a trait that is transferred via a recessive allele, such as the waxy starch characteristic, requires growing and selfing the first backcross generation to determine which plants carry the recessive alleles. Recessive traits may require additional progeny testing in successive backcross generations to determine the presence of the locus of interest. The last backcross generation is usually selfed to give pure breeding progeny for the gene(s) being transferred, although a backcross conversion with a stably introgressed trait may also be maintained by further backcrossing to the recurrent parent with selection for the converted trait.

Along with selection for the trait of interest, progeny are selected for the phenotype and/or genotype of the recurrent parent. While occasionally additional polynucleotide

sequences or genes may be transferred along with the backcross conversion, the backcross conversion variety "fits into the same hybrid combination as the recurrent parent inbred variety and contributes the effect of the additional gene added through the backcross." Poehiman et al. (1995, page 334). It has been proposed that in general there should be at least four backcrosses when it is important that the recovered varieties be essentially identical to the recurrent parent except for the characteristic being transferred (Fehr 1987, Principles of Cultivar Development). However, as noted above, the number of backcrosses necessary can be reduced with the use of molecular markers. Other factors, such as a genetically similar donor parent, may also reduce the number of backcrosses necessary.

One process for adding or modifying a trait or locus in maize inbred variety PHE2E comprises crossing PHE2E plants grown from PHE2E seed with plants of another maize variety that comprise the desired trait or locus, selecting F1 progeny plants that comprise the desired trait or locus to produce selected F1 progeny plants, crossing the selected progeny plants with the PHE2E plants to produce backcross progeny plants, selecting for backcross progeny plants that have the desired trait or locus and the morphological characteristics of maize inbred variety PHE2E to produce selected backcross progeny plants; and backcrossing to PHE2E three or more times in succession to produce selected fourth or higher backcross progeny plants that comprise said trait or locus. The modified PHE2E may be further characterized as having the physiological and morphological characteristics of maize inbred variety PHE2E listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions and/or may be characterized by percent similarity or identity to PHE2E as determined by SSR markers.

Traits are also used by those of ordinary skill in the art to characterize progeny. Traits are commonly evaluated at a significance level, such as a 1%, 5% or 10% significance level, when measured in plants grown in the same environmental conditions. For example, a locus conversion of PHE2E may be characterized as having the same morphological and physiological traits as PHE2E. The traits used for comparison may be those traits shown in Table 1, Table 3, Table 4 or Table 5. Molecular markers can also be used during the breeding process for the selection of qualitative traits. For example, markers closely linked to alleles or markers containing sequences within the actual alleles of interest can be used to select plants that contain the alleles of interest during a backcrossing breeding program. The markers can also be used to select for the genome of the recurrent parent and against the genome of the donor parent. Using this procedure can minimize the amount of genome from the donor parent that remains in the selected plants.

The above method may be utilized with fewer backcrosses in appropriate situations, such as when the donor parent is highly related or markers are used in the selection step. Desired traits that may be used include those nucleic acids known in the art, some of which are listed herein, that will affect traits through nucleic acid expression or inhibition. Desired loci include the introgression of FRT, Lox and other sites for site specific integration.

In addition, the above process and other similar processes described herein may be used to produce F1 hybrid maize seed by adding a step at the end of the process that comprises crossing PHE2E with the introgressed trait or locus with a different maize plant and harvesting the resultant F1 hybrid maize seed.

Male Sterility and Hybrid Seed Production

Hybrid seed production requires elimination or inactivation of pollen produced by the female inbred parent. Incomplete removal or inactivation of the pollen provides the potential for self-pollination. A reliable method of controlling male fertility in plants offers the opportunity for improved seed production.

PHE2E can be produced in a male-sterile form. There are several ways in which a maize plant can be manipulated so that it is male sterile. These include use of manual or mechanical emasculation (or detasseling), use of one or more genetic factors that confer male sterility, including cytoplasmic genetic and/or nuclear genetic male sterility, use of gametocides and the like. A male sterile inbred designated PHE2E may include one or more genetic factors, which result in cytoplasmic genetic and/or nuclear genetic male sterility. All of such embodiments are within the scope of the present claims. The male sterility may be either partial or complete male sterility.

Hybrid maize seed is often produced by a male sterility system incorporating manual or mechanical detasseling. Alternate strips of two maize inbreds are planted in a field, and the pollen-bearing tassels are removed from one of the inbreds (female). Provided that there is sufficient isolation from sources of foreign maize pollen, the ears of the detasseled inbred will be fertilized only from the other inbred (male), and the resulting seed is therefore hybrid and will form hybrid plants.

The laborious detasseling process can be avoided by using cytoplasmic male-sterile (CMS) inbreds. Plants of a CMS inbred are male sterile as a result of genetic factors in the cytoplasm, as opposed to the nucleus, and so nuclear linked genes are not transferred during backcrossing. Thus, this characteristic is inherited exclusively through the female parent in maize plants, since only the female provides cytoplasm to the fertilized seed. CMS plants are fertilized with pollen from another inbred that is not male-sterile. Pollen from the second inbred may or may not contribute genes that make the hybrid plants male-fertile, and either option may be preferred depending on the intended use of the hybrid. The same hybrid seed, a portion produced from detasseled fertile maize and a portion produced using the CMS system, can be blended to insure that adequate pollen loads are available for fertilization when the hybrid plants are grown. CMS systems have been successfully used since the 1950's, and the male sterility trait is routinely backcrossed into inbred varieties. See Wych, p. 585-586, 1998.

There are several methods of conferring genetic male sterility available, such as multiple mutant genes at separate locations within the genome that confer male sterility, as disclosed in U.S. Pat. Nos. 4,654,465 and 4,727,219 to Brar et al. and chromosomal translocations as described by Patterson in U.S. Pat. Nos. 3,861,709 and 3,710,511. In addition to these methods, Albertsen et al., U.S. Pat. No. 5,432,068, describe a system of nuclear male sterility which includes: identifying a gene which is critical to male fertility; silencing this native gene which is critical to male fertility; removing the native promoter from the essential male fertility gene and replacing it with an inducible promoter; inserting this genetically engineered gene back into the plant; and thus creating a plant that is male sterile because the inducible promoter is not "on" resulting in the male fertility gene not being transcribed. Fertility is restored by inducing, or turning "on", the promoter, which in turn allows the gene that confers male fertility to be transcribed.

These, and the other methods of conferring genetic male sterility in the art, each possess their own benefits and draw-

backs. Some other methods use a variety of approaches such as delivering into the plant a gene encoding a cytotoxic substance associated with a male tissue specific promoter or an antisense system in which a gene critical to fertility is identified and an antisense to that gene is inserted in the plant (see Fabinjanski, et al. EPO 89/3010153.8 publication no. 329, 308 and PCT application PCT/CA90/00037 published as WO 90/08828).

Another system for controlling male sterility makes use of gametocides. Gametocides are not a genetic system, but rather a topical application of chemicals. These chemicals affect cells that are critical to male fertility. The application of these chemicals affects fertility in the plants only for the growing season in which the gametocide is applied (see Carlson, Glenn R., U.S. Pat. No. 4,936,904). Application of the gametocide, timing of the application and genotype specificity often limit the usefulness of the approach and it is not appropriate in all situations.

Incomplete control over male fertility may result in self-pollinated seed being unintentionally harvested and packaged with hybrid seed. This would typically be only female parent seed, because the male plant is grown in rows that are typically destroyed prior to seed development. Once the seed from the hybrid bag is planted, it is possible to identify and select these self-pollinated plants. These self-pollinated plants will be one of the inbred varieties used to produce the hybrid. Though the possibility of inbred PHE2E being included in a hybrid seed bag exists, the occurrence is very low because much care is taken by seed companies to avoid such inclusions. It is worth noting that hybrid seed is sold to growers for the production of grain or forage and not for breeding or seed production. These self-pollinated plants can be identified and selected by one skilled in the art due to their less vigorous appearance for vegetative and/or reproductive characteristics, including shorter plant height, small ear size, ear and kernel shape, cob color, or other characteristics.

Identification of these self-pollinated varieties can also be accomplished through molecular marker analyses. See, "The Identification of Female Selfs in Hybrid Maize: A Comparison Using Electrophoresis and Morphology", Smith, J. S. C. and Wych, R. D., Seed Science and Technology 14, 1-8 (1995), the disclosure of which is expressly incorporated herein by reference. Through these technologies, the homozygosity of the self pollinated variety can be verified by analyzing allelic composition at various loci along the genome. Those methods allow for rapid identification of the invention disclosed herein. See also, "Identification of Atypical Plants in Hybrid Maize Seed by Postcontrol and Electrophoresis" Sarca, V. et al., Probleme de Genetica Teoritica si Aplicata Vol. 20 (1) p. 29-42.

An embodiment of this invention is a process for producing seed of PHE2E comprising planting a collection of seed comprising seed of a hybrid, one of whose parents is inbred PHE2E said collection also comprising seed of said inbred, growing plants from said collection of seed, identifying inbred parent plants, selecting said inbred parent plant; and controlling pollination to preserve the homozygosity of said inbred parent plant.

Transformation

The advent of new molecular biological techniques has allowed the isolation and characterization of genetic elements with specific functions, such as encoding specific protein products. Scientists in the field of plant biology developed a strong interest in engineering the genome of plants to contain and express foreign genetic elements, or additional, or modified versions of native or endogenous genetic elements in order to alter the traits of a plant in a specific manner. Any DNA sequences, whether from a different species or from the same species, which are inserted into the genome using transformation are referred to herein collectively as "transgenes". In some embodiments of the invention, a transformed variant of PHE2E may comprise at least one transgene but could contain at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 and/or no more than 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2. Over the last fifteen to twenty years several methods for producing transgenic plants have been developed, and the present invention also relates to transformed versions of the claimed inbred maize variety PHE2E as well as hybrid combinations thereof.

Numerous methods for plant transformation have been developed, including biological and physical plant transformation protocols. See, for example, Miki et al., "Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology*, Glick, B. R. and Thompson, J. E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 67-88 and Armstrong, "The First Decade of Maize Transformation: A Review and Future Perspective" (Maydica 44:101-109, 1999). In addition, expression vectors and in vitro culture methods for plant cell or tissue transformation and regeneration of plants are available. See, for example, Gruber et al., "Vectors for Plant Transformation" in *Methods in Plant Molecular Biology and Biotechnology*, Glick, B. R. and Thompson, J. E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 89-119.

The most prevalent types of plant transformation involve the construction of an expression vector. Such a vector comprises a DNA sequence that contains a gene under the control of or operatively linked to a regulatory element, for example a promoter. The vector may contain one or more genes and one or more regulatory elements.

A genetic trait which has been engineered into the genome of a particular maize plant using transformation techniques, could be moved into the genome of another variety using traditional breeding techniques that are well known in the plant breeding arts. For example, a backcrossing approach is commonly used to move a transgene from a transformed maize plant to an elite inbred variety, and the resulting progeny would then comprise the transgene(s). Also, if an inbred variety was used for the transformation then the transgenic plants could be crossed to a different inbred in order to produce a transgenic hybrid maize plant.

Various genetic elements can be introduced into the plant genome using transformation. These elements include, but are not limited to genes; coding sequences; inducible, constitutive, and tissue specific promoters; enhancing sequences; and signal and targeting sequences. For example, see the traits, genes and transformation methods listed in U.S. Pat. Nos. 6,118,055 and 6,284,953, which are herein incorporated by reference. In addition, transformability of a variety can be increased by introgressing the trait of high transformability from another variety known to have high transformability, such as Hi-II. See U.S. Patent Application Publication US2004/0016030 (2004).

With transgenic plants according to the present invention, a foreign protein can be produced in commercial quantities. Thus, techniques for the selection and propagation of transformed plants, which are well understood in the art, yield a plurality of transgenic plants that are harvested in a conventional manner, and a foreign protein then can be extracted from a tissue of interest or from total biomass. Protein extraction from plant biomass can be accomplished by known methods which are discussed, for example, by Heney and Orr, *Anal. Biochem.* 114: 92-6 (1981).

Transgenes can be mapped by one of ordinary skill in the art and such techniques are well known to those of ordinary skill in the art. For exemplary methodologies in this regard, see for example, Glick and Thompson, Methods in Plant Molecular Biology and Biotechnology 269-284 (CRC Press, Boca Raton, 1993).

Likewise, by means of the present invention, plants can be genetically engineered to express various phenotypes of agronomic interest. Through the transformation of maize the expression of genes can be altered to enhance disease resistance, insect resistance, herbicide resistance, agronomic traits, grain quality and other traits. Transformation can also be used to insert DNA sequences which control or help control male-sterility. DNA sequences native to maize as well as non-native DNA sequences can be transformed into maize and used to alter levels of native or non-native proteins. Various promoters, targeting sequences, enhancing sequences, and other DNA sequences can be inserted into the maize genome for the purpose of altering the expression of proteins. Reduction of the activity of specific genes (also known as gene silencing, or gene suppression) is desirable for several aspects of genetic engineering in plants.

Many techniques for gene silencing are well known to one of skill in the art, including but not limited to knock-outs (such as by insertion of a transposable element such as mu (Vicki Chandler, *The Maize Handbook* ch. 118 (Springer-Verlag 1994) or other genetic elements such as a FRT, Lox or other site specific integration site, antisense technology (see, e.g., Sheehy et al. (1988) *PNAS* USA 85:8805-8809; and U.S. Pat. Nos. 5,107,065; 5,453,566; and 5,759,829); co-suppression (e.g., Taylor (1997) *Plant Cell* 9:1245; Jorgensen (1990) *Trends Biotech.* 8(12):340-344; Flavell (1994) *PNAS* USA 91:3490-3496; Finnegan et al. (1994) *Bio/Technology* 12: 883-888; and Neuhuber et al. (1994) *Mol. Gen. Genet.* 244: 230-241); RNA interference (Napoli et al. (1990) *Plant Cell* 2:279-289; U.S. Pat. No. 5,034,323; Sharp (1999) *Genes Dev.* 13:139-141; Zamore et al. (2000) *Cell* 101:25-33; and Montgomery et al. (1998) *PNAS* USA 95:15502-15507), virus-induced gene silencing (Burton, et al. (2000) *Plant Cell* 12:691-705; and Baulcombe (1999) *Curr. Op. Plant Bio.* 2:109-113); target-RNA-specific ribozymes (Haseloff et al. (1988) *Nature* 334: 585-591); hairpin structures (Smith et al. (2000) *Nature* 407:319-320; WO 99/53050; and WO 98/53083); MicroRNA (Aukerman & Sakai (2003) Plant Cell 15:2730-2741); ribozymes (Steinecke et al. (1992) *EMBO J.* 11:1525; and Perriman et al. (1993) *Antisense Res. Dev.* 3:253); oligonucleotide mediated targeted modification (e.g., WO 03/076574 and WO 99/25853); Zn-finger targeted molecules (e.g., WO 01/52620; WO 03/048345; and WO 00/42219); and other methods or combinations of the above methods known to those of skill in the art.

