United States Patent	12382913
Kind Code	B2
Date of Patent	August 12, 2025
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Variety corn lines

Abstract

The present invention provides an inbred corn line designated TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, methods for producing a corn plant by crossing plants of the inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with plants of another corn plant. The invention further encompasses all parts of inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, including culturable cells. Additionally, provided herein are methods for introducing transgenes into inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, and plants produced according to these methods.

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Appl. No.: **18/143811**

Filed: **May 05, 2023**

Prior Publication Data

Document Identifier	Publication Date
US 20230337615 A1	Oct. 26, 2023

Related U.S. Application Data

continuation parent-doc US 17308619 20210505 US 11678631 child-doc US 18143811
us-provisional-application US 63022804 20200511

Publication Classification

Int. Cl.: **A01H6/46** (20180101); **A01H5/10** (20180101)

U.S. Cl.:

CPC **A01H6/4684** (20180501); **A01H5/10** (20130101);

Field of Classification Search

USPC: None

References Cited

U.S. PATENT DOCUMENTS

Patent No.	Issued Date	Patentee Name	U.S. Cl.	CPC
9591826	12/2016	Delzer	N/A	N/A
2017/0135302	12/2016	Miller	N/A	C12N 15/8241

Primary Examiner: Logsdon; Charles

Background/Summary

RELATED APPLICATION INFORMATION (1) This application is a continuation of U.S. application Ser. No. 17/308,619, filed May 5, 2021, which claims benefit of U.S. Provisional Patent Application No. 63/022,804, filed May 11, 2021, the contents of which are herein incorporated by reference.

FIELD OF THE INVENTION
(1) This invention is in the field of corn breeding. Specifically, the present invention provides a maize plant and its seed designated TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, as well as derivatives and hybrids thereof.
BACKGROUND OF THE INVENTION
(2) Maize (or corn; *Zea mays* L.) plant breeding is a process to develop improved maize germplasm in an inbred or hybrid plant. Maize plants can be self-pollinating or cross pollinating. Self pollination for several generations produces homozygosity at almost all gene loci, forming a uniform population of true breeding progeny, known as inbreds. Hybrids are developed by crossing two homozygous inbreds to produce heterozygous gene loci in hybrid plants and seeds. In this process, the inbred is emasculated and the pollen from the other inbred pollinates the emasculated inbred. Emasculation of the inbred can be done by chemical treatment of the plant, detasseling the seed parent, or the parent inbred can comprise a male sterility trait or transgene imparting sterility, eliminating the need for detasseling. This emasculated inbred, often referred to as the female, produces the hybrid seed, F1. The hybrid seed that is produced is heterozygous. However, the grain produced by a plant grown from F1 hybrid seed is referred to as F2 grain. F2 grain which is a plant part produced on the F1 plant will comprise segregating maize germplasm, even though the hybrid plant is heterozygous.
(3) Such heterozygosity in hybrids results in robust and vigorous plants. Inbred plants on the other hand are mostly homozygous, rendering them less vigorous. Inbred seed can be difficult to produce

due to such decreased vigor. However, when two inbred lines are crossed, the resulting hybrid plant shows greatly increased vigor and seed yield compared to open pollinated, segregating maize plants. An important consequence of the homozygosity and homogeneity of inbred maize lines is that all hybrid seed and plants produced from any cross of two such lines will be the same. Thus the use of inbreds allows for the production of hybrid seed that can be readily reproduced.

(4) There are numerous stages in the development of any novel, desirable plant germplasm. Plant breeding begins with the analysis and definition of problems and weaknesses of the current germplasm, the establishment of program goals, and the definition of specific breeding objectives. The next step is selection of germplasm that possess the traits to meet the program goals. The aim is to combine in a single variety an improved combination of desirable traits from the parental germplasm. These important traits may include, for example, higher yield, resistance to diseases, fungus, bacteria and insects, better stems and roots, tolerance to drought and heat, improved nutritional quality, and better agronomic characteristics.

(5) Choice of breeding methods depends on the mode of plant reproduction, the heritability of the trait(s) being improved, and the type of cultivar used commercially (e.g., F1 hybrid cultivar, pure line cultivar, etc.). For highly heritable traits, a choice of superior individual plants evaluated at a single location may be effective, whereas for traits with low heritability, selection can be based on mean values obtained from replicated evaluations of families of related plants. Popular selection methods commonly include pedigree selection, modified pedigree selection, mass selection, and recurrent selection.

(6) The complexity of inheritance influences the choice of breeding method. Backcross breeding is used to transfer one or a few favorable genes for a highly heritable trait into a desirable cultivar. This approach has been used extensively for breeding disease-resistant cultivars and introducing transgenic events into maize germplasm. Thus, backcross breeding is useful for transferring genes for a simply inherited, highly heritable trait into a desirable homozygous cultivar or inbred line which is the recurrent parent. The source of the trait to be transferred is called the donor parent. After the initial cross, individuals possessing the phenotype of the donor parent are selected and repeatedly crossed (backcrossed) to the recurrent parent. The resulting plant is expected to have the attributes of the recurrent parent (e.g., cultivar) and the desirable trait transferred from the donor parent.

(7) Each breeding program generally includes a periodic, objective evaluation of the efficiency of the breeding procedure. Evaluation criteria vary depending on the goals and objectives, but should include gain from selection per year based on comparisons to an appropriate standard, overall value of the advanced breeding lines, and number of successful cultivars produced per unit of input (e.g., per year, per dollar expended, etc.).

(8) The ultimate objective of commercial corn breeding programs is to produce high yield, agronomically sound plants that perform well in particular regions of the U.S. Corn Belt, such as a plant of this invention.