Exemplary nucleotide sequences that may be altered by genetic engineering include, but are not limited to, those categorized below.

1. Transgenes that Confer Resistance to Insects or Disease and that Encode:

(A) Plant disease resistance genes. Plant defenses are often activated by specific interaction between the product of a disease resistance gene (R) in the plant and the product of a corresponding avirulence (Avr) gene in the pathogen. A plant variety can be transformed with cloned resistance gene to engineer plants that are resistant to specific pathogen strains. See, for example Jones et al., Science 266: 789 (1994) (cloning of the tomato Cf-9 gene for resistance to *Cladosporium fulvum*); Martin et al., Science 262: 1432 (1993) (tomato Pto gene for resistance to *Pseudomonas syringae* pv. tomato encodes a protein kinase); Mindrinos et al., Cell 78: 1089 (1994) (*Arabidopsis* RSP2 gene for resistance to *Pseudomonas syringae*); McDowell & Woffenden, (2003) Trends Biotechnol. 21(4): 178-83 and Toyoda et al., (2002) Transgenic Res. 11 (6):567-82. A plant resistant to a disease is one that is more resistant to a pathogen as compared to the wild type plant.

(B) A *Bacillus thuringiensis* protein, a derivative thereof or a synthetic polypeptide modeled thereon. See, for example, Geiser et al., *Gene* 48: 109 (1986), who disclose the cloning and nucleotide sequence of a Bt delta-endotoxin gene. Moreover, DNA molecules encoding delta-endotoxin genes can be purchased from American Type Culture Collection (Rockville, Md.), for example, under ATCC Accession Nos. 40098, 67136, 31995 and 31998. Other examples of *Bacillus thuringiensis* transgenes being genetically engineered are given in the following patents and patent applications and hereby are incorporated by reference for this purpose: U.S. Pat. Nos. 5,188,960; 5,689,052; 5,880,275; WO 91/14778; WO 99/31248; WO 01/12731; WO 99/24581; WO 97/40162 and U.S. application Ser. Nos. 10/032,717; 10/414,637; and 10/606,320.

(C) An insect-specific hormone or pheromone such as an ecdysteroid and juvenile hormone, a variant thereof, a mimetic based thereon, or an antagonist or agonist thereof. See, for example, the disclosure by Hammock et al., Nature 344: 458 (1990), of baculovirus expression of cloned juvenile hormone esterase, an inactivator of juvenile hormone.

(D) An insect-specific peptide which, upon expression, disrupts the physiology of the affected pest. For example, see the disclosures of Regan, *J. Biol. Chem.* 269: 9 (1994) (expression cloning yields DNA coding for insect diuretic hormone receptor); Pratt et al., *Biochem. Biophys. Res. Comm.* 163: 1243 (1989) (an allostatin is identified in *Diploptera puntata*); Chattopadhyay et al. (2004) Critical Reviews in Microbiology 30 (1): 33-54 2004; Zjawiony (2004) J Nat Prod 67 (2): 300-310; Carlini & Grossi-de-Sa (2002) Toxicon, 40 (11): 1515-1539; Ussuf et al. (2001) Curr Sci. 80 (7): 847-853; and Vasconcelos & Oliveira (2004) Toxicon 44 (4): 385-403. See also U.S. Pat. No. 5,266,317 to Tomalski et al., who disclose genes encoding insect-specific toxins.

(E) An enzyme responsible for a hyperaccumulation of a monterpene, a sesquiterpene, a steroid, hydroxamic acid, a phenylpropanoid derivative or another non-protein molecule with insecticidal activity.

(F) An enzyme involved in the modification, including the post-translational modification, of a biologically active molecule; for example, a glycolytic enzyme, a proteolytic enzyme, a lipolytic enzyme, a nuclease, a cyclase, a transaminase, an esterase, a hydrolase, a phosphatase, a kinase, a phosphorylase, a polymerase, an elastase, a chitinase and a glucanase, whether natural or synthetic. See PCT application WO 93/02197 in the name of Scott et al., which discloses the nucleotide sequence of a callase gene. DNA molecules which contain chitinase-encoding sequences can be obtained, for example, from the ATCC under Accession Nos. 39637 and 67152. See also Kramer et al., *Insect Biochem. Molec. Biol.* 23: 691 (1993), who teach the nucleotide sequence of a cDNA encoding tobacco hookworm chitinase, and Kawalleck et al., *Plant Molec. Biol.* 21: 673 (1993), who provide the nucleotide sequence of the parsley ubi4-2 polyubiquitin gene, U.S. application Ser. Nos. 10/389,432, 10/692,367, and U.S. Pat. No. 6,563,020.

(G) A molecule that stimulates signal transduction. For example, see the disclosure by Botella et al., *Plant Molec. Biol.* 24: 757 (1994), of nucleotide sequences for mung bean calmodulin cDNA clones, and Griess et al., *Plant Physiol.*

104: 1467 (1994), who provide the nucleotide sequence of a maize calmodulin cDNA clone.

(H) A hydrophobic moment peptide. See PCT application WO 95/16776 and U.S. Pat. No. 5,580,852 (disclosure of peptide derivatives of Tachyplesin which inhibit fungal plant pathogens) and PCT application WO 95/18855 and U.S. Pat. No. 5,607,914) (teaches synthetic antimicrobial peptides that confer disease resistance).

(I) A membrane permease, a channel former or a channel blocker. For example, see the disclosure by Jaynes et al., *Plant Sci.* 89: 43 (1993), of heterologous expression of a cecropin-beta lytic peptide analog to render transgenic tobacco plants resistant to *Pseudomonas solanacearum.*

(J) A viral-invasive protein or a complex toxin derived therefrom. For example, the accumulation of viral coat proteins in transformed plant cells imparts resistance to viral infection and/or disease development effected by the virus from which the coat protein gene is derived, as well as by related viruses. See Beachy et al., *Ann. Rev. Phytopathol.* 28: 451 (1990). Coat protein-mediated resistance has been conferred upon transformed plants against alfalfa mosaic virus, cucumber mosaic virus, tobacco streak virus, potato virus X, potato virus Y, tobacco etch virus, tobacco rattle virus and tobacco mosaic virus. Id.

(K) An insect-specific antibody or an immunotoxin derived therefrom. Thus, an antibody targeted to a critical metabolic function in the insect gut would inactivate an affected enzyme, killing the insect. Cf. Taylor et al., Abstract #497, SEVENTH INT'L SYMPOSIUM ON MOLECULAR PLANT-MICROBE INTERACTIONS (Edinburgh, Scotland, 1994) (enzymatic inactivation in transgenic tobacco via production of single-chain antibody fragments).

(L) A virus-specific antibody. See, for example, Tavladoraki et al., *Nature* 366: 469 (1993), who show that transgenic plants expressing recombinant antibody genes are protected from virus attack.

(M) A developmental-arrestive protein produced in nature by a pathogen or a parasite. Thus, fungal endo alpha-1,4-D-polygalacturonases facilitate fungal colonization and plant nutrient release by solubilizing plant cell wall homo-alpha-1,4-D-galacturonase. See Lamb et al., *Bio/Technology* 10: 1436 (1992). The cloning and characterization of a gene which encodes a bean endopolygalacturonase-inhibiting protein is described by Toubart et al., *Plant J.* 2: 367 (1992).

(N) A developmental-arrestive protein produced in nature by a plant. For example, Logemann et al., *Bio/Technology* 10: 305 (1992), have shown that transgenic plants expressing the barley ribosome-inactivating gene have an increased resistance to fungal disease.

(O) Genes involved in the Systemic Acquired Resistance (SAR) Response and/or the pathogenesis related genes. Briggs, S., Current Biology, 5(2):128-131 (1995), Pieterse & Van Loon (2004) Curr. Opin. Plant Bio. 7(4):456-64 and Somssich (2003) Cell 113(7):815-6.

(P) Antifungal genes (Cornelissen and Melchers, Pl. Physiol. 101:709-712, (1993) and Parijs et al., Planta 183: 258-264, (1991) and Bushnell et al., Can. J. of Plant Path. 20(2):137-149 (1998). Also see U.S. Pat. No. 6,875,907.

(Q) Detoxification genes, such as for fumonisin, beauvericin, moniliformin and zearalenone and their structurally related derivatives. For example, see U.S. Pat. No. 5,792,931.

(R) Cystatin and cysteine proteinase inhibitors. See U.S. application Ser. No. 10/947,979.

(S) Defensin genes. See WO03000863 and U.S. application Ser. No. 10/178,213.

(T) Genes conferring resistance to nematodes. See WO 03/033651 and Urwin et. al., Planta 204:472-479 (1998), Williamson (1999) Curr Opin Plant Bio. 2(4):327-31.

(U) Genes such as rcg1 conferring resistance to Anthracnose stalk rot, which is caused by the fungus *Colletotrichum graminiola*. See M. Jung et al., Generation-means analysis and quantitative trait locus mapping of Anthracnose Stalk Rot genes in Maize, *Theor. Appl. Genet.* (1994) 89:413-418 which is incorporated by reference for this purpose, as well as U.S. Patent Application 60/675,664, which is also incorporated by reference for this purpose.

2. Transgenes that Confer Resistance to a Herbicide, for Example:

(A) A herbicide that inhibits the growing point or meristem, such as an imidazolinone or a sulfonylurea. Exemplary genes in this category code for mutant ALS and AHAS enzyme as described, for example, by Lee et al., *EMBO J.* 7: 1241 (1988), and Miki et al., *Theor. Appl. Genet.* 80: 449 (1990), respectively. See also, U.S. Pat. Nos. 5,605,011; 5,013,659; 5,141,870; 5,767,361; 5,731,180; 5,304,732; 4,761,373; 5,331,107; 5,928,937; and 5,378,824; and international publication WO 96/33270, which are incorporated herein by reference for this purpose.

(B) Glyphosate (resistance imparted by mutant 5-enolpyruvl-3-phosphikimate synthase (EPSP) and aroA genes, respectively) and other phosphono compounds such as glufosinate (phosphinothricin acetyl transferase (PAT) and *Streptomyces hygroscopicus* phosphinothricin acetyl transferase (bar) genes), and pyridinoxy or phenoxy proprionic acids and cycloshexones (ACCase inhibitor-encoding genes). See, for example, U.S. Pat. No. 4,940,835 to Shah et al., which discloses the nucleotide sequence of a form of EPSPS which can confer glyphosate resistance. U.S. Pat. No. 5,627,061 to Barry et al. also describes genes encoding EPSPS enzymes. See also U.S. Pat. Nos. 6,566,587; 6,338,961; 6,248,876 B1; 6,040,497; 5,804,425; 5,633,435; 5,145,783; 4,971,908; 5,312,910; 5,188,642; 4,940,835; 5,866,775; 6,225,114 B1; 6,130,366; 5,310,667; 4,535,060; 4,769,061; 5,633,448; 5,510,471; Re. 36,449; RE 37,287 E; and 5,491,288; and international publications EP1173580; WO 01/66704; EP1173581 and EP1173582, which are incorporated herein by reference for this purpose. Glyphosate resistance is also imparted to plants that express a gene that encodes a glyphosate oxido-reductase enzyme as described more fully in U.S. Pat. Nos. 5,776,760 and 5,463,175, which are incorporated herein by reference for this purpose. In addition glyphosate resistance can be imparted to plants by the over expression of genes encoding glyphosate N-acetyltransferase. See, for example, U.S. application Ser. Nos. 01/46227; 10/427,692 and 10/427,692. A DNA molecule encoding a mutant aroA gene can be obtained under ATCC accession No. 39256, and the nucleotide sequence of the mutant gene is disclosed in U.S. Pat. No. 4,769,061 to Comai. European Patent Application No. 0 333 033 to Kumada et al. and U.S. Pat. No. 4,975,374 to Goodman et al. disclose nucleotide sequences of glutamine synthetase genes which confer resistance to herbicides such as L-phosphinothricin. The nucleotide sequence of a phosphinothricin-acetyl-transferase gene is provided in European Patent No. 0 242 246 and 0 242 236 to Leemans et al. De Greef et al., *Bio/Technology* 7: 61 (1989), describe the production of transgenic plants that express chimeric bar genes coding for phosphinothricin acetyl transferase activity. See also, U.S. Pat. Nos. 5,969,213; 5,489,520; 5,550,318; 5,874,265; 5,919,675; 5,561,236; 5,648,477; 5,646,024; 6,177,616 B1; and 5,879,903, which are incorporated herein by reference for this purpose. Exem-

plary genes conferring resistance to phenoxy proprionic acids and cycloshexones, such as sethoxydim and haloxyfop, are the Acc1-S1, Acc1-S2 and Acc1-S3 genes described by Marshall et al., *Theor. Appl. Genet.* 83: 435 (1992).

(C) A herbicide that inhibits photosynthesis, such as a triazine (psbA and gs+ genes) and a benzonitrile (nitrilase gene). Przibilla et al., *Plant Cell* 3: 169 (1991), describe the transformation of *Chlamydomonas* with plasmids encoding mutant psbA genes. Nucleotide sequences for nitrilase genes are disclosed in U.S. Pat. No. 4,810,648 to Stalker, and DNA molecules containing these genes are available under ATCC Accession Nos. 53435, 67441 and 67442. Cloning and expression of DNA coding for a glutathione S-transferase is described by Hayes et al., *Biochem. J.* 285:173 (1992).

(D) Acetohydroxy acid synthase, which has been found to make plants that express this enzyme resistant to multiple types of herbicides, has been introduced into a variety of plants (see, e.g., Hattori et al. (1995) Mol Gen Genet 246: 419). Other genes that confer resistance to herbicides include: a gene encoding a chimeric protein of rat cytochrome P4507A1 and yeast NADPH-cytochrome P450 oxidoreductase (Shiota et al. (1994) Plant Physiol. 106(1):17-23), genes for glutathione reductase and superoxide dismutase (Aono et al. (1995) Plant Cell Physiol 36:1687, and genes for various phosphotransferases (Datta et al. (1992) Plant Mol Biol 20:619).

(E) Protoporphyrinogen oxidase (protox) is necessary for the production of chlorophyll, which is necessary for all plant survival. The protox enzyme serves as the target for a variety of herbicidal compounds. These herbicides also inhibit growth of all the different species of plants present, causing their total destruction. The development of plants containing altered protox activity which are resistant to these herbicides are described in U.S. Pat. Nos. 6,288,306 B1; 6,282,837 B1; and 5,767,373; and international publication WO 01/12825.

3. Transgenes that Confer or Contribute to an Altered Grain Characteristic, Such as:

(A) Altered fatty acids, for example, by

(1) Down-regulation of stearoyl-ACP desaturase to increase stearic acid content of the plant. See Knultzon et al., *Proc. Natl. Acad. Sci. USA* 89: 2624 (1992) and WO99/64579 (Genes for Desaturases to Alter Lipid Profiles in Corn),

(2) Elevating oleic acid via FAD-2 gene modification and/or decreasing linolenic acid via FAD-3 gene modification (see U.S. Pat. Nos. 6,063,947; 6,323,392; 6,372,965 and WO 93/11245),

(3) Altering conjugated linolenic or linoleic acid content, such as in WO 01/12800,

(4) Altering LEC1, AGP, Dek1, Superal1, mi1ps, various Ipa genes such as Ipa1, Ipa3, hpt or hggt. For example, see WO 02/42424, WO 98/22604, WO 03/011015, U.S. Pat. No. 6,423,886, U.S. Pat. No. 6,197,561, U.S. Pat. No. 6,825,397, US2003/0079247, US2003/0204870, WO02/057439, WO03/011015 and Rivera-Madrid, R. et. al. Proc. Natl. Acad. Sci. 92:5620-5624 (1995).

(B) Altered phosphorus content, for example, by the

(1) Introduction of a phytase-encoding gene would enhance breakdown of phytate, adding more free phosphate to the transformed plant. For example, see Van Hartingsveldt et al., *Gene* 127: 87 (1993), for a disclosure of the nucleotide sequence of an *Aspergillus niger* phytase gene.

(2) Up-regulation of a gene that reduces phytate content. In maize, this, for example, could be accomplished, by cloning and then re-introducing DNA associated with one or more of the alleles, such as the LPA alleles, identified in maize mutants characterized by low levels of phytic acid, such as in Raboy et al., *Maydica* 35: 383 (1990) and/or by altering inositol kinase activity as in WO 02/059324, US2003/0009011, WO 03/027243, US2003/0079247, WO 99/05298, U.S. Pat. No. 6,197,561, U.S. Pat. No. 6,291,224, U.S. Pat. No. 6,391,348, WO2002/059324, US2003/0079247, Wo98/45448, WO99/55882, WO01/04147.

(C) Altered carbohydrates effected, for example, by altering a gene for an enzyme that affects the branching pattern of starch or a gene altering thioredoxin such as NTR and/or TRX (see U.S. Pat. No. 6,531,648 which is incorporated by reference for this purpose) and/or a gamma zein knock out or mutant such as cs27 or TUSC27 or en27 (See U.S. Pat. No. 6,858,778 and US2005/0160488, US2005/0204418; which are incorporated by reference for this purpose). See Shiroza et al., J. Bacteriol. 170: 810 (1988) (nucleotide sequence of *Streptococcus mutans* fructosyltransferase gene), Steinmetz et al., Mol. Gen. Genet. 200: 220 (1985) (nucleotide sequence of *Bacillus subtilis* levansucrase gene), Pen et al., Bio/Technology 10: 292 (1992) (production of transgenic plants that express *Bacillus licheniformis* alpha-amylase), Elliot et al., Plant Molec. Biol. 21: 515 (1993) (nucleotide sequences of tomato invertase genes), Søgaard et al., J. Biol. Chem. 268: 22480 (1993) (site-directed mutagenesis of barley alpha-amylase gene), and Fisher et al., Plant Physiol. 102: 1045 (1993) (maize endosperm starch branching enzyme II), WO 99/10498 (improved digestibility and/or starch extraction through modification of UDP-D-xylose 4-epimerase, Fragile 1 and 2, Ref1, HCHL, C4H), U.S. Pat. No. 6,232,529 (method of producing high oil seed by modification of starch levels (AGP)). The fatty acid modification genes mentioned above may also be used to affect starch content and/or composition through the interrelationship of the starch and oil pathways.

(D) Altered antioxidant content or composition, such as alteration of tocopherol or tocotrienols. For example, see U.S. Pat. No. 6,787,683, US2004/0034886 and WO 00/68393 involving the manipulation of antioxidant levels through alteration of a phytl prenyl transferase (ppt), WO 03/082899 through alteration of a homogentisate geranyl geranyl transferase (hggt).

(E) Altered essential seed amino acids. For example, see U.S. Pat. No. 6,127,600 (method of increasing accumulation of essential amino acids in seeds), U.S. Pat. No. 6,080,913 (binary methods of increasing accumulation of essential amino acids in seeds), U.S. Pat. No. 5,990,389 (high lysine), WO99/40209 (alteration of amino acid compositions in seeds), WO99/29882 (methods for altering amino acid content of proteins), U.S. Pat. No. 5,850,016 (alteration of amino acid compositions in seeds), WO98/20133 (proteins with enhanced levels of essential amino acids), U.S. Pat. No. 5,885,802 (high methionine), U.S. Pat. No. 5,885,801 (high threonine), U.S. Pat. No. 6,664,445 (plant amino acid biosynthetic enzymes), U.S. Pat. No. 6,459,019 (increased lysine and threonine), U.S. Pat. No. 6,441,274 (plant tryptophan synthase beta subunit), U.S. Pat. No. 6,346,403 (methionine metabolic enzymes), U.S. Pat. No. 5,939,599 (high sulfur), U.S. Pat. No. 5,912,414 (increased methionine), WO98/56935 (plant amino acid biosynthetic enzymes), WO98/45458 (engineered seed protein having higher percentage of essential amino acids), WO98/42831 (increased lysine), U.S. Pat. No. 5,633,436 (increasing sulfur amino acid content), U.S. Pat. No. 5,559,223 (synthetic storage proteins with defined structure containing programmable levels of essential amino acids for improvement of the nutritional value of plants), WO96/01905 (increased threonine), WO95/15392

(increased lysine), US2003/0163838, US2003/0150014, US2004/0068767, U.S. Pat. No. 6,803,498, WO01/79516, and WO00/09706 (Ces A: cellulose synthase), U.S. Pat. No. 6,194,638 (hemicellulose), U.S. Pat. No. 6,399,859 and US2004/0025203 (UDPGdH), U.S. Pat. No. 6,194,638 (RGP).

4. Genes that Control Male-Sterility

There are several methods of conferring genetic male sterility available, such as multiple mutant genes at separate locations within the genome that confer male sterility, as disclosed in U.S. Pat. Nos. 4,654,465 and 4,727,219 to Brar et al. and chromosomal translocations as described by Patterson in U.S. Pat. Nos. 3,861,709 and 3,710,511. In addition to these methods, Albertsen et al., U.S. Pat. No. 5,432,068, describe a system of nuclear male sterility which includes: identifying a gene which is critical to male fertility; silencing this native gene which is critical to male fertility; removing the native promoter from the essential male fertility gene and replacing it with an inducible promoter; inserting this genetically engineered gene back into the plant; and thus creating a plant that is male sterile because the inducible promoter is not "on" resulting in the male fertility gene not being transcribed. Fertility is restored by inducing, or turning "on", the promoter, which in turn allows the gene that confers male fertility to be transcribed.

(A) Introduction of a deacetylase gene under the control of a tapetum-specific promoter and with the application of the chemical N-Ac-PPT (WO 01/29237).

(B) Introduction of various stamen-specific promoters (WO 92/13956, WO 92/13957).

(C) Introduction of the barnase and the barstar gene (Paul et al. Plant Mol. Biol. 19:611-622, 1992).

For additional examples of nuclear male and female sterility systems and genes, see also, U.S. Pat. Nos. 5,859,341; 6,297,426; 5,478,369; 5,824,524; 5,850,014; and 6,265,640; all of which are hereby incorporated by reference.

5. Genes that create a site for site specific DNA integration. This includes the introduction of FRT sites that may be used in the FLP/FRT system and/or Lox sites that may be used in the Cre/Loxp system. For example, see Lyznik, et al., Site-Specific Recombination for Genetic Engineering in Plants, Plant Cell Rep (2003) 21:925-932 and WO 99/25821, which are hereby incorporated by reference. Other systems that may be used include the Gin recombinase of phage Mu (Maeser et al., 1991; Vicki Chandler, *The Maize Handbook* ch. 118 (Springer-Verlag 1994), the Pin recombinase of *E. coli* (Enomoto et al., 1983), and the R/RS system of the pSR1 plasmid (Araki et al., 1992).

6. Genes that affect abiotic stress resistance (including but not limited to flowering, ear and seed development, enhancement of nitrogen utilization efficiency, altered nitrogen responsiveness, drought resistance or tolerance, cold resistance or tolerance, and salt resistance or tolerance) and increased yield under stress. For example, see: WO 00/73475 where water use efficiency is altered through alteration of malate; U.S. Pat. No. 5,892,009, U.S. Pat. No. 5,965,705, U.S. Pat. No. 5,929,305, U.S. Pat. No. 5,891,859, U.S. Pat. No. 6,417,428, U.S. Pat. No. 6,664,446, U.S. Pat. No. 6,706,866, U.S. Pat. No. 6,717,034, U.S. Pat. No. 6,801,104, WO2000060089, WO2001026459, WO2001035725, WO2001034726, WO2001035727, WO2001036444, WO2001036597, WO2001036598, WO2002015675, WO2002017430, WO2002077185, WO2002079403, WO2003013227, WO2003013228, WO2003014327, WO2004031349, WO2004076638, WO9809521, and WO9938977 describing genes, including CBF genes and transcription factors effective in mitigating the negative effects of freezing, high salinity, and drought on plants, as well as conferring other positive effects on plant phenotype; US2004/0148654 and WO01/36596 where abscisic acid is altered in plants resulting in improved plant phenotype such as increased yield and/or increased tolerance to abiotic stress; WO2000/006341, WO04/090143, U.S. application Ser. Nos. 10/817,483 and 09/545,334 where cytokinin expression is modified resulting in plants with increased stress tolerance, such as drought tolerance, and/or increased yield. Also see WO0202776, WO2003052063, JP2002281975, U.S. Pat. No. 6,084,153, WO0164898, U.S. Pat. No. 6,177,275, and U.S. Pat. No. 6,107,547 (enhancement of nitrogen utilization and altered nitrogen responsiveness). For ethylene alteration, see US20040128719, US20030166197 and WO200032761. For plant transcription factors or transcriptional regulators of abiotic stress, see e.g. US20040098764 or US20040078852.

Other genes and transcription factors that affect plant growth and agronomic traits such as yield, flowering, plant growth and/or plant structure, can be introduced or introgressed into plants, see e.g. WO97/49811 (LHY), WO98/56918 (ESD4), WO97/10339 and U.S. Pat. No. 6,573,430 (TFL), U.S. Pat. No. 6,713,663 (FT), WO96/14414 (CON), WO96/38560, WO01/21822 (VRN1), WO00/44918 (VRN2), WO99/49064 (GI), WO00/46358 (FRI), WO97/29123, U.S. Pat. No. 6,794,560, U.S. Pat. No. 6,307,126 (GAI), WO99/09174 (D8 and Rht), and WO2004076638 and WO2004031349 (transcription factors).

Using PHE2E to Develop Another Maize Plant

Inbred maize varieties such as PHE2E are typically developed for use in the production of hybrid maize varieties. However, inbred varieties such as PHE2E also provide a source of breeding material that may be used to develop new maize inbred varieties. Plant breeding techniques known in the art and used in a maize plant breeding program include, but are not limited to, recurrent selection, mass selection, bulk selection, mass selection, backcrossing, pedigree breeding, open pollination breeding, restriction fragment length polymorphism enhanced selection, genetic marker enhanced selection, making double haploids, and transformation. Often combinations of these techniques are used. The development of maize hybrids in a maize plant breeding program requires, in general, the development of homozygous inbred varieties, the crossing of these varieties, and the evaluation of the crosses. There are many analytical methods available to evaluate the result of a cross. The oldest and most traditional method of analysis is the observation of phenotypic traits but genotypic analysis may also be used.

This invention is also directed to methods for producing a maize plant by crossing a first parent maize plant with a second parent maize plant wherein either the first or second parent maize plant is an inbred maize plant of the variety PHE2E. The other parent may be any other maize plant, such as another inbred variety or a plant that is part of a synthetic or natural population. Any such methods using the inbred maize variety PHE2E are part of this invention: selfing, sibbing, backcrosses, mass selection, pedigree breeding, bulk selection, hybrid production, crosses to populations, and the like. These methods are well known in the art and some of the more commonly used breeding methods are described below. Descriptions of breeding methods can also be found in one of several reference books (e.g., Allard, *Principles of Plant Breeding*, 1960; Simmonds, *Principles of Crop Improvement*, 1979; Fehr, "Breeding Methods for Cultivar Development",

Production and Uses, 2nd ed., Wilcox editor, 1987 the disclosure of which is incorporated herein by reference).

Pedigree Breeding

Pedigree breeding starts with the crossing of two genotypes, such as PHE2E and one other elite inbred variety having one or more desirable characteristics that is lacking or which complements PHE2E. If the two original parents do not provide all the desired characteristics, other sources can be included in the breeding population. In the pedigree method, superior plants are selfed and selected in successive filial generations. In the succeeding filial generations the heterozygous condition gives way to homogeneous varieties as a result of self-pollination and selection. Typically in the pedigree method of breeding, five or more successive filial generations of selfing and selection is practiced: F1→F2; F2→F3; F3→F4; F4→F5, etc. After a sufficient amount of inbreeding, successive filial generations will serve to increase seed of the developed inbred. Preferably, the inbred variety comprises homozygous alleles at about 95% or more of its loci.

In addition to being used to create a backcross conversion, backcrossing can also be used in combination with pedigree breeding to modify PHE2E and a hybrid that is made using the modified PHE2E. As discussed previously, backcrossing can be used to transfer one or more specifically desirable traits from one variety, the donor parent, to an inbred called the recurrent parent, which has overall good agronomic characteristics yet lacks that desirable trait or traits. However, the same procedure can be used to move the progeny toward the genotype of the recurrent parent but at the same time retain many components of the non-recurrent parent by stopping the backcrossing at an early stage and proceeding with selfing and selection. For example, an F1, such as a commercial hybrid, is created. This commercial hybrid may be backcrossed to one of its parent varieties to create a BC1 or BC2. Progeny are selfed and selected so that the newly developed inbred has many of the attributes of the recurrent parent and yet several of the desired attributes of the non-recurrent parent. This approach leverages the value and strengths of the recurrent parent for use in new hybrids and breeding.