SUMMARY OF THE INVENTION

(9) In one aspect, the present invention provides a seed of the maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, representative seed of said variety are deposited.

(10) In a further aspect, the present invention provides a plant of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, representative seed of said TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 variety are deposited. Further provided is a plant part of the plant of this invention, which includes but is not limited to a pollen grain, a silk, a protoplast, a cell, a tassel, an anther, or an ovule. Also provided is a maize seed produced on the plant of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684.

(11) Another aspect of the invention provides a maize plant having essentially all the physiological

and morphological characteristics of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and further comprising an additional trait, wherein the additional trait is selected from the group consisting of increased water stress resistance, waxy starch, male sterility or restoration of male fertility, modified carbohydrate metabolism, modified protein metabolism, modified fatty acid metabolism, altered starch, thermotolerant amylase, herbicide resistance, insect resistance, nematode resistance, bacterial disease resistance, fungal disease resistance, and viral disease resistance. In some embodiments, the additional trait is conferred by introducing a transgene. Some embodiments of the invention provide a seed produced by the maize plant having essentially all the physiological and morphological characteristics of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and further comprising an additional trait. Additional aspects of this invention include a process for producing an F1 hybrid maize seed, said process comprising crossing a plant of maize inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with a different maize plant and harvesting the resultant F1 hybrid maize seed. A maize plant or plant part produced by growing the F1 hybrid maize seed is also provided herein. The present invention also provides a maize seed produced by crossing the plant of this invention with a different maize plant.

(12) The present invention further provides an F1 hybrid maize seed comprising an inbred maize plant cell of inbred maize plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684. Further provided is a process of crossing the maize inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with another plant. Additionally provided herein is the seed produced by crossing the maize inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with another plant. Additionally, a plant produced by germinating the seed produced by crossing the maize inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with another plant is provided

(13) A method is also provided for producing maize seed comprising growing the plant of this invention until seed is produced and harvesting the seed, wherein the harvested seed is inbred or hybrid or haploid seed.

(14) The present invention also provides a method of producing seed, comprising crossing the plant of the invention with itself or a second maize plant. Seed produced by this method are also provided herein. Additional aspects of this invention include hybrid seed produced by crossing the invention with a second distinct corn plant and the plant and plant parts on this hybrid plant grown from the hybrid seed.

(15) In some aspects, the present invention provides a progeny maize plant of the maize plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 that comprises at least 95% of the alleles of the maize plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, wherein the progeny maize plant has essentially the same characteristics as table 1.

(16) Additional aspects of this invention include a process of introducing an additional trait into maize inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, comprising: (a) crossing TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 plants grown from TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 seed with plants of another maize plant that comprise an additional trait to produce hybrid progeny plants, (b) selecting hybrid progeny plants that have the additional trait to produce selected hybrid progeny plants; (c) crossing the selected progeny plants with the TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 plants to produce backcross progeny plants; (d) selecting for backcross progeny plants that have the additional trait to produce selected backcross progeny plants; and (e) repeating step(s) (c) and (d) one or more times to produce backcross progeny plants of subsequent generations that comprise the additional trait and all of the physiological and morphological characteristics of maize inbred plant

TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 when grown in the same environmental conditions. In some embodiments of this invention, the desired trait can be, but is not limited to, waxy starch, male sterility, increased tolerance to water stress, herbicide resistance, nematode resistance, modified amylase, altered starch, thermotolerant amylase, insect resistance, modified carbohydrate metabolism, protein metabolism, fatty acid metabolism, bacterial resistance, disease resistance, fungal disease resistance, viral disease resistance, or any combination thereof. A plant produced by this process is also provided herein. A conversion of this maize variety is provided, wherein representative seed of said maize variety comprising at least one new trait wherein said conversions had the morphological and physiological traits of the maize plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and said trait confers a characteristic selected from the group consisting of altered amylase, abiotic stress and biotic stress tolerance, herbicide, insect, fungal, bacterial and disease resistance.

(17) Furthermore, the present invention provides a maize plant having all the physiological and morphological characteristics of inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, wherein a sample of the seed of inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 was deposited. The maize plant of this invention can comprise a genome which further comprises at least one transgene and/or the maize plant can exhibit a trait conferred by a transgene. In some embodiments of this invention, the transgene can confer a trait of herbicide resistance or tolerance; insect resistance or tolerance; resistance or tolerance to bacterial, fungal, nematode or viral disease; waxy starch; altered starch, male sterility or restoration of male fertility, modified carbohydrate metabolism, modified fatty acid metabolism, or any combination thereof.

(18) Additionally provided herein is a method of producing a maize plant derived from the inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, comprising the steps of: (a) growing a progeny plant wherein the inbred plant is one parent of the progeny; (b) crossing the progeny plant with itself or a different plant to produce a seed of a progeny plant of a subsequent generation; (c) repeating step (b) one or more times, and (d) growing a progeny plant of a subsequent generation from said seed and crossing the progeny plant of a subsequent generation with itself or a different plant to produce a maize plant derived from the inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684.

(19) In some aspects, the present invention provides a converted seed, plant, plant part or plant cell of inbred maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, representative seed of the maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 having been deposited, wherein the converted seed, plant, plant part or plant cell comprises a locus conversion, and wherein the plant or a plant grown from the converted seed, plant part or plant cell comprises the locus conversion and otherwise comprises the phenotypic characteristics of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 listed in Table 1 when grown under the same environmental conditions.

(20) Another aspect of this invention includes a method for developing a maize plant in a maize plant breeding program, comprising applying plant breeding techniques comprising recurrent selection, backcrossing, pedigree breeding, marker enhanced selection, haploid/dihaploid production, or transformation to the maize plant of this invention, or its parts, wherein application of said techniques results in development of a maize plant.

(21) Furthermore, the present invention provides a method of producing a commodity plant product comprising growing the plant from the seed of this invention or a part thereof and producing said commodity plant product, wherein said commodity plant product can be, but is not limited to a protein concentrate, a protein isolate, starch, meal, flour, oil therefrom, or any combination thereof.

(22) A method is also provided of producing a treated seed of this invention, comprising obtaining the seed of TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and

treating said seed. According to one aspect, the present invention provides a method of producing a genetic marker profile comprising extracting nucleic acids from the seed produced by maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 or the plant grown from said seed and genotyping said nucleic acids, thereby producing a genetic marker profile.

(23) According to another aspect, the present invention provides a method of plant breeding comprising: isolating nucleic acids from a seed produced by maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 or a plant grown from the seed, identifying one or more polymorphisms from the isolated nucleic acids, and selecting a plant having one or more poly morphisms wherein the plant is used in a plant breeding method.

(24) In some aspects, the invention provides a method of producing nucleic acids comprising extracting nuclei acids from an F1 maize plant or seed produced by maize plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684.

(25) In a still further aspect, the present invention provides a method of producing an inbred maize plant derived from the inbred maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 the method comprising: crossing a progeny plant wherein the inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 is one parent of the progeny, wherein said plant may have one or more traits, with an inducer maize plant to produce haploid seed; and doubling the haploid seed to produce an inbred maize plant.

Description

DETAILED DESCRIPTION OF THE INVENTION

(1) Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. The terminology used in the description of the invention herein is for the purpose of describing particular embodiments only and is not intended to be limiting of the invention. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

(2) In the description and examples that follow, a number of terms are used. In order to provide a clear and consistent understanding of the specifications and claims, including the scope to be given such terms, the following definitions are provided.

(3) Definitions of Plant Characteristics

(4) Early Season Trait Codes

(5) Emergence Rating (EMRGR): Recorded when 50% of the plots in the trial are at V1 (1 leaf collar) growth stage. Various responses include, but are not limited to, (1) All plants have emerged and are uniform in size; (2) All plants have emerged but are not completely uniform; (3) Most plants have emerged with some just beginning to break the soil surface, noticeable lack of uniformity; (4) Less than 50% of the plants have emerged, and lack of uniformity is very noticeable; or (5) A few plants have emerged but most remain under the soil surface.

(6) Seedling Growth (SVGRR or Vigor): Recorded between V3 and V5 (3-5 leaf stage) giving greatest weight to seedling plant size and secondary weight to uniform growth. Various responses include, but are not limited to, (1) Large plant size and uniform growth; (2) Acceptable plant size and uniform growth; (3) Acceptable plant size and might be a little non-uniform; (4) Weak looking plants and non-uniform growth; or (5) Small plants with poor uniformity.

(7) Purpling (PRPLR): Emergence and/or early growth rating. Purpling is more pronounced on the under sides of leaf blades especially on midribs. Various responses include, but are not limited to, (1) No plants showing purple color; (2) 30% plants showing purple color; (3) 50% plants showing purple color; (4) 70% plants showing purple color; or (5) 90+% plants showing purple color.

(8) Herbicide Injury (HRBDR): List the herbicide type that is being rated. Then rate each hybrid/variety injury as indicated below. (1) No apparent reduction in biomass or other injury symptoms; (2) Moderate reduction in biomass with some signs of sensitivity; (3) Severe reduction in biomass with some mortality.
(9) Mid-Season Trait Codes
(10) Heat Units to 50% Silk (HU5SN): Recorded the day when 50% of all plants within a plot show 2 cm or more silk protruding from the ear. Converted days to accumulated heat units from planting.
(11) Heat units to 50% Pollen Shed (HUPSN): Recorded the day when 50% of all plants within a plot are shedding pollen. Converted days to accumulated heat units from planting.
(12) Plant Height (PLHTN): After pollination, recorded average plant height of each plot. Measured from ground to tassel tip in cm.
(13) Plant Ear Height (ERHTN) in cm: After pollination, record average ear height of each plot. Measure from ground to base of ear node (shank).
(14) Root Lodging Early % (ERTLP): Early root lodging occurs up to about two weeks after flowering and usually involves goosenecking. The number of root lodged plants are counted and converted to a percentage.
(15) Shed Duration (Shed Duration): Sum of daily heat units for days when plants in the plot are actively shedding pollen.
(16) Foliar Disease (LFDSR): Foliar disease ratings taken one month before harvest and through harvest. The predominant disease should be listed in the trial information and individual hybrid ratings should be given. Various responses include, but are not limited to, (9) No lesions to two lesions per leaf; (8) A few scattered lesions on the leaf. About five to ten percent of the leaf surface is affected; (7) A moderate number of lesions are on the leaf. About 15 to 20 percent of the leaf surface is affected; (6) abundant lesions are on the leaf. About 30 to 40 percent of the leaf surface is affected; or (5) Highly abundant lesions (>50 percent) on the leaf. Lesions are highly coalesced. Plants may be prematurely killed. Alternatively, the response to diseases can also be rated as: R=Resistant=9 to 8 rating; MR=Moderately Resistant=7 to 6 rating; MS=Moderately Susceptible=5 to 4 rating; S=Susceptible=3 to 1 rating
(17) Preharvest Trait Codes
(18) Heat units to Black Layer (HUBLN): The day when 50% of all plants within a plot reach the black layer stage is recorded. Convert days to accumulated heat units from planting.
(19) Harvest Population (HAVPN): The number of plants in yield rows, excluding tillers, in each plot is counted.
(20) Barren Plants (BRRNP): The number of plants in yield rows having no ears and/or abnormal ears with less than 50 kernels is counted.
(21) Dropped Ears (DROPP): The numbers of ears lying on the ground in yield rows are counted.
(22) Stalk Lodging % (STKLP): Stalk lodging will be reported as number of plants broken below the ear without pushing, excluding green snapped plants. The number of broken plants in yield rows is counted and converted to percent.
(23) Root Lodging Late % (LRTLP): Late root lodging can usually start to occur about two weeks after flowering and involves lodging at the base of the plant. Plants leaning at a 30-degree angle or more from the vertical are considered lodged. The number of root lodged plants in yield rows is counted and converted to percent.
(24) Push Test for Stalk and Root Quality on Erect Plants % (PSTSP or PCT Push or % Pushtest): The push test is applied to trials with approximately five percent or less average stalk lodging. Plants are pushed that are not root lodged or broken prior to the push test. Standing next to the plant, the hand is placed at the top ear and pushed to arm's length. Push one of the border rows (four-row small plot) into an adjacent plot border row. The number of plants leaning at a 30-degree angle or more from the vertical, including plants with broken stalks prior to pushing is counted.