Therefore, an embodiment of this invention is a method of obtaining a molecular marker profile of maize inbred variety PHE2E and using the molecular marker profile to select for a progeny plant with the desired trait and the molecular marker profile of PHE2E.

Recurrent Selection and Mass Selection

Recurrent selection is a method used in a plant breeding program to improve a population of plants. PHE2E is suitable for use in a recurrent selection program. The method entails individual plants cross pollinating with each other to form progeny. The progeny are grown and the superior progeny selected by any number of selection methods, which include individual plant, half-sib progeny, full-sib progeny, selfed progeny and topcrossing. The selected progeny are cross pollinated with each other to form progeny for another population. This population is planted and again superior plants are selected to cross pollinate with each other. Recurrent selection is a cyclical process and therefore can be repeated as many times as desired. The objective of recurrent selection is to improve the traits of a population. The improved population can then be used as a source of breeding material to obtain inbred varieties to be used in hybrids or used as parents for a synthetic cultivar. A synthetic cultivar is the resultant progeny formed by the intercrossing of several selected inbreds.

PHE2E is suitable for use in mass selection. Mass selection is a useful technique when used in conjunction with molecular marker enhanced selection. In mass selection seeds from individuals are selected based on phenotype and/or genotype. These selected seeds are then bulked and used to grow the next generation. Bulk selection requires growing a population of plants in a bulk plot, allowing the plants to self-pollinate, harvesting the seed in bulk and then using a sample of the seed harvested in bulk to plant the next generation. Instead of self pollination, directed pollination could be used as part of the breeding program.

Mutation Breeding

Mutation breeding is one of many methods that could be used to introduce new traits into PHE2E. PHE2E is suitable for use in a mutation breeding program. Mutations that occur spontaneously or are artificially induced can be useful sources of variability for a plant breeder. The goal of artificial mutagenesis is to increase the rate of mutation for a desired characteristic. Mutation rates can be increased by many different means including temperature, long-term seed storage, tissue culture conditions, radiation; such as X-rays, Gamma rays (e.g. cobalt 60 or cesium 137), neutrons, (product of nuclear fission by uranium 235 in an atomic reactor), Beta radiation (emitted from radioisotopes such as phosphorus 32 or carbon 14), or ultraviolet radiation (preferably from 2500 to 2900 nm), or chemical mutagens (such as base analogues (5-bromo-uracil), related compounds (8-ethoxy caffeine), antibiotics (streptonigrin), alkylating agents (sulfur mustards, nitrogen mustards, epoxides, ethylenamines, sulfates, sulfonates, sulfones, lactones), azide, hydroxylamine, nitrous acid, or acridines. Once a desired trait is observed through mutagenesis the trait may then be incorporated into existing germplasm by traditional breeding techniques, such as backcrossing. Details of mutation breeding can be found in "Principles of Cultivar Development" Fehr, 1993 Macmillan Publishing Company, the disclosure of which is incorporated herein by reference. In addition, mutations created in other varieties may be used to produce a backcross conversion of PHE2E that comprises such mutation.

Breeding with Molecular Markers

Molecular markers, which includes markers identified through the use of techniques such as Isozyme Electrophoresis, Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs), may be used in plant breeding methods utilizing PHE2E.

Isozyme Electrophoresis and RFLPs as discussed in Lee, M., "Inbred Lines of Maize and Their Molecular Markers," *The Maize Handbook*, (Springer-Verlag, New York, Inc. 1994, at 423-432), have been widely used to determine genetic composition. Isozyme Electrophoresis has a relatively low number of available markers and a low number of allelic variants among maize inbreds. RFLPs allow more discrimination because they have a higher degree of allelic variation in maize and a larger number of markers can be found. Both of these methods have been eclipsed by SSRs as discussed in Smith et al., "An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays* L.): comparisons with data from RFLPs and pedigree", *Theoretical and Applied Genetics* (1997) vol. 95 at 163-173 and by Pejic et al., "Comparative analysis of genetic similarity among maize inbreds detected by RFLPs, RAPDs, SSRs, and AFLPs,"

Theoretical and Applied Genetics (1998) at 1248-1255 incorporated herein by reference. SSR technology is more efficient and practical to use than RFLPs; more marker loci can be routinely used and more alleles per marker locus can be found using SSRs in comparison to RFLPs. Single Nucleotide Polymorphisms may also be used to identify the unique genetic composition of the invention and progeny varieties retaining that unique genetic composition. Various molecular marker techniques may be used in combination to enhance overall resolution.

Maize DNA molecular marker linkage maps have been rapidly constructed and widely implemented in genetic studies. One such study is described in Boppenmaier, et al., "Comparisons among strains of inbreds for RFLPs", Maize Genetics Cooperative Newsletter, 65:1991, pg. 90, is incorporated herein by reference.

One use of molecular markers is Quantitative Trait Loci (QTL) mapping. QTL mapping is the use of markers, which are known to be closely linked to alleles that have measurable effects on a quantitative trait. Selection in the breeding process is based upon the accumulation of markers linked to the positive effecting alleles and/or the elimination of the markers linked to the negative effecting alleles from the plant's genome.

Molecular markers can also be used to reduce the number of crosses back to the recurrent parent needed in a backcrossing program. With backcrossing, the expected contribution of PHE2E after 2, 3, 4 and 5 doses (or 1, 2, 3 and 4 backcrosses) would be 75%, 87.5%, 93.75% and 96.875% respectively. Actual genetic contribution may be much higher than the genetic contribution expected by pedigree, especially if molecular markers are used in selection. The use of molecular markers in the selection process is often called genetic marker enhanced selection. Molecular markers could also be used to confirm and/or determine the pedigree of the progeny variety.

Production of Double Haploids

The production of double haploids can also be used for the development of inbreds in the breeding program. For example, an F1 hybrid for which PHE2E is a parent can be used to produce double haploid plants. Double haploids are produced by the doubling of a set of chromosomes (1N) from a heterozygous plant to produce a completely homozygous individual. For example, see Wan et al., "Efficient Production of Doubled Haploid Plants Through Colchicine Treatment of Anther-Derived Maize Callus", Theoretical and Applied Genetics, 77:889-892, 1989 and US2003/0005479. This can be advantageous because the process omits the generations of selfing needed to obtain a homozygous plant from a heterozygous source.

Haploid induction systems have been developed for various plants to produce haploid tissues, plants and seeds. The haploid induction system can produce haploid plants from any genotype by crossing a selected variety (as female) with an inducer variety. Such inducer varieties for maize include Stock 6 (Coe, 1959, *Am. Nat.* 93:381-382; Sharkar and Coe, 1966, *Genetics* 54:453-464) RWS (see world wide web site www.uni-hohenheim.de/%7Eipspwww/350b/indexe.html#Project3), KEMS (Deimling, Roeber, and Geiger, 1997, *Vortr. Pflanzenzuchtg* 38:203-224), or KMS and ZMS (Chalyk, Bylich & Chebotar, 1994, *MNL* 68:47; Chalyk & Chebotar, 2000, *Plant Breeding* 119:363-364), and indeterminate gametophyte (ig) mutation (Kermicle 1969 *Science* 166:1422-1424). The disclosures of which are incorporated herein by reference.

Methods for obtaining haploid plants are also disclosed in Kobayashi, M. et al., *Journ. of Heredity* 71(1):9-14, 1980, Pollacsek, M., Agronomie (Paris) 12(3):247-251, 1992; Cho-Un-Haing et al., *Journ. of Plant Biol.*, 1996, 39(3):185-188; Verdoodt, L., et al., February 1998, 96(2):294-300; Genetic Manipulation in Plant Breeding, Proceedings International Symposium Organized by EUCARPIA, Sep. 8-13, 1985, Berlin, Germany; Chalyk et al., 1994, Maize Genet Coop. Newsletter 68:47; Chalyk, S. T., 1999, *Maize Genet. Coop. Newsletter* 73:53-54; Coe, R. H., 1959, *Am. Nat.* 93:381-382; Deimling, S. et al., 1997, *Vortr. Pflanzenzuchtg* 38:203-204; Kato, A., 1999, *J. Hered.* 90:276-280; Lashermes, P. et al., 1988, *Theor. Appl. Genet.* 76:570-572 and 76:405-410; Tyrnov, V. S. et al., 1984, Dokl. Akad. Nauk. SSSR 276:735-738; Zabirova, E. R. et al., 1996, Kukuruza I Sorgo N4, 17-19; Aman, M. A., 1978, *Indian J. Genet Plant Breed* 38:452-457; Chalyk S. T., 1994, Euphytica 79:13-18; Chase, S. S., 1952, *Agron. J.* 44:263-267; Coe, E. H., 1959, *Am. Nat.* 93:381-382; Coe, E. H., and Sarkar, K. R., 1964 *J. Hered.* 55:231-233; Greenblatt, I. M. and Bock, M., 1967, *J. Hered.* 58:9-13; Kato, A., 1990, *Maize Genet. Coop. Newsletter* 65:109-110; Kato, A., 1997, *Sex. Plant Reprod.* 10:96-100; Nanda, D. K. and Chase, S. S., 1966, *Crop Sci.* 6:213-215; Sarkar, K. R. and Coe, E. H., 1966, *Genetics* 54:453-464; Sarkar, K. R. and Coe, E. H., 1971, *Crop Sci.* 11:543-544; Sarkar, K. R. and Sachan J. K. S., 1972, *Indian J. Agric. Sci.* 42:781-786; Kermicle J. L., 1969, Mehta Yeshwant, M. R., Genetics and Molecular Biology, September 2000, 23(3):617-622; Tahir, M. S. et al. Pakistan Journal of Scientific and Industrial Research, August 2000, 43(4):258-261; Knox, R. E. et al. Plant Breeding, August 2000, 119(4):289-298; U.S. Pat. No. 5,639,951 and U.S. patent application Ser. No. 10/121,200, the disclosures of which are incorporated herein by reference.

Thus, an embodiment of this invention is a process for making a homozygous PHE2E progeny plant substantially similar to PHE2E by producing or obtaining a seed from the cross of PHE2E and another maize plant and applying double haploid methods to the F1 seed or F1 plant or to any successive filial generation. Such methods decrease the number of generations required to produce an inbred with similar genetics or characteristics to PHE2E. See Bernardo, R. and Kahler, A. L., Theor. Appl. Genet. 102:986-992, 2001.

In particular, a process of making seed substantially retaining the molecular marker profile of maize inbred variety PHE2E is contemplated, such process comprising obtaining or producing F1 hybrid seed for which maize inbred variety PHE2E is a parent, inducing double haploids to create progeny without the occurrence of meiotic segregation, obtaining the molecular marker profile of maize inbred variety PHE2E, and selecting progeny that retain the molecular marker profile of PHE2E.

Use of PHE2E in Tissue Culture

This invention is also directed to the use of PHE2E in tissue culture. As used herein, the term "tissue culture" includes plant protoplasts, plant cell tissue culture, cultured microspores, plant calli, plant clumps, and the like. As used herein, phrases such as "growing the seed" or "grown from the seed" include embryo rescue, isolation of cells from seed for use in tissue culture, as well as traditional growing methods.

Duncan, Williams, Zehr, and Widholm, Planta (1985) 165: 322-332 reflects that 97% of the plants cultured that produced callus were capable of plant regeneration. Subsequent experiments with both inbreds and hybrids produced 91% regenerable callus that produced plants. In a further study in 1988, Songstad, Duncan & Widholm in *Plant Cell Reports* (1988), 7:262-265 reports several media additions that enhance regenerability of callus of two inbred varieties. Other pub-

lished reports also indicated that "nontraditional" tissues are capable of producing somatic embryogenesis and plant regeneration. K. P. Rao, et al., *Maize Genetics Cooperation Newsletter,* 60:64-65 (1986), refers to somatic embryogenesis from glume callus cultures and B. V. Conger, et al., *Plant Cell Reports,* 6:345-347 (1987) indicates somatic embryogenesis from the tissue cultures of maize leaf segments. Thus, it is clear from the literature that the state of the art is such that these methods of obtaining plants are, and were, "conventional" in the sense that they are routinely used and have a very high rate of success.

Tissue culture of maize, including tassel/anther culture, is described in U.S. 2002/0062506A1 and European Patent Application, publication EP0160,390, each of which are incorporated herein by reference for this purpose. Maize tissue culture procedures are also described in Green and Rhodes, "Plant Regeneration in Tissue Culture of Maize," *Maize for Biological Research* (Plant Molecular Biology Association, Charlottesville, Va. 1982, at 367-372) and in Duncan, et al., "The Production of Callus Capable of Plant Regeneration from Immature Embryos of Numerous *Zea Mays* Genotypes," 165 *Planta* 322-332 (1985). Thus, another aspect of this invention is to provide cells which upon growth and differentiation produce maize plants having the genotype and/or physiological and morphological characteristics of inbred variety PHE2E.

INDUSTRIAL APPLICABILITY

Maize is used as human food, livestock feed, and as raw material in industry. The food uses of maize, in addition to human consumption of maize kernels, include both products of dry- and wet-milling industries. The principal products of maize dry milling are grits, meal and flour. The maize wet-milling industry can provide maize starch, maize syrups, and dextrose for food use. Maize oil is recovered from maize germ, which is a by-product of both dry- and wet-milling industries.

Maize, including both grain and non-grain portions of the plant, is also used extensively as livestock feed, primarily for beef cattle, dairy cattle, hogs, and poultry.

Industrial uses of maize include production of ethanol, maize starch in the wet-milling industry and maize flour in the dry-milling industry. The industrial applications of maize starch and flour are based on functional properties, such as viscosity, film formation, adhesive properties, and ability to suspend particles. The maize starch and flour have application in the paper and textile industries. Other industrial uses include applications in adhesives, building materials, foundry binders, laundry starches, explosives, oil-well muds, and other mining applications.

Plant parts other than the grain of maize are also used in industry: for example, stalks and husks are made into paper and wallboard and cobs are used for fuel and to make charcoal.

The seed of inbred maize variety PHE2E, the plant produced from the inbred seed, the hybrid maize plant produced from the crossing of the inbred, hybrid seed, and various parts of the hybrid maize plant and transgenic versions of the foregoing, can be utilized for human food, livestock feed, and as a raw material in industry.