Plants that have strong rinds that snap rather than bend over easily are not counted. The goal of the push test is to identify stalk rot and stalk lodging potential, NOT ECB injury. Data may be collected for the push test in the following manner:
(25) PUSXN: Push ten plants and enter the number of plants that do not remain upright.
(26) Intactness (INTLR): Responses can include, but are not limited to, (1) Healthy appearance, tops unbroken; (2) 25% of tops broken; or (3) Majority of tops broken
(27) Plant Appearance (PLTAR): This is a visual rating based on general plant appearance, taking into account all factors of intactness, pest and disease pressure. Various responses include, but are not limited to, (1) Complete plant with healthy appearance; (2) Plants look okay; or (3) Plants are not acceptable.
(28) Green Snap (GRSNP or PCTGS or % GreenSnap): Count the number of plants in yield rows that snap below the ear due to brittleness associated with high winds.
(29) Stay-green (STGRP): This is an assessment of the ability of a grain hybrid to retain green color as maturity approaches (taken near the time of black-layer formation) and should not be a reflection of hybrid maturity or leaf disease. Record as a percentage of green tissue. This may be listed as a Stay Green Rating instead of a percentage.
(30) Stay Green Rating (STGRR): This is an assessment of the ability of a grain hybrid to retain green color as maturity is approached (taken near the time of black layer formation or if major differences are noted later). This rating should not be a reflection of the hybrid maturity or leaf disease. Ratings are 1-9. (1=best, 9=worst) 1=solid Green Plant 9=no green tissue
(31) Ear/Kernel Rots (KRDSR): If ear or kernel rot is present, husk ten consecutive ears in each plot and count the number that have evidence of ear or kernel rot, multiply by 10, and round up to the nearest rating as described below. Identify and record the disease primarily responsible for the rot. The rot response can include but is not limited to (1) No rot, 0% of the ears infected; (2) Up to 10% of the ears infected; (3) 11 to 20% of the ears infected; (4) 21 to 35% of the ears infected; or (5) 36% or more of the ears infected.
(32) Grain Quality (GRQUR): Observations taken on husked ears after black layer stage. The kernel cap integrity and relative amount of soft starch endosperm along the sides of kernels are rated. Grain quality ratings can include but are not limited to (1) Smooth kernel caps and or 10% or less soft starch; (2) Slight kernel wrinkles and or 30% soft starch; (3) Moderate kernel wrinkles and or 70% soft starch; or (4) Severe kernel wrinkled and or 90% or more soft starch.
(33) Preharvest Hybrid Trait Codes
(34) Ear Shape (DESHR): Description of ear shape can include, but is not limited to, (1) Blocky; (2) Semi-blocky; or (3) Slender.
(35) Ear Type (EARFR): Description of ear type can include, but is not limited to, (1) Flex; (2) Semi-flex; or (3) Fixed.
(36) Husk Cover (HSKCR):): Description of husk cover can include, but is not limited to, (1) Long; (2) Medium; or (3) Short.
(37) Kernel Depth (KRLNR): Description of kernel depth can include, but is not limited to, (1) Deep; (2) Medium; or (3) Short (shallow).
(38) Shank Length (SHLNR): Description of shank length can include, but is not limited to, (1) Short; (2) Medium; or (3) Long.
(39) Kernel Row Number (KRRWN): The average number of kernel rows on 3 ears.
(40) Cob diameter (COBDR): Cob diameter is to be taken with template. Description of cob diameter can include, but is not limited to, (1) Small; (2) Medium; or (3) Large.
(41) Harvest Trait Codes
(42) Number of Rows Harvested (NRHAN)
(43) Plot Width (RWIDN)
(44) Plot Length (RLENN)
(45) Yield Lb/Plot (YGSMN): Bushels per acre adjusted to 15.5% moisture.