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DEPOSITS

Applicant has made a deposit of at least 2500 seeds of Inbred Maize Variety PHE2E with the American Type Culture Collection (ATCC), Manassas, Va. 20110 USA, ATCC Deposit No. PTA-7521. The seeds deposited with the ATCC on Apr. 14, 2006 will be taken from the deposit maintained by Pioneer Hi-Bred International, Inc., 7250 NW 62nd Avenue, Johnston, Iowa, 50131 since prior to the filing date of this application. Access to this deposit will be available during the pendency of the application to the Commissioner of Patents and Trademarks and persons determined by the Commissioner to be entitled thereto upon request. Upon allowance of any claims in the application, the Applicant will make the deposit available to the public pursuant to 37 C.F.R. §1.808. This deposit of the Inbred Maize Variety PHE2E will be maintained in the ATCC depository, which is a public depository, for a period of 30 years, or 5 years after the most recent request, or for the enforceable life of the patent, whichever is longer, and will be replaced if it becomes nonviable during that period. Additionally, Applicant has or will satisfy all of the requirements of 37 C.F.R. §§1.801-1.809, including providing an indication of the viability of the sample upon deposit. Applicant has no authority to waive any restrictions imposed by law on the transfer of biological material or its transportation in commerce. Applicant does not waive any infringement of rights granted under this patent or under the Plant Variety Protection Act (7 USC 2321 et seq.). U.S. Plant Variety Protection of Inbred Maize Variety PHE2E has been applied for. Unauthorized seed multiplication prohibited.

TABLE 1

VARIETY DESCRIPTION INFORMATION
PHE2E

1. TYPE: (Describe intermediate types in comments section)					AVG	STDEV	N
1 = Sweet, 2 = Dent, 3 = Flint, 4 = Flour, 5 = Pop and 6 = Ornamental.					3		
Comments: Flint-Dent							
2. MATURITY: DAYS HEAT UNITS					Days	H. Units	
Emergence to 50% of plants in silk					65	1,509	
Emergence to 50% of plants in pollen shed					63	1,463	
10% to 90% pollen shed					2	56	
50% Silk to harvest at 25% moisture							
3. PLANT:							
Plant Height (to tassel tip) (cm)					244.0	11.99	25
Ear Height (to base of top ear node) (cm)					87.6	8.86	25
Length of Top Ear Internode (cm)					16.2	1.94	25
Average Number of Tillers per Plant					0.0	0.02	5
Average Number of Ears per Stalk					1.1	0.20	5
Anthocyanin of Brace Roots: 1 = Absent, 2 = Faint,					4		
3 = Moderate, 4 = Dark							
4. LEAF:							
Width of Ear Node Leaf (cm)					9.6	0.65	25
Length of Ear Node Leaf (cm)					86.8	5.43	25
Number of Leaves above Top Ear					7.1	0.76	25
Leaf Angle: (at anthesis, 2nd leaf above ear to					26.1	3.96	25
stalk above leaf) (Degrees)							
*Leaf Color:	V. Dark Green	Munsell:	5GY34				
Leaf Sheath Pubescence: 1 = none to 9 = like peach fuzz					2		
5. TASSEL:							
Number of Primary Lateral Branches					5.4	1.80	25
Branch Angle from Central Spike					42.8	11.00	25
Tassel Length: (from peduncle node to tassel tip), (cm).					58.8	3.30	25
Pollen Shed: 0 = male sterile, 9 = heavy shed					5		
*Anther Color:	Light Red	Munsell:	2.5R58				
*Glume Color:	Red	Munsell:	7.5RP38				
*Bar Glumes (glume bands): 1 = absent, 2 = present					1		
Peduncle Length: (from top leaf node to lower florets or					22.9	2.08	25
branches), (cm).							
6a. EAR (Unhusked ear)							
*Silk color:	Light Red	Munsell:	5R58				
(3 days after silk emergence)							
*Fresh husk color:	Med. Green	Munsell:	5GY68				
*Dry husk color:	Buff	Munsell:	2.5Y84				
(65 days after 50% silking)							
Ear position at dry husk stage: 1 = upright, 2 = horizontal,					1		
3 = pendant							
Husk Tightness: (1 = very loose, 9 = very tight)					7		
Husk Extension (at harvest): 1 = short(ears exposed),					2		
2 = medium (<8 cm), 3 = long (8-10 cm), 4 = v. long (>10 cm)							

TABLE 1-continued

VARIETY DESCRIPTION INFORMATION
PHE2E

6b. EAR (Husked ear data)			
Ear Length (cm):	14.9	1.04	25
Ear Diameter at mid-point (mm)	45.0	1.31	25
Ear Weight (gm):	138.4	19.23	25
Number of Kernel Rows:	14.1	0.70	25
Kernel Rows: 1 = indistinct, 2 = distinct	2		
Row Alignment: 1 = straight, 2 = slightly curved, 3 = spiral	2		
Shank Length (cm):	8.7	1.54	25
Ear Taper: 1 = slight cylind., 2 = average, 3 = extreme conic.	2		
7. KERNEL (Dried):			
Kernel Length (mm):	12.3	0.68	25
Kernel Width (mm):	8.9	0.70	25
Kernel Thickness (mm):	4.3	0.56	25
Round Kernels (shape grade) (%)	41.4	15.49	5
Aleurone Color Pattern: 1 = homozygous, 2 = segregating	1		
*Aleurone Color: Yellow Munsell: 10YR714			
*Hard Endo. Color: Yellow Munsell: 10YR610			
Endosperm Type:	3		
1 = sweet (su1), 2 = extra sweet (sh2), 3 = normal starch,			
4 = high amylose starch, 5 = waxy starch, 6 = high protein,			
7 = high lysine, 8 = super sweet (se), 9 = high oil, 10 = other			
Weight per 100 Kernels (unsized sample) (gm):	33.8	1.64	5
8. COB:			
*Cob Diameter at mid-point (mm):	23.4	0.71	25
*Cob Color: Red Munsell: 2.5YR38			

9. DISEASE RESISTANCE:

(Rate from 1 = most-susceptable to 9 = most-resistant. Leave blank if not tested,

leave race or strain options blank if polygenic.)

A. LEAF BLIGHTS, WILTS, AND LOCAL INFECTION DISEASES

Anthracnose Leaf Blight (*Colletotrichum graminicola*)

6 Common Rust (*Puccinia sorghi*)

9 Common Smut (*Ustilago maydis*)

Eyespot (*Kabatiella zeae*)

Goss's Wilt (*Clavibacter michiganense* spp. *nebraskense*)

5 Gray Leaf Spot (*Cercospora zeae-maydis*)

Helminthosporium Leaf Spot (*Bipolaris zeicola*) Race:

5 Northern Leaf Blight (*Exserohilum turcicum*) Race:

6 Southern Leaf Blight (*Bipolaris maydis*) Race:

Southern Rust (*Puccinia polysora*)

6 Stewart's Wilt (*Erwinia stewartii*)

Other (Specify): _____

B. SYSTEMIC DISEASES

Corn Lethal Necrosis (MCMV and MDMV)

5 Head Smut (*Sphacelotheca reiliana*) (% infected)

Maize Chlorotic Dwarf Virus (MDV)

Maize Chlorotic Mottle Virus (MCMV)

Maize Dwarf Mosaic Virus (MDMV)

Sorghum Downy Mildew of Corn (*Peronosclerospora sorghi*)

Other (Specify): _____

C. STALK ROTS

6 Anthracnose Stalk Rot (*Colletotrichum graminicola*)

Diplodia Stalk Rot (*Stenocarpella maydis*)

Fusarium Stalk Rot (*Fusarium moniliforme*)

Gibberella Stalk Rot (*Gibberella zeae*)

Other (Specify): _____

D. EAR AND KERNEL ROTS

Aspergillus Ear and Kernel Rot (*Aspergillus flavus*)

4 Diplodia Ear Rot (*Stenocarpella maydis*)

6 *Fusarium* Ear and Kernel Rot (*Fusarium moniliforme*)

Gibberella Ear Rot (*Gibberella zeae*)

Other (Specify): _____

10. INSECT RESISTANCE:

(Rate from 1 = most-suscept. to 9 = most-resist., leave blank if not tested.)

Corn Worm (*Helicoverpa zea*)

__ Leaf Feeding

__ Silk Feeding

__ Ear Damage

Corn Leaf Aphid (*Rophalosiphum maydis*)

Corn Sap Beetle (*Capophilus dimidiatus*)

European Corn Borer (*Ostrinia nubilalis*)

1st. Generation (Typically whorl leaf feeding)

2nd. Generation (Typically leaf sheath-collar feeding)

__ Stalk Tunneling

__ cm tunneled/plant

Fall armyworm (*Spodoptera fruqiperda*)

TABLE 1-continued

VARIETY DESCRIPTION INFORMATION
PHE2E

__ Leaf Feeding
__ Silk Feeding
__ mg larval wt.
Maize Weevil (*Sitophilus zeamaize*)
Northern Rootworm (*Diabrotica barberi*)
Southern Rootworm (*Diabrotica undecimpunctata*)
Southwestern Corn Borer (*Diatreaea grandiosella*)
__ Leaf Feeding
__ Stalk Tunneling
__ cm tunneled/plant
Two-spotted Spider Mite (*Tetranychus utricae*)
Western Rootworm (*Diabrotica virgifrea virgifrea*)
Other (Specify): _____

11. AGRONOMIC TRAITS:

7	Staygreen (at 65 days after anthesis; rate from 1-worst to 9-excellent)
	% Dropped Ears (at 65 days after anthesis)
	% Pre-anthesis Brittle Snapping
0	% Pre-anthesis Root Lodging
8	% Post-anthesis Root Lodging (at 65 days after anthesis)
0	% Post-anthesis Stalk Lodging
6,075.0	Kg/ha (Yield at 12-13% grain moisture)

*Munsell Glossy Book of Color, (A standard color reference). Kollmorgen Inst. Corp. New Windsor, NY.

TABLE 2

SSR PROFILE DATA FOR PHE2E.

Marker Name	Chromosome	Location	Base Pairs
BNLG1014	1	82.8	132.8
PHI427913	1	108.3	130.3
BNLG1127	1	167.5	115.8
BNLG1953	1	170	248.5
BNLG1064	1	201.3	223.1
BNLG439	1	259.1	234.6
PHI339017	1	270.6	146.6
BNLG1886	1	377.2	146.8
BNLG1832	1	381.3	217
BNLG2086	1	401.2	218.7
BNLG1615	1	557.6	212.5
PHI323065	1	777.4	329.8
PHI335539	1	805.3	89.1
BNLG1720	1	834.5	238.1
PHI308707	1	927.4	129.6
PHI265454	1	973	236.2
PHI227562	1	1097.4	308.4
PHI064	1	1103	96.2
PHI402893	2	3.8	219.3
PHI96100	2	28.1	285.9
BNLG1017	2	65.7	196.3
BNLG1909	2	270.7	304.5
PHI083	2	284.7	132.3
BNLG1396	2	372.8	138
BNLG1141	2	374.9	154.3
BNLG1138	2	379.2	223.2
PHI127	2	422.7	110.1
PHI328189	2	422.7	116.3
PHI251315	2	453.8	125.1
PHI435417	2	520.5	218.8
PHI090	2	548.3	139.1
BNLG1940	2	577.6	215.2
BNLG1520	2	605.8	286.7
PHI427434	2	712.1	131.5
PHI101049	2	712.1	236.1
PHI404206	3	11	304.1
BNLG1523	3	81.5	265.6
PHI243966	3	163.8	220.3
BNLG1452	3	190.8	126.3
PHI029	3	192.3	147.7
PHI073	3	229.7	186.4
PHI053	3	297.9	172.4

TABLE 2-continued

SSR PROFILE DATA FOR PHE2E.

Marker Name	Chromosome	Location	Base Pairs
BNLG1951	3	481.6	121.8
BNLG1160	3	491.4	223.5
PHI193225	3	791.6	138.5
PHI213984	4	130.1	285.7
BNLG1937	4	232	228.7
PHI096	4	232.2	235.5
PHI079	4	254	179.2
BNLG1265	4	268.4	225
BNLG1755	4	299.9	216
PHI438301	4	452.9	212.8
PHI093	4	522.1	287.3
PHI314704	4	655	153.9
PHI396160	5	307	299.2
PHI331888	5	324.3	131.2
PHI330507	5	389.9	142.4
BNLG1711	5	666.5	177
PHI423796	6	72.7	129.7
PHI389203	6	269.8	306.7
PHI452693	6	278	131.7
PHI445613	6	375.8	98.3
PHI364545	6	428.4	132.7
PHI299852	6	450.7	118.2
BNLG2271	7	383.8	235.4
PHI328175	7	472.9	99.4
PHI420701	8	99.6	290.3
PHI100175	8	274.9	138.3
PHI233376	8	609.1	137.5
PHI448880	9	536.8	187.2
PHI236654	9	538.5	124.5
BNLG1129	9	633.6	301.5
PHI059	10	143.5	154.4
PHI301654	10	309	129.2
PHI323152	10	468.4	141.2
BNLG1450	10	483.7	178.2
BNLG1185	10	529.1	189.9

TABLE 3A

PAIRED INBRED COMPARISON REPORT
Variety #1: PHE2E
Variety #2: PH6CF

Stat	YIELD BU/A 56# ABS	GLFSPT SCORE ABS	YIELD BU/A 56# % MN	MST PCT ABS	TSTWT LB/BU ABS	FUSERS SCORE ABS
Mean1	99.9	4.8	105.4	27.9	55.0	7.6
Mean2	62.6	4.4	66.2	26.8	53.3	8.0
Locs	27	5	27	27	6	5
Reps	52	5	52	52	12	5
Diff	37.3	0.4	39.2	−1.1	1.7	−0.4
Prob	0.000	0.374	0.000	0.055	0.379	0.178

Stat	EGRWTH SCORE ABS	STWWLT SCORE ABS	ESTCNT COUNT ABS	TILLER PCT ABS	GDUSHD GDU ABS	GDUSLK GDU ABS
Mean1	6.4	6.0	31.2	9.3	151.5	153.6
Mean2	6.5	7.0	34.6	1.3	146.5	150.6
Locs	15	1	16	27	58	56
Reps	15	1	18	27	58	56
Diff	−0.1	−1.0	−3.4	−8.0	5.0	3.0
Prob	0.582	.	0.040	0.004	0.000	0.000

Stat	SLFBLT SCORE ABS	POLWT VALUE ABS	POLWT VALUE % MN	TASBLS SCORE ABS	SOURST SCORE ABS	TASSZ SCORE ABS
Mean1	7.0	116.5	89.0	9.0	6.0	4.7
Mean2	7.0	120.6	90.1	9.0	7.0	4.9
Locs	1	10	10	1	1	55
Reps	1	19	19	1	1	55
Diff	0.0	−4.1	−1.2	0.0	−1.0	−0.2
Prob	.	0.750	0.914	.	.	0.175

Stat	PLTHT CM ABS	COMRST SCORE ABS	EARHT CM ABS	STAGRN SCORE ABS	BRTSTK % NOT ABS	SCTGRN SCORE ABS
Mean1	249.6	8.0	90.9	6.7	98.3	8.3
Mean2	226.8	7.5	82.9	6.2	99.6	7.0
Locs	44	2	28	9	2	6
Reps	45	2	29	9	4	6
Diff	22.8	0.5	7.9	0.4	−1.3	1.3
Prob	0.000	0.795	0.003	0.104	0.500	0.043

Stat	STLPCN % NOT ABS	BARPLT % NOT ABS	LRTLPN % NOT ABS	CLDTST PCT ABS	ERTLPN % NOT ABS	CLDTST PCT % MN
Mean1	100.0	91.2	93.3	94.4	99.4	99.9
Mean2	100.0	81.3	98.3	95.3	100.0	
Locs	1	28	3	9	4	
Reps	2	29	6	9	5	
Diff	0.0	9.8	−5.0	−0.9	−0.6	
Prob	.	0.033	0.423	0.673	0.391	

TABLE 3B

PAIRED INBRED COMPARISON REPORT
Variety #1: PHE2E
Variety #2: PHC77

Stat	YIELD BU/A 56# ABS	GLFSPT SCORE ABS	YIELD BU/A 56# % MN	NLFBLT SCORE ABS	MST PCT ABS	TSTWT LB/BU ABS
Mean1	105.7	5.0	107.9	5.5	26.7	60.5
Mean2	73.2	5.0	76.0	4.1	25.0	59.5
Locs	30	15	30	4	37	1
Reps	157	23	157	8	166	2
Diff	32.5	0.0	31.9	1.4	−1.7	1.0
Prob	0.000	0.885	0.000	0.115	0.008	.