(46) Test Weight (TSTWN or TWT): Test weight at harvest in pounds per bushel.
(47) Moisture % (MST_P): Percent moisture of grain at harvest.
(48) Adjusted Yield in Bu/A (YBUAN) listing of bushels per acre of harvested seed at standard moisture
(49) Kernel Type (KRTPN): Description of kernal type can include, but is not limited to, (1) Dent; (2) Flint; (3) Sweet; (4) Flour; (5) Pop; (6) Ornamental; (7) Pipecorn; or (8) Other.
(50) Endosperm Type (KRTEN): Description of endosperm type can include, but is not limited to, (1) Normal; (2) Amylose (high); (3) Waxy (4) Sweet; (5) Extra sweet; (6) High protein; (7) High lysine; (8) Super sweet; (9) High oil; or (10) Other.
(51) Sterile Type (MSCT): Description of sterile type can include, but is not limited to, (1) No; If yes, cytoplasm type can include but is not limited to, (2)C-type or (3) S-type if other (4) for example, transgene
(52) Anthocyanin of Brace Roots (PBRCC): Refers to the presence of color on 60% of the brace roots during pollen shed. The description of the anthocyanin of brace roots can include, but is not limited to, (1) Absent; (2) Faint; (3) Moderate; (4) Dark; (5) Brace Roots not present; (6) Green; (7) Red; or (8) Purple.
(53) Anther Color (ANTCC): At 50 percent pollen shed observe the color of newly extruded anthers, pollen not yet shed. The description of the anther color can include, but is not limited to, (1) Yellow; (2) Red; (3) Pink; or (4) Purple
(54) Glume Color (GLMCC): Color of glumes prior to pollen shed. The description of the glume color can include, but is not limited to, (1) Red or (2) Green.
(55) Silk Color (SLKCC; SLKCN): Taken at a late flowering stage when all plants have fully extruded silk. Silks at least 2″ long but still fresh. The description of the silk color can include, but is not limited to, (1) Yellow; (2) Pink; or (3) Red (e.g., Munsell value).
(56) Kernel Color (KERCC): The main color of the kernel from at least three ears per ear family. The description of the kernel color can include, but is not limited to, (1) Yellow; or (2) White.
(57) Cob Color (COBCC; COBCC): The main color of the cob after shelling from at least three ears per ear family. The description of the cob color can include, but is not limited to, (1) Red; (2) Pink; or (3) White (e.g., Munsell value).
(58) Additional Definitions Relating to Plant Culture and Plant Characteristics
(59) Final number of plants per plot EMRGN
(60) Region Developed (REGNN): Various response can include, but are not limited to, (1) Northwest; (2) Northcentral; (3) Northeast; (4) Southeast; (5) Southcentral; (6) Southwest; or (7) Other.
(61) Cross type (CRTYN); The cross types include, but are not limited to, (1) sc 2; (2) dc; (3) 3w; (4) msc; (5) m3w; (6) inbred; (7) rel. line; or (8) Other.
(62) Days to Emergence (EMERN).
(63) Percent Root lodging (before anthesis) (ERTLP).
(64) Percent Brittle snapping (before anthesis) (GRSNP).
(65) Tassel branch angle (degree) of 2nd primary lateral branch (at anthesis) (TBANN).
(66) Days to 50% silk in adapted zone (DSAZN).
(67) Heat units to 90% pollen shed (from emergence) (HU9PN).
(68) Days from 10% to 90% pollen shed (DA19N).
(69) Heat units from 10% to 90% pollen shed (HU19N).
(70) Heat units to 10% pollen shed: (from emergence) (HU1PN) Leaf sheath pubescence of second leaf above the ear (at anthesis) 1-9 (1=none) (LSPUR).
(71) Angle (degree) between stalk and 2nd leaf above the ear (at anthesis) (ANGBN).
(72) Color of second leaf above the ear (at anthesis) (CR2LN) (Munsell value).
(73) Glume color bars perpendicular to their veins (glume bands) (GLCBN): can be described as (1) absent or (2) present.

(74) Anther color (Munsell value) (ANTCN).
(75) Pollen Shed (PLQUR): Can be described numerically, for example, 1-9 (0=male sterile).
(76) Number of leaves above the top ear node (LAERN).
(77) Number of lateral tassel branches that originate from the central spike (LTBRN).
(78) Number of ears per stalk (EARPN).
(79) Husk color (Munsell value) 25 days after 50% silk (fresh) (HSKCN).
(80) Husk color (Munsell value) 65 days after 50% silk: (dry) (HSKDN).
(81) Leaf marginal waves: Can be described numerically, for example, 1-9 (1=none) (MLWVR).
(82) Leaf longitudinal creases (LFLCR): Can be described numerically, for example, 1-9 (1=none).
(83) Length (cm) of ear leaf at the top ear node (ERLLN).
(84) Width (cm) of ear leaf at the top ear node at the widest point (ERLWN).
(85) Plant height (cm) to tassel tip (PLHTN).
(86) Plant height (cm) to the top ear node (ERHCN).
(87) Length (cm) of the internode between the ear node and the node above (LTEIN).
(88) Length (cm) of the tassel from top leaf collar to tassel tip (LTASN).
(89) Days from 50% silk to 25% grain moisture in adapted zone (DSGMN).
(90) Shank length (cm) (SHLNN).
(91) Ear length (cm) (ERLNN).
(92) Diameter (mm) of the ear at the midpoint (ERDIN).
(93) Weight (gm) of a husked ear (EWGTN).
(94) Kernel rows (KRRWR): Can be described as, for example, (1) Indistinct or (2) Distinct.
(95) Kernel row alignment (KRNAR): Can be described as, for example, (1) Straight; (2) Slightly Curved; or (3) Curved.
(96) Ear taper (ETAPR): Can be described as, for example, (1) Slight; (2) Average; or (3) Extreme.
(97) Number of kernel rows (KRRWN).
(98) Husk tightness 65 days after 50% silk (HSKTR): Can be described numerically, for example, 1-9 (1=loose).
(99) Diameter (mm) of the cob at the midpoint (COBDN).
(100) Yield (YKGHN) (kg/ha) Kg per Hectare.
(101) Hard endosperm color (KRCLN) (Munsell value)
(102) Aleurone color (ALECN) (Munsell value)
(103) Aleurone color pattern (ALCPR): Can be described, for example, as (1) homozygous or (2) segregating.
(104) Kernel length (mm) (KRLNN).
(105) Kernel width (mm) (KRWDN).
(106) Kernel thickness (mm) (KRDPN).
(107) One hundred kernel weight (gm) (K1KHN)
(108) Husk extension (HSKCR): Can be described as, for example, (1) Short (ear exposed); (2) Medium (8 cm); (3) Long (8-10 cm); or (4) Very long (>10 cm).
(109) Percent round kernels on 13/64 slotted screen (KRPRN).
(110) Position of ear 65 days after 50% silk (HEPSR): Can be described as, for example, (1) Upright; (2) Horizontal; or (3) Pendent.
(111) Percent dropped ears 65 days after anthesis (DPOPP).
(112) Percent root lodging 65 days after anthesis (LRTRP).
(113) Heat units to 25% grain moisture (from emergence) (HU25N).
(114) Heat units from 50% silk to 25% grain moisture in adapted zone (HUSGN).
Other Definitions
(115) A, AN, THE—As used herein, “a,” “an” or “the” can mean one or more than one. For example, a cell can mean a single cell or a multiplicity of cells.
(116) AND/OR—As used herein, “and/or” refers to and encompasses any and all possible

combinations of one or more of the associated listed items, as well as the lack of combinations when interpreted in the alternative (or).

(117) ABOUT—The term "about," as used herein when referring to a measurable value such as an amount of a compound or agent, dose, time, temperature, and the like, is meant to encompass variations of ±20%, ±10%, ±5%, ±1%, ±0.5%, or even ±0.1% of the specified amount.

(118) PLANT—The term "plant" is intended to encompass plants at any stage of maturity or development, including a plant that has been detasseled or from which seed or grain have been removed. A seed or embryo that will produce the plant is also included within the term plant.

(119) PLANT PART—As used herein, the term "plant part" includes but is not limited to pollen, tassels, seeds, branches, fruit, kernels, ears, cobs, husks, stalks, root tips, anthers, stems, roots, flowers, ovules, stamens, leaves, embryos, meristematic regions, callus tissue, anther cultures, gametophytes, sporophytes, microspores, protoplasts, and the like. Tissue culture of various tissues of plants and regeneration of plants therefrom is well known in the art. Plant cell as used herein includes plant cells that are intact in plants and/or parts of plants, plant protoplasts, plant tissues, plant cell tissue cultures, plant calli, plant clumps, and the like. Further, as used herein, "plant cell" refers to a structural and physiological unit of the plant, which comprises a cell wall and also may refer to a protoplast. A plant cell of the present invention can be in the form of an isolated single cell or can be a cultured cell or can be a part of a higher-organized unit such as, for example, a plant tissue or a plant organ. Thus, as used herein, a "plant cell" includes, but is not limited to, a protoplast, a gamete producing cell, and a cell that regenerates into a whole plant.

(120) ALLELE—Any alternative forms of sequence. Diploid cells carry two alleles of the genetic sequence. These two sequence alleles correspond to the same locus (i.e., position) on homologous chromosomes.

(121) ELITE INBRED, ELITE LINE—Maize plant that is substantially homozygous and which contributes useful agronomic and/or phenotypic qualities when used to produce hybrids that are commercially acceptable.

(122) GENE SILENCING—The loss or inhibition of the expression of a gene.

(123) GENOTYPE—genetic makeup.

(124) LINKAGE—The tendency of a segment of DNA on the same chromosome to not separate during meiosis of homologous chromosomes. Thus during meiosis this segment of DNA remains unbroken more often than expected by chance.

(125) LINKAGE DISEQUILIBRIUM—The tendency of alleles to remain in linked groups when segregating from parents to progeny more often than expected from chance.

(126) LOCUS—A defined segment of DNA. This segment is often associated with an allele position on a chromosome.

(127) PHENOTYPE—The detectable characteristics of a maize plant. These characteristics often are manifestations of the genotype/environment interaction.

(128) BACKCROSS and BACKCROSSING refer to the process whereby a progeny plant is repeatedly crossed back to one of its parents. In a backcrossing scheme, the "donor" parent refers to the parental plant with the desired gene or locus to be introduced. The "recipient" parent (used one or more times) or "recurrent" parent (used two or more times) refers to the parental plant into which the gene or locus is being introduced. For example, see Ragot, M. et al. Marker-assisted Backcrossing: A Practical Example, in Techniques et Utilisations des Marqueurs Moleculaires Les Colloques, Vol. 72, pp. 45-56 (1995); and Openshaw et al., Marker-assisted Selection in Backcross Breeding, in Proceedings of the Symposium "Analysis of Molecular Marker Data," pp. 41-43 (1994). The initial cross gives rise to the F1 generation. The term "BC1" refers to the second use of the recurrent parent, "BC2" refers to the third use of the recurrent parent, and so on.