TABLE 3B-continued

PAIRED INBRED COMPARISON REPORT
Variety #1: PHE2E
Variety #2: PHC77

Stat	FUSERS SCORE ABS	EGRWTH SCORE ABS	STWWLT SCORE ABS	ESTCNT COUNT ABS	DIPERS SCORE ABS	TILLER PCT ABS
Mean1	5.9	6.4	5.8	27.3	4.5	11.2
Mean2	5.5	6.2	3.5	27.0	4.6	0.3
Locs	10	15	3	18	6	28
Reps	14	15	4	28	11	28
Diff	0.4	0.2	2.3	0.3	−0.1	−10.9
Prob	0.153	0.550	0.020	0.736	0.856	0.002

Stat	ANTROT SCORE ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	GIBROT SCORE ABS	SLFBLT SCORE ABS	HDSMT % NOT ABS
Mean1	6.2	151.6	153.8	8.0	7.0	93.2
Mean2	6.2	151.1	155.3	7.3	6.5	88.2
Locs	3	68	66	2	2	6
Reps	5	68	66	4	3	12
Diff	0.0	0.5	−1.4	0.8	0.5	5.0
Prob	1.000	0.342	0.025	0.205	0.500	0.229

Stat	TASBLS SCORE ABS	SOURST SCORE ABS	TASSZ SCORE ABS	PLTHT CM ABS	COMRST SCORE ABS	EARHT CM ABS
Mean1	9.0	6.0	4.7	249.7	7.0	91.2
Mean2	9.0	4.0	4.3	237.1	7.3	87.9
Locs	2	1	62	54	3	36
Reps	2	1	62	54	3	36
Diff	0.0	2.0	0.4	12.6	−0.3	3.3
Prob	1.000	.	0.005	0.000	0.742	0.134

Stat	STAGRN SCORE ABS	BRTSTK % NOT ABS	SCTGRN SCORE ABS	STLPCN % NOT ABS	STLLPN % NOT ABS	BARPLT % NOT ABS
Mean1	6.8	98.3	8.4	100.0	90.0	87.1
Mean2	5.8	97.1	9.0	100.0	87.5	85.0
Locs	12	2	5	3	1	38
Reps	12	4	5	35	2	114
Diff	1.0	1.3	−0.6	0.0	2.5	2.1
Prob	0.020	0.220	0.208	1.000	.	0.281

Stat	LRTLPN % NOT ABS	CLDTST PCT ABS	ERTLPN % NOT ABS	STKLDG % NOT ABS	CLDTST PCT % MN
Mean1	85.0	93.5	99.4	100.0	100.7
Mean2	92.8	93.3	96.4	100.0	
Locs	2	8	4	1	
Reps	23	8	5	12	
Diff	−7.8	0.3	3.0	0.0	
Prob	0.464	0.870	0.297	.	

TABLE 4

GENERAL COMBINING ABILITY REPORT FOR PHE2E

PRM Day ABS	Mean	118
PRM Day ABS	Reps	2842
PRMSHD Day ABS	Mean	116
PRMSHD Day ABS	Reps	2569
YIELD bu/a 56# ABS	Mean	193.8
YIELD bu/a 56# ABS	Reps	1465
YIELD bu/a 56# ABS	Years	4
YIELD bu/a 56# % MN	Mean	102.1
YIELD bu/a 56# % MN	Reps	1465
MST pct ABS	Mean	22.7
MST pct ABS	Reps	1480
MST pct % MN	Mean	101.9

TABLE 4-continued

GENERAL COMBINING ABILITY REPORT FOR PHE2E

MST pct % MN	Reps	1480
YLDMST ABS	Mean	100
YLDMST ABS	Reps	1469
STLPCN % NOT % MN	Mean	109
STLPCN % NOT % MN	Reps	239
STLLPN % NOT % MN	Mean	108
STLLPN % NOT % MN	Reps	312
ERTLPN % NOT % MN	Mean	96
ERTLPN % NOT % MN	Reps	211
LRTLPN % NOT % MN	Mean	106
LRTLPN % NOT % MN	Reps	486
TSTWT lb/bu % MN	Mean	99.1

TABLE 4-continued

GENERAL COMBINING ABILITY REPORT FOR PHE2E		
TSTWT lb/bu % MN	Reps	1079
STKCNT count % MN	Mean	100
STKCNT count % MN	Reps	2568
PLTHT in % MN	Mean	102
PLTHT in % MN	Reps	506
EARHT in % MN	Mean	99
EARHT in % MN	Reps	512
BRTSTK % NOT % MN	Mean	97
BRTSTK % NOT % MN	Reps	79

TABLE 4-continued

GENERAL COMBINING ABILITY REPORT FOR PHE2E		
GLFSPT score ABS	Mean	5
GLFSPT score ABS	Reps	161
STAGRN score ABS	Mean	5
STAGRN score ABS	Reps	224
HSKCVR score ABS	Mean	6
HSKCVR score ABS	Reps	173
ECBLSI score ABS	Mean	6
ECBLSI score ABS	Reps	229

TABLE 5A

INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PHE2E
Variety #2: 33N56

Stat	YIELD BU/A 56# ABS	GLFSPT SCORE ABS	YIELD BU/A 56# % MN	NLFBLT SCORE ABS	MST PCT ABS	TSTWT LB/BU ABS	ESTCNT COUNT ABS	STKCNT COUNT ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	PLTHT CM ABS
Mean1	192.2	5.0	106.0	5.3	20.6	57.2	48.7	55.5	136.3	134.0	333.5
Mean2	180.3	5.0	99.6	5.3	20.7	56.7	51.7	55.7	141.0	139.5	318.5
Locs	34	2	34	2	34	24	3	47	4	2	13
Reps	34	2	34	3	34	24	3	54	4	2	14
Diff	11.8	0.0	6.3	0.0	0.1	0.5	−3.0	−0.2	−4.8	−5.5	15.0
Prob	0.009	1.000	0.014	1.000	0.819	0.121	0.122	0.182	0.095	0.500	0.000

Stat	EARHT CM ABS	STAGRN SCORE ABS	STLLPN % NOT ABS	STLPCN % NOT ABS	ERTLPN % NOT ABS	ECBLSI SCORE ABS	LRTLPN % NOT ABS	HSKCVR SCORE ABS
Mean1	136.8	5.3	87.8	89.1	92.4	6.1	77.1	6.0
Mean2	142.8	4.3	86.5	74.5	86.0	4.9	68.2	4.0
Locs	13	10	6	11	5	7	7	1
Reps	14	10	8	13	6	7	8	1
Diff	−6.0	1.0	1.3	14.5	6.4	1.3	8.9	2.0
Prob	0.067	0.085	0.873	0.097	0.516	0.063	0.599	.

TABLE 5B

INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PHE2E
Variety #2: 31D24

Stat	YIELD BU/A 56# ABS	GLFSPT SCORE ABS	YIELD BU/A 56# % MN	NLFBLT SCORE ABS	SLFBLT SCORE ABS	MST PCT ABS
Mean1	193.9	4.6	103.4	5.6	5.0	22.0
Mean2	196.2	4.6	104.6	5.6	7.0	23.1
Locs	50	3	50	5	1	50
Reps	58	7	58	8	1	59
Diff	−2.3	0.1	−1.2	0.0	−2.0	1.1
Prob	0.538	0.840	0.556	1.000	.	0.000

Stat	TSTWT LB/BU ABS	ANTROT SCORE ABS	EGRWTH SCORE ABS	FUSERS SCORE ABS	ESTCNT COUNT ABS	STKCNT COUNT ABS
Mean1	55.7	5.7	6.0	6.0	53.0	50.1
Mean2	55.1	4.2	5.0	5.0	59.5	50.8
Locs	35	3	5	1	2	77
Reps	43	4	5	2	2	122
Diff	0.6	1.5	1.0	1.0	−6.5	−0.7
Prob	0.148	0.356	0.230	.	0.144	0.017

Stat	DIPERS SCORE ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	PLTHT CM ABS	EARHT CM ABS	STAGRN SCORE ABS
Mean1	5.5	136.7	136.9	349.3	143.8	5.2
Mean2	4.5	137.9	137.5	325.3	138.5	4.8

TABLE 5B-continued

INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PHE2E
Variety #2: 31D24

Locs	2	10	10	12	12	5
Reps	4	13	13	13	13	5
Diff	1.0	−1.3	−0.6	24.0	5.3	0.4
Prob	1.000	0.110	0.357	0.000	0.150	0.587

Stat	GIBROT SCORE ABS	HDSMT % NOT ABS	STLLPN % NOT ABS	STLPCN % NOT ABS	ERTLPN % NOT ABS	ECBLSI SCORE ABS
Mean1	6.3	93.0	88.6	92.5	48.9	5.9
Mean2	7.0	74.9	80.4	50.0	90.0	5.7
Locs	1	3	6	2	7	11
Reps	3	8	16	3	10	11
Diff	−0.7	18.1	8.2	42.5	−41.1	0.2
Prob	.	0.062	0.376	0.460	0.024	0.691

Stat	LRTLPN % NOT ABS	BRTSTK % NOT ABS	HSKCVR SCORE ABS
Mean1	80.6	98.4	5.2
Mean2	85.3	98.4	5.3
Locs	20	2	6
Reps	29	2	6
Diff	−4.7	0.0	−0.2
Prob	0.481	0.982	0.363

TABLE 5C

INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PHE2E
Variety #2: 31G98

Stat	YIELD BU/A 56# ABS	GLFSPT SCORE ABS	YIELD BU/A 56# % MN	NLFBLT SCORE ABS	SLFBLT SCORE ABS	MST PCT ABS
Mean1	193.7	4.6	103.5	5.6	5.0	21.9
Mean2	185.4	4.6	99.5	6.3	3.0	21.8
Locs	51	3	51	5	1	51
Reps	60	7	60	8	1	60
Diff	8.2	0.0	4.0	−0.7	2.0	−0.1
Prob	0.037	1.000	0.052	0.052	.	0.789

Stat	TSTWT LB/BU ABS	ANTROT SCORE ABS	EGRWTH SCORE ABS	FUSERS SCORE ABS	ESTCNT COUNT ABS	STKCNT COUNT ABS
Mean1	55.7	5.7	6.0	6.0	53.0	50.6
Mean2	55.1	5.7	6.2	5.0	58.5	51.7
Locs	36	3	5	1	2	84
Reps	44	5	5	2	2	135
Diff	0.6	0.0	−0.2	1.0	−5.5	−1.1
Prob	0.090	1.000	0.621	.	0.058	0.000

Stat	DIPERS SCORE ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	PLTHT CM ABS	EARHT CM ABS	STAGRN SCORE ABS
Mean1	5.5	136.7	136.9	340.7	143.1	5.2
Mean2	4.8	141.2	141.4	333.0	152.5	3.8
Locs	2	10	10	18	18	5
Reps	4	13	13	23	23	5
Diff	0.8	−4.5	−4.4	7.7	−9.4	1.4
Prob	0.500	0.000	0.000	0.124	0.011	0.280

Stat	GIBROT SCORE ABS	HDSMT % NOT ABS	STLLPN % NOT ABS	STLPCN % NOT ABS	ERTLPN % NOT ABS	ECBLSI SCORE ABS
Mean1	6.3	93.0	88.6	91.3	48.9	5.9
Mean2	9.0	92.9	79.2	72.5	82.1	4.7
Locs	1	3	6	4	7	11

TABLE 5C-continued

INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PHE2E
Variety #2: 31G98

Reps	3	8	17	5	10	11
Diff	−2.7	0.0	9.4	18.8	−33.2	1.2
Prob	.	0.985	0.283	0.122	0.037	0.019

Stat	LRTLPN % NOT ABS	BRTSTK % NOT ABS	HSKCVR SCORE ABS
Mean1	80.3	98.4	5.2
Mean2	64.7	94.6	5.2
Locs	22	2	5
Reps	31	2	5
Diff	15.7	3.7	0.0
Prob	0.036	0.688	1.000

TABLE 5D

INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PHE2E
Variety #2: 32B14

Stat	YIELD BU/A 56# ABS	GLFSPT SCORE ABS	YIELD BU/A 56# % MN	NLFBLT SCORE ABS	SLFBLT SCORE ABS	MST PCT ABS
Mean1	193.3	4.6	103.3	5.6	5.0	21.9
Mean2	180.5	4.0	96.6	5.0	4.0	22.7
Locs	52	3	52	5	1	52
Reps	60	7	60	8	1	60
Diff	12.7	0.6	6.7	0.6	1.0	0.8
Prob	0.000	0.311	0.001	0.284	.	0.002

Stat	TSTWT LB/BU ABS	ANTROT SCORE ABS	EGRWTH SCORE ABS	FUSERS SCORE ABS	ESTCNT COUNT ABS	STKCNT COUNT ABS
Mean1	55.7	5.7	6.0	6.0	53.0	50.5
Mean2	56.4	3.5	6.4	3.5	61.0	51.3
Locs	37	3	5	1	2	85
Reps	44	5	5	2	2	133
Diff	−0.7	2.2	−0.4	2.5	−8.0	−0.8
Prob	0.011	0.329	0.374	.	0.295	0.010

Stat	DIPERS SCORE ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	PLTHT CM ABS	EARHT CM ABS	STAGRN SCORE ABS
Mean1	5.5	136.7	136.9	340.7	143.1	5.2
Mean2	3.8	140.3	140.8	324.9	145.0	5.4
Locs	2	10	10	18	18	5
Reps	4	13	13	23	23	5
Diff	1.8	−3.6	−3.8	15.8	−1.8	−0.2
Prob	0.258	0.004	0.001	0.002	0.558	0.749

Stat	GIBROT SCORE ABS	HDSMT % NOT ABS	STLLPN % NOT ABS	STLPCN % NOT ABS	ERTLPN % NOT ABS	ECBLSI SCORE ABS
Mean1	6.3	93.0	88.6	91.3	48.9	5.9
Mean2	8.7	89.8	93.3	85.0	53.1	6.5
Locs	1	3	6	4	7	11
Reps	3	8	17	4	10	11
Diff	−2.3	3.2	−4.7	6.3	−4.2	−0.5
Prob	.	0.296	0.444	0.194	0.834	0.052

Stat	LRTLPN % NOT ABS	BRTSTK % NOT ABS	HSKCVR SCORE ABS
Mean1	81.0	98.4	5.2
Mean2	77.6	100.0	5.3
Locs	23	2	6
Reps	32	2	6

TABLE 5D-continued

INBREDS IN HYBRID COMBINATION REPORT Variety #1: HYBRID CONTAINING PHE2E Variety #2: 32B14			
Diff	3.4	−1.6	−0.2
Prob	0.444	0.500	0.611

TABLE 6

PHENOTYPIC DATA FROM HYBRIDS PRODUCED WITH PHE2E.