(129) CROSS or CROSSED refer to the fusion of gametes via pollination to produce progeny (e.g., cells, seeds or plants). The term encompasses both sexual crosses (the pollination of one plant by another) and selfing (self-pollination, e.g., when the pollen and ovule are from the same plant) and

use of haploid inducer to form haploid seeds. The term “crossing” refers to the act of using gametes via pollination to produce progeny.
(130) CULTIVAR and VARIETY refer to a group of similar plants that by structural or genetic features and/or performance can be distinguished from other varieties within the same species.
(131) TRANSGENE refers to any nucleotide sequence used in the transformation of a plant (e.g., maize), animal, or other organism. Thus, a transgene can be a coding sequence, a non-coding sequence, a cDNA, a gene or fragment or portion thereof, a genomic sequence, a regulatory element and the like. A “transgenic” organism, such as a transgenic plant, is an organism into which a transgene has been delivered or introduced and the transgene can be expressed in the transgenic organism to produce a product, the presence of which can impart an effect and/or a phenotype in the organism.
(132) INTRODUCE OR INTRODUCING (and grammatical equivalents thereof) in the context of a plant cell, plant and/or plant part means contacting a nucleic acid molecule with the plant, plant part, and/or plant cell in such a manner that the nucleic acid molecule gains access to the interior of the plant cell and/or a cell of the plant and/or plant part i.e. transformation. It also refers to both the natural and artificial transmission of a desired allele, transgene, or combination of desired alleles of a genetic locus or genetic loci, or combination of desired transgenes from one genetic background to another. For example, a desired allele or transgene at a specified locus can be transmitted to at least one progeny via a sexual cross between two parents of the same species, where at least one of the parents has the desired allele or transgene in its genome. Alternatively, for example, transmission of an allele or transgene can occur by recombination between two donor genomes, e.g., in a fused protoplast, where at least one of the donor protoplasts has the desired allele in its genome. The desired allele may be a selected allele of a marker, a QTL, a transgene, or the like. Offspring comprising the desired allele or transgene can be repeatedly backcrossed to a line having a desired genetic background and selected for the desired allele or transgene, with the result being that the desired allele or transgene becomes fixed in the desired genetic background.
I. Embodiments of the Invention
(133) A. Inbred and Hybrid Production
(134) Certain regions of the Corn Belt can have specific difficulties related to grain production that other regions may not have. Thus, the corn hybrids developed from inbreds should have traits that overcome or at least minimize these regional growing problems. Examples of these problems include Gray Leaf Spot infection in the eastern Corn Belt, cool temperatures during seedling emergence in the northern Corn Belt, Corn Lethal Necrosis (CLN) disease in the Nebraska region and soil with excessively high pH levels in the west. Hybrid combinations employ inbreds that address these specific issues resulting in the development of hybrids which are well adapted to niche production challenges. However, the aim of seed producers is to provide a number of traits to each inbred so that the corresponding hybrid combinations can be useful across broad regions of the Corn Belt. Biotechnology techniques offer tools, such as microsatellites, SNPs, RFLPs, RAPDs and the like, to breeders to accomplish the goal of providing desirable traits in inbreds.
(135) To produce hybrids, inbreds are developed using numerous methods, which allow for the introduction of needed traits into the inbreds used in the hybrid combination. Hybrids are not often uniformly adapted for use throughout the entire U.S. Corn Belt, but most often are adapted for specific regions of the Corn Belts because for example, northern regions of the Corn Belt require shorter season hybrids than do southern regions. Hybrids that grow well in Colorado and Nebraska soils may not flourish in richer Illinois and lowa soils. Thus, several different major agronomic traits are important in hybrid combination for growth in the various Corn Belt regions, and these traits have an impact on hybrid performance.
(136) If there is a pool of desirable maize varieties for use as parents then development of a corn hybrid involves one step crossing the selected maize variety with at least one different maize variety to produce the hybrid progeny. This single crossing step is possible because breeders have

been developing inbreds from different maize germplasm pools since the early 1900s, which can be used in hybrid combinations. However, to keep producing better and higher yielding hybrids, better inbreds must be developed. Inbred development involves the step of selecting plants from various germplasm pools, or from the same germplasm pool for making initial breeding crosses; and then either producing haploid seed from the cross and selfing as needed, or selfing the breeding crosses for several generations to produce a series of inbred lines, which, although different from each other, breed true and are highly uniform. During plant selection in each generation, uniformity of plant type is maintained to ensure homozygosity and phenotypic stability. A consequence of the homozygosity and homogeneity of the inbred lines is that the hybrid between a defined pair of inbreds, regardless of the method by which the inbreds were produced, will always be the same.
(137) The maize variety and seed of the present invention can be employed to carry an agronomic package of this invention into a hybrid. Additionally, as described herein the inbred line can comprise one or more transgenes that are then introduced into the hybrid seed. When the maize variety parents that give a superior hybrid have been identified, the hybrid seed can be reproduced indefinitely as long as the homogeneity of the maize variety parents is maintained.
(138) Any breeding methods using the maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, and its progeny are part of this invention. Inbred development can be accomplished by different methods, for example, pedigree selection, backcrossing, recurrent selection, haploid/doubled haploid production. An inbred plant with similar genetic or characteristics to maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 could be produced by applying double haploid methods to the progeny of a cross between maize inbred TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and a different plant. Double haploid methods produce substantially homozygous plants without repeated backcrossing steps. The haploid/doubled haploid process of developing inbreds starts with the induction of a haploid by using, for example, KWS inducers lines, Krasnador inducers lines, stock six inducer lines (Coe, 1959, Am. Nat. 93:381-382). The haploid cell is then doubled, and the doubled haploid plant is produced. In some embodiments, a method of producing an maize plant with doubled haploid chromosomes derived from the maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 the method comprising: (a) crossing a plant, wherein said plant may have one or more traits, with an inducer maize plant to produce a progeny with haploid chromosomes; and (b) doubling the haploid chromosomes in the progeny to produce a maize plant with doubled haploid chromosomes. In some embodiments, the progeny may be for example a cell, seed, embryo or plant. In further embodiments, the maize plant with doubled haploid chromosomes produced by step (b) above is a maize inbred plant with the characteristics of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684. In other embodiments, the plant crossed with an inducer in step (a) is a hybrid maize plant produced by crossing maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with a different plant.
(139) For examples of the use of double hybrid methods, see Prasanna et al. (eds) *Doubled Haploid Technology in Maize Breeding: Theory and Practice* Mexico, D.F.: CIMMYT, Barnabus et al. “Colchicine, an efficient genome doubling agent for maize microsporescultured in anthero”, Plant Cell Reports, v. 18:858-862, 1999 or US patent application 2003/0005479. Sometimes this doubled haploid can be used as an inbred but sometimes it is further self pollinated to finish the inbred development. Another breeding process is pedigree selection which uses the selection in an F2 population produced from a cross of two genotypes (often elite inbred lines), or selection of progeny of synthetic varieties, open pollinated, composite, or backcrossed populations. Pedigree selection is effective for highly heritable traits but other traits, such as yield, require replicated test crosses at a variety of stages for accurate selection.
(140) The maize variety and hybrid corn lines of the present invention can be employed in a variety of breeding methods that can be selected, depending on the mode of reproduction, the trait and/or

the condition of the germplasm. Thus, any breeding methods using the inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 or its progeny are part of this invention. Such methods can include, but are not limited to, marker assisted breeding, selection, selfing, backcrossing, hybrid production, and crosses to populations.

(141) All plants and plant cells produced using maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 are encompassed within the present invention, which also encompasses the corn variety used in crosses with other, different, corn varieties to produce corn hybrid seeds and hybrid plants and the grain produced on the hybrid plant. This invention includes progeny plants and plant cells, which upon growth and differentiation produce corn plants having the physiological and morphological characteristics of the maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 when grown in the same environmental conditions.

(142) Maize breeders select for a variety of traits in inbred plants that impact hybrid performance in addition to selecting for acceptable parental traits. Such traits include, but are not limited, to yield potential in hybrid combination, dry down, maturity, grain moisture at harvest, green snap, resistance to root lodging, resistance to stalk lodging, grain quality, disease and insect resistance, ear, and plant height. Additionally, because hybrid performance may differ in different soil types such as those having low levels of organic matter, clay, sand, black, high pH, or low pH; or in different environments such as wet environments, drought environments, and no tillage conditions multiple trials testing for agronomic traits must be run to assert hybrid performance across environments. These traits are governed by a complex genetic system that makes selection and breeding of an inbred line extremely difficult. However, even if an inbred, in hybrid combination, has excellent yield (a desired characteristic), it may not be useful for hybrid seed production if the inbred lacks acceptable parental traits, for example, seed size, pollen production, good silks, plant height, etc.

(143) The following example is provided to illustrate the difficulty of breeding and developing inbred lines. Two inbreds compared for similarity of 29 traits differed significantly for 18 traits between the two lines. If 18 simply inherited single gene traits were polymorphic with gene frequencies of 0.5 in the parental lines, and assuming independent segregation (as would essentially be the case if each trait resided on a different chromosome arm), then the specific combination of these traits as embodied in an inbred would only be expected to become fixed at a rate of one in 262,144 possible homozygous genetic combinations. Selection of the specific inbred combination is also influenced by the specific selection environment on many of these 18 traits which makes the probability of obtaining this one inbred even more remote. In addition, most traits in the corn genome are not single dominant genes; they are multi-genetic with additive gene action but not dominant gene action. Thus, the general approach of producing a non-segregating F1 generation and self pollinating to produce an F2 generation that segregates for traits and then selecting progeny from the F2 generation with the desired visual traits does not easily lead to a useful inbred. Great care and breeder expertise must be used in the selection of breeding material to continue to increase yield and enhance desirable agronomic features of inbreds and resultant commercial hybrids.

(144) In one embodiment, a method of producing a plant of this invention is by planting the seed of TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, which is substantially homozygous, self-pollinating or sib pollinating the resultant plant in isolate environment, and harvesting the resultant seed. The F1 hybrid seed can be produced using two distinct inbreds, the male inbred contributing pollen to the female seed producing parent, the female seed producing parent, on the other hand, is not contributing pollen to the seed. Thus, in some embodiments, a method is provided for producing an hybrid maize seed by crossing a plant of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with a different maize plant (e.g., a different inbred line), and harvesting the resultant hybrid maize

seed. A maize plant of the present invention can act as a male or female part in hybrid production.
(145) A method is also provided for producing maize seed comprising growing the plant of this invention until seed is produced and harvesting the seed, wherein the harvested seed is inbred or hybrid or haploid seed. Plants and plant parts produced by the seed of this method is also provided herein. Additionally, provided herein is a method of producing hybrid seed corn from this inbred corn line and producing hybrid plants and seeds from the hybrid seed corn of this invention.
(146) Thus, in some embodiments, the invention provides hybrid seed, produced by planting, in pollinating proximity, seeds of corn inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and seeds of another inbred line. The corn plants resulting from said planting are cultivated; emasculation of one of the inbred lines (i.e., the selected inbred plant) and allowing pollination to occur. Seeds produced by plants of the selected inbred can be harvested. In further embodiments, seeds of corn inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 are planted and cultivated. Alternatively, emasculated plants are pollinated with preserved maize pollen (as described in U.S. Pat