	PRM Day ABS MEAN	PRM Day ABS REPS	PRMSHD Day ABS MEAN	PRMSHD Day ABS REPS	YIELD bu/a 56# ABS MEAN	YIELD bu/a 56# ABS REPS	YIELD bu/a 56# ABS YRS	YIELD bu/a 56# % MN MEAN	YIELD bu/a 56# % MN REPS
Hybrid 1	118	10			170.9	6	1	95.2	6
Hybrid 2	114	86	115	69	192.5	37	2	100	37
Hybrid 3	112	57			186	9	1	92.8	9
Hybrid 4	117	18			198.7	13	1	96.5	13
Hybrid 5	119	60	109	60	184.2	31	1	96.3	31
Hybrid 6	115	19			181.9	11	1	97.3	11
Hybrid 7	119	55			198.2	25	1	98.2	25
Hybrid 8	113	98			196.6	62	1	102.7	62
Hybrid 9	117	27	110	10	179.8	14	2	96.3	14
Hybrid 10	112	38			185.5	21	1	98.2	21
Hybrid 11	116	18			213	13	1	105.1	13
Hybrid 12	114	19			198.1	13	1	97.8	13
Hybrid 13	117	19			199.2	13	1	98.6	13
Hybrid 14	116	19			197.1	14	1	97.4	14
Hybrid 15	114	18			198.6	12	1	97.3	12
Hybrid 16	120	171	116	171	192.4	118	3	101.9	118
Hybrid 17	118	47			191.6	80	2	103	80
Hybrid 18	119	55	121	36	189	84	3	100.4	84
Hybrid 19	116	38			192.5	20	1	101.5	20
Hybrid 20	119	38			203.8	25	2	103.5	25
Hybrid 21	121	60			196.8	30	2	103	30
Hybrid 22	118	41			186.9	19	1	96.6	19
Hybrid 23	123	60			200.9	30	2	105.2	30
Hybrid 24	119	95	111	95	196.4	63	2	101.8	63
Hybrid 25	117	18			207.7	13	1	103.2	13
Hybrid 26	119	19			195.9	13	1	97.2	13
Hybrid 27	117	19			208.9	12	1	102	12
Hybrid 28	116	18			200.1	12	1	99.3	12
Hybrid 29	115	19			203.3	13	1	101.1	13
Hybrid 30	115	19			205	12	1	101.8	12
Hybrid 31	114	19			203.1	11	1	101.1	11
Hybrid 32	119	19			192.5	13	1	94.9	13
Hybrid 33	115	18			197.6	12	1	99.5	12
Hybrid 34	111	19			199.6	13	1	99	13
Hybrid 35	118	18			212.1	13	1	105.1	13
Hybrid 36	121	19			206.1	14	1	102	14
Hybrid 37	118	19			199.6	13	1	99.1	13
Hybrid 38	118	19			201.8	12	1	100.5	12
Hybrid 39	115	18			203.8	7	1	97.6	7
Hybrid 40	114	18			193.6	13	1	95.9	13
Hybrid 41	117	19			204.9	14	1	101.7	14
Hybrid 42	115	18			211.1	11	1	98.6	11
Hybrid 43	115	19			209.1	13	1	104.1	13
Hybrid 44	117	19			201.8	12	1	99.9	12
Hybrid 45	119	18			211.9	13	1	104.7	13
Hybrid 46	118	33	115	17	187.7	18	2	100.2	18
Hybrid 47	117	37	115	37	197.4	38	2	99.7	38
Hybrid 48	117	191	115	171	192.4	87	3	98.5	87
Hybrid 49	115	27	114	27	185	19	1	104.1	19
Hybrid 50	117	76			200.1	38	2	100.1	38
Hybrid 51	116	71	113	54	201.6	40	3	102.7	40
Hybrid 52	112	92	113	52	192.5	44	2	103.6	44
Hybrid 53	118	71	112	36	199.6	40	3	102.8	40
Hybrid 54	119	72	122	36	197.5	39	3	100.4	39
Hybrid 55	118	21			192.1	12	1	100.3	12
Hybrid 56	114	36			189.7	22	1	99.4	22
Hybrid 57	116	60	116	60	196	35	1	101.6	35
Hybrid 58	117	60			200.3	30	2	104.2	30
Hybrid 59	115	57			193	31	2	101.3	31

TABLE 6-continued

PHENOTYPIC DATA FROM HYBRIDS PRODUCED WITH PHE2E.

Hybrid 60	116	38		208.8	24	2	105.9	24
Hybrid 61	116	57		199.9	30	2	104.5	30
Hybrid 62	117	10		173.6	5	1	94	5
Hybrid 63	120	10		159.9	6	1	88.9	6
Hybrid 64	118	10		182	5	1	98.6	5

	MST pct ABS MEAN	MST pct ABS REPS	MST pct % MN MEAN	MST pct % MN REPS	YLDMST Value ABS MEAN	YLDMST Value ABS REPS	STLPCN % NOT % MN MEAN	STLPCN % NOT % MN REPS
Hybrid 1	21.3	6	95.3	6	99.9	6	29	1
Hybrid 2	21	37	99.5	37	100.5	37	104	11
Hybrid 3	22.3	9	95.1	9	97.7	9	94	2
Hybrid 4	22.5	14	102.3	14	94.2	13	110	4
Hybrid 5	23	31	105.9	31	90.4	31	104	6
Hybrid 6	22.1	11	102.4	11	94.8	11	102	2
Hybrid 7	25.6	26	109.1	26	89.2	25	110	8
Hybrid 8	21.8	66	100.5	66	102.3	62	112	21
Hybrid 9	22.3	14	102	14	94.3	14	111	3
Hybrid 10	21.8	22	95.8	22	102.4	21	111	8
Hybrid 11	23	14	98.8	14	106.4	13	99	3
Hybrid 12	21.9	14	94.1	14	103.8	13	87	3
Hybrid 13	23	14	99.1	14	99.5	13	102	3
Hybrid 14	22.6	15	94.1	15	103.4	14	114	4
Hybrid 15	22.6	13	95.6	13	102.1	12	129	3
Hybrid 16	23.5	121	108.2	121	93.8	118	113	17
Hybrid 17	22.3	82	104.5	82	98.5	80	113	14
Hybrid 18	22.5	86	103.3	86	97	84	106	17
Hybrid 19	21.9	22	102.2	22	99	20	124	8
Hybrid 20	23.2	26	99.8	26	103.5	25	118	4
Hybrid 21	23.7	32	103.2	32	99.8	30	115	7
Hybrid 22	22.6	21	101	21	95.6	19	117	8
Hybrid 23	24.2	32	106.2	32	98.9	30	125	7
Hybrid 24	23	64	106.6	64	95.3	63	114	12
Hybrid 25	23.4	14	100.7	14	102.6	13	143	3
Hybrid 26	24	14	103	14	94.1	13	87	3
Hybrid 27	23.7	13	100.4	13	101.6	12	124	3
Hybrid 28	22.1	14	102.7	14	96.9	12	108	4
Hybrid 29	22.9	14	98.6	14	103	13	133	3
Hybrid 30	21.5	14	100.3	14	101.1	12	160	4
Hybrid 31	21.1	14	98.3	14	103.5	11	135	4
Hybrid 32	23.8	14	102.4	14	92.3	13	138	3
Hybrid 33	22.5	14	96.8	14	102.8	12	143	2
Hybrid 34	21.4	14	92.7	14	106.4	13	138	3
Hybrid 35	23.5	14	100.4	14	104.5	13	72	3
Hybrid 36	24.1	15	99.9	15	102.3	14	125	4
Hybrid 37	23.6	14	101.4	14	97.5	13	97	3
Hybrid 38	23.2	13	101	13	99.2	12	138	3
Hybrid 39	23.1	8	98.8	8	98.3	7	143	2
Hybrid 40	22.2	14	95.9	14	100.1	13	128	3
Hybrid 41	23.1	15	95.9	15	106.2	14	86	4
Hybrid 42	22.4	13	100.8	13	97.8	11	119	4
Hybrid 43	22.8	14	98.3	14	105.7	13	85	3
Hybrid 44	23.3	14	100.5	14	100	12	120	3
Hybrid 45	24.1	14	103.4	14	101.3	13	138	3
Hybrid 46	21	18	100.6	18	99.6	18	58	4
Hybrid 47	21.7	40	101	40	98.7	38	112	12
Hybrid 48	22.3	91	101.1	91	97.6	87	113	13
Hybrid 49	21.5	19	98.9	19	105.2	19	100	4
Hybrid 50	24	38	103.9	38	96.2	38	106	12
Hybrid 51	21.2	40	100.7	40	102	40	111	12
Hybrid 52	20.6	46	96.9	46	106.8	44	113	21
Hybrid 53	22.7	41	100.2	41	103	40	97	10
Hybrid 54	23.6	41	104.5	41	95.2	40	112	10
Hybrid 55	25.5	13	106.6	13	93.1	12	125	5
Hybrid 56	22.3	23	98.1	23	101.1	22	129	5
Hybrid 57	23.6	36	111.1	36	90.5	35	106	7
Hybrid 58	22.2	32	99.7	32	104.5	30	118	8
Hybrid 59	21.2	33	99.6	33	101.8	31	110	8
Hybrid 60	22	25	98.2	25	107.7	24	117	3
Hybrid 61	21.6	33	100.8	33	103.6	30	125	8
Hybrid 62	23.8	5	105.6	5	88.5	5	88	1
Hybrid 63	22.3	6	99.6	6	89.3	6	132	1
Hybrid 64	21.4	5	105.1	5	93.5	5	43	1

TABLE 6-continued

PHENOTYPIC DATA FROM HYBRIDS PRODUCED WITH PHE2E.

	STLLPN % NOT % MN MEAN	STLLPN % NOT % MN REPS	ERTLPN % NOT % MN MEAN	ERTLPN % NOT % MN REPS	LRTLPN % NOT % MN MEAN	LRTLPN % NOT % MN REPS	TSTWT lb/bu % MN MEAN	TSTWT lb/bu % MN REPS
Hybrid 1	88	3					97.3	5
Hybrid 2	123	13	81	5	95	9	97.9	35
Hybrid 3	134	2			112	1	98.3	6
Hybrid 4	124	2	126	4	79	3	97.8	14
Hybrid 5	83	4			42	1	98.7	26
Hybrid 6	107	6			108	1	98.4	8
Hybrid 7	119	7			96	7	99.4	20
Hybrid 8	101	13	90	5	83	17	97.2	55
Hybrid 9	123	6	117	1	106	2	98.4	13
Hybrid 10	121	9			118	5	100.7	18
Hybrid 11	123	2	95	4	61	3	100.2	13
Hybrid 12	72	2	111	4	115	3	99.7	13
Hybrid 13	106	2	118	4	95	3	99.5	13
Hybrid 14	117	2	96	4	71	3	101	14
Hybrid 15	100	2	92	4	119	3	100.6	12
Hybrid 16	112	42	94	17	115	41	99.1	103
Hybrid 17	98	21	114	8	110	13	99.9	72
Hybrid 18	116	25	82	10	102	26	101	73
Hybrid 19	97	4	79	4	88	6	98.5	21
Hybrid 20	120	4	115	4	98	10	99.9	25
Hybrid 21	109	6	79	4	115	13	99.5	31
Hybrid 22	115	4	87	4	71	6	100.8	19
Hybrid 23	104	6	63	4	109	13	98.4	31
Hybrid 24	137	9	122	3	99	6	98.4	56
Hybrid 25	157	2	83	4	113	3	100.9	12
Hybrid 26	129	2	83	4	69	3	99.6	13
Hybrid 27	117	2	89	4	88	3	100.4	12
Hybrid 28	121	2	69	4	71	3	101.1	14
Hybrid 29	100	2	99	4	73	3	100.6	13
Hybrid 30	109	2	42	4	183	3	101.4	14
Hybrid 31	181	2	136	4	64	3	99.9	14
Hybrid 32	100	2	115	4	98	3	98.9	13
Hybrid 33	129	2	121	4	156	3	99.4	13
Hybrid 34	72	2	109	4	142	3	97.9	13
Hybrid 35	83	2	97	4	69	3	101.3	13
Hybrid 36	114	2	99	4	112	3	99.6	14
Hybrid 37	95	2	91	4	83	3	99.4	13
Hybrid 38	111	2	115	3	109	3	99.9	12
Hybrid 39			127	3	108	1	100.5	8
Hybrid 40	100	2	114	4	106	3	101.5	13
Hybrid 41	88	2	101	4	74	3	101	13
Hybrid 42	93	2	73	4	43	3	99.1	13
Hybrid 43	123	2	78	4	72	3	97.8	13
Hybrid 44	106	2	105	4	142	3	98.8	12
Hybrid 45	77	2	108	4	134	3	98	12
Hybrid 46	80	9	62	2	92	4	98.8	15
Hybrid 47	77	5	103	3	110	6	99.1	34
Hybrid 48	115	21	102	17	108	40	98.3	80
Hybrid 49	102	4			92	1	97.6	17
Hybrid 50	112	13	86	3	103	12	99.8	31
Hybrid 51	102	14	134	5	112	7	96.9	35
Hybrid 52	119	11	106	9	96	14	100.3	43
Hybrid 53	112	11	92	6	106	19	98.1	35
Hybrid 54	103	11	120	6	109	19	99.3	35
Hybrid 55	110	4			112	4	99	10
Hybrid 56	94	7	111	4	90	4	99.1	19
Hybrid 57	98	9	99	3	103	7	98.4	31
Hybrid 58	113	6	87	4	97	13	99.8	30
Hybrid 59	102	6	112	5	90	13	99.1	32
Hybrid 60	89	4	89	4	116	10	100.4	24
Hybrid 61	117	6	104	4	108	13	98.8	32
Hybrid 62	125	3					99.1	4
Hybrid 63	123	3					96.3	5
Hybrid 64	110	3					101.5	4

	STKCNT count % MN MEAN	STKCNT count % MN REPS	PLTHT in % MN MEAN	PLTHT in % MN REPS	EARHT in % MN MEAN	EARHT in % MN REPS	BRTSTK % NOT % MN MEAN	BRTSTK % NOT % MN REPS
Hybrid 1	100	8	102	4	99	4	74	1
Hybrid 2	100	61	102	17	106	17	9	1

TABLE 6-continued

PHENOTYPIC DATA FROM HYBRIDS PRODUCED WITH PHE2E.

Hybrid 3	99	11	98	4	94	4		
Hybrid 4	100	17	95	7	89	7		
Hybrid 5	99	43	100	11	98	11	90	4
Hybrid 6	100	16	101	7	103	7		
Hybrid 7	102	51	101	17	99	17	99	1
Hybrid 8	100	100	102	35	100	35	101	1
Hybrid 9	101	22	103	12	98	12	55	1
Hybrid 10	100	38	100	20	97	20	98	2
Hybrid 11	101	18	101	8	101	8		
Hybrid 12	100	18	103	8	103	8		
Hybrid 13	100	18	102	8	99	8		
Hybrid 14	101	18	103	8	101	8		
Hybrid 15	99	18	104	8	106	8		
Hybrid 16	100	319	102	75	100	69	99	13
Hybrid 17	101	190	102	39	96	34	101	12
Hybrid 18	100	156	99	23	93	24	87	6
Hybrid 19	100	29	103	9	102	9		
Hybrid 20	101	36	104	14	103	14		
Hybrid 21	100	47	103	14	104	14		
Hybrid 22	100	29	107	8	109	8		
Hybrid 23	100	47	102	14	103	14		
Hybrid 24	100	78	103	26	102	26	104	5
Hybrid 25	101	18	100	8	101	8		
Hybrid 26	101	18	102	8	101	8		
Hybrid 27	101	18	103	8	101	8		
Hybrid 28	101	17	101	7	102	7		
Hybrid 29	101	18	102	8	98	8		
Hybrid 30	100	17	107	7	103	7		
Hybrid 31	99	17	104	7	101	7		
Hybrid 32	101	18	105	8	105	8		
Hybrid 33	100	17	101	8	98	8		
Hybrid 34	101	18	100	7	98	8		
Hybrid 35	101	18	106	8	100	8		
Hybrid 36	101	18	101	8	97	8		
Hybrid 37	101	18	100	8	97	8		
Hybrid 38	101	17	105	8	103	8		
Hybrid 39	100	9	99	6	101	6		
Hybrid 40	100	18	105	8	105	8		
Hybrid 41	101	18	104	8	103	8		
Hybrid 42	101	17	105	7	106	7		
Hybrid 43	101	18	105	8	102	8		
Hybrid 44	100	18	100	8	103	8		
Hybrid 45	101	18	104	8	103	8		
Hybrid 46	99	27	103	8	106	8	38	1
Hybrid 47	100	51	101	20	98	20	102	3
Hybrid 48	97	171	102	31	100	31	102	5
Hybrid 49	100	24	106	7	106	7	101	3
Hybrid 50	99	61	99	17	99	17	101	1
Hybrid 51	100	62	103	18	101	18	82	4
Hybrid 52	101	73	102	19	98	19		
Hybrid 53	101	63	103	12	103	12	80	3
Hybrid 54	101	64	107	12	104	12	79	3
Hybrid 55	99	24	101	13	100	13	101	1
Hybrid 56	100	32	103	13	102	13	57	1
Hybrid 57	101	62	104	12	109	12	90	7
Hybrid 58	100	47	100	14	101	14		
Hybrid 59	100	46	105	15	100	15		
Hybrid 60	100	34	103	14	100	14		
Hybrid 61	101	46	102	15	98	15		
Hybrid 62	98	8	106	4	107	4	42	1
Hybrid 63	101	8	101	4	102	4	46	1
Hybrid 64	102	7	104	4	103	4	57	1

	BORBMN % NOT % MN MEAN	BORBMN % NOT % MN REPS	BRLPNE % NOT % MN MEAN	BRLPNE % NOT % MN REPS	BRLPNL % NOT % MN MEAN	BRLPNL % NOT % MN REPS	GLFSPT score ABS MEAN	GLFSPT score ABS REPS
Hybrid 1								
Hybrid 2	51	6					5	2
Hybrid 3								
Hybrid 4							4	1
Hybrid 5	92	6						
Hybrid 6							3	1
Hybrid 7	71	6					5	1
Hybrid 8	84	6					6	5
Hybrid 9								

TABLE 6-continued

PHENOTYPIC DATA FROM HYBRIDS PRODUCED WITH PHE2E.

Hybrid 10								
Hybrid 11							5	1
Hybrid 12							6	1
Hybrid 13							5	1
Hybrid 14							4	1
Hybrid 15							5	1
Hybrid 16	80	16	38	18	119	18	5	15
Hybrid 17	106	18	66	18	104	17	6	4
Hybrid 18	106	12					6	9
Hybrid 19							6	2
Hybrid 20							5	3
Hybrid 21							6	4
Hybrid 22							5	2
Hybrid 23							5	4
Hybrid 24								
Hybrid 25							5	1
Hybrid 26							5	1
Hybrid 27							6	1
Hybrid 28							5	1
Hybrid 29							6	1
Hybrid 30							4	1
Hybrid 31							4	1
Hybrid 32							4	1
Hybrid 33							6	1
Hybrid 34							4	1
Hybrid 35							5	1
Hybrid 36							5	1
Hybrid 37							6	1
Hybrid 38								
Hybrid 39								
Hybrid 40							5	1
Hybrid 41							5	1
Hybrid 42							5	1
Hybrid 43							5	1
Hybrid 44							4	1
Hybrid 45							5	1
Hybrid 46								
Hybrid 47							5	5
Hybrid 48	103	4					5	14
Hybrid 49								
Hybrid 50	108	6					5	2
Hybrid 51							5	5
Hybrid 52	106	6					5	4
Hybrid 53							5	5
Hybrid 54							6	5
Hybrid 55								
Hybrid 56							5	1
Hybrid 57	85	6					5	3
Hybrid 58							6	4
Hybrid 59							6	4
Hybrid 60							5	3
Hybrid 61							5	4
Hybrid 62								
Hybrid 63								
Hybrid 64								

	STAGRN score ABS MEAN	STAGRN score ABS REPS	HSKCVR score ABS MEAN	HSKCVR score ABS REPS	ECBLSI score ABS MEAN	ECBLSI score ABS REPS
Hybrid 1	5	2				
Hybrid 2	5	12	6	1		
Hybrid 3	3	4				
Hybrid 4	4	4	5	4		
Hybrid 5	6	4				
Hybrid 6	4	3				
Hybrid 7	6	8	6	1		
Hybrid 8	5	18	5	10		
Hybrid 9	5	5				
Hybrid 10	5	6				
Hybrid 11	4	4	6	4		
Hybrid 12	4	4	6	4		
Hybrid 13	4	4	7	4		
Hybrid 14	4	4	7	4		
Hybrid 15	5	4	7	4		
Hybrid 16	6	20	7	22	6	6
Hybrid 17	5	13	5	12	6	4

TABLE 6-continued

PHENOTYPIC DATA FROM HYBRIDS PRODUCED WITH PHE2E.

Hybrid 18	5	19	5	17	6	4
Hybrid 19	5	6	7	5		
Hybrid 20	4	7	6	7		
Hybrid 21	5	8	6	8		
Hybrid 22	6	5	6	5		
Hybrid 23	5	8	6	8		
Hybrid 24	6	9	6	2		
Hybrid 25	5	4	6	4		
Hybrid 26	6	4	6	4		
Hybrid 27	5	4	6	4		
Hybrid 28	5	4	6	4		
Hybrid 29	5	4	6	4		
Hybrid 30	5	4	6	4		
Hybrid 31	5	4	6	4		
Hybrid 32	5	4	6	4		
Hybrid 33	4	4	7	4		
Hybrid 34	3	4	7	4		
Hybrid 35	4	4	6	4		
Hybrid 36	5	4	6	4		
Hybrid 37	4	4	6	4		
Hybrid 38	4	4	6	3		
Hybrid 39	4	3	6	3		
Hybrid 40	4	4	7	4		
Hybrid 41	5	4	7	4		
Hybrid 42	4	4	6	4		
Hybrid 43	4	4	6	4		
Hybrid 44	5	4	5	4		
Hybrid 45	5	4	6	4		
Hybrid 46	5	5				
Hybrid 47	6	6	6	6		
Hybrid 48	5	9	6	11	8	2
Hybrid 49	5	2				
Hybrid 50	5	9	6	1		
Hybrid 51	5	9	6	4		
Hybrid 52	5	15	6	5		
Hybrid 53	5	9	5	6		
Hybrid 54	5	9	5	6		
Hybrid 55	5	3				
Hybrid 56	5	6	6	4		
Hybrid 57	5	9	5	3		
Hybrid 58	5	8	6	8		
Hybrid 59	4	8	6	8		
Hybrid 60	3	7	6	7		
Hybrid 61	5	9	6	8		
Hybrid 62	6	2				
Hybrid 63	4	2				
Hybrid 64	5	1				

All publications, patents and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All such publications, patents and patent applications are incorporated by reference herein for the purpose cited to the same extent as if each was specifically and individually indicated to be incorporated by reference herein.

The foregoing invention has been described in detail by way of illustration and example for purposes of clarity and understanding. As is readily apparent to one skilled in the art, the foregoing are only some of the methods and compositions that illustrate the embodiments of the foregoing invention. It will be apparent to those of ordinary skill in the art that variations, changes, modifications and alterations may be applied to the compositions and/or methods described herein without departing from the true spirit, concept and scope of the invention.

What is claimed is:

1. Maize inbred variety PHE2E, representative seed of said variety having been deposited under ATCC accession number PTA-7521.

2. A seed of the maize inbred variety of claim **1**.

3. A plant of the maize inbred variety of claim **1**.

4. A plant part of the maize inbred variety of claim **1**.

5. A plant of maize inbred variety PHE2E, representative seed of said variety having been deposited under ATCC accession number PTA-7521 further comprising at least one locus conversion, wherein said locus conversion is selected from the group consisting of male sterility, site-specific recombination, abiotic stress tolerance, altered phosphorus, altered antioxidants, altered fatty acids, altered essential amino acids, altered carbohydrates, herbicide resistance, insect resistance and disease resistance, and wherein the plant further comprising at least one locus conversion has all the other morphological and physiological characteristics of maize inbred variety PHE2E.

6. A maize plant having all the morphological and physiological characteristics of the plant of claim **3**.

7. A maize seed produced by crossing the plant of claim **3** with a different maize plant.

8. A maize plant produced by growing the maize seed of claim **7**.

9. A plant part of the maize plant of claim **8**.

10. A process of producing a conversion of maize inbred variety PHE2E comprising at least one new trait, the process comprising:

(a) crossing a plant of maize inbred variety PHE2E, representative seed of which has been deposited under ATCC Accession Number PTA-7521, with a plant of another maize variety that comprises at least one new trait to produce progeny seed;

(b) harvesting and planting the progeny seed to produce at least one progeny plant of a subsequent generation, said progeny plant comprising the at least one new trait;

(c) crossing the progeny plant with a plant of maize inbred variety PHE2E to produce backcross progeny seed;

(d) harvesting and planting the backcross progeny seed to produce at least one backcross progeny plant; and

(e) repeating steps (c) and (d) for at least three additional generations to

produce a converted plant of inbred variety PHE2E, wherein the converted plant of inbred variety PHE2E comprises the at least one new trait and all other morphological and physiological characteristics of maize inbred variety PHE2E.

11. The converted plant of inbred variety PHE2E produced by the process of claim 10.

12. A plant part of the plant of claim 11.

13. A maize seed produced by crossing the plant of claim 11 with a different maize plant.

14. A maize plant produced by growing the maize seed of claim 13.

15. The plant of claim 11, wherein said at least one new trait is selected from the group consisting of male sterility, site-specific recombination, abiotic stress tolerance, altered phosphorus, altered antioxidants, altered fatty acids, altered essential amino acids, altered carbohydrates, herbicide resistance, insect resistance and disease resistance.

16. A method for developing a second maize plant in a maize plant breeding program comprising applying plant breeding techniques to a first maize plant, or parts thereof, wherein said first maize plant is the maize plant of claim 8, and wherein application of said techniques results in development of said second maize plant.

17. The method of claim 16, further comprising producing an inbred maize plant derived from the maize variety PHE2E, the method further comprising the steps of:

(a) crossing said second maize plant with itself or a second plant to produce seed of a subsequent generation;

(b) harvesting and planting the seed of the subsequent generation to produce at least one plant of the subsequent generation;

(c) repeating steps (a) and (b) for an additional 2-10 generations to produce an inbred maize plant derived from maize variety PHE2E.

18. The seed of claim 2, further comprising a transgene.

19. The seed of claim 18, wherein the transgene confers a trait selected from the group consisting of male sterility, site-specific recombination, abiotic stress tolerance, altered phosphorus, altered antioxidants, altered fatty acids, altered essential amino acids, altered carbohydrates, herbicide resistance, insect resistance and disease resistance.

20. The plant of claim 3, further comprising a transgene.

21. The plant of claim 20, wherein the transgene confers a trait selected from the group consisting of male sterility, site-specific recombination, abiotic stress tolerance, altered phosphorus, altered antioxidants, altered fatty acids, altered essential amino acids, altered carbohydrates, herbicide resistance, insect resistance and disease resistance.

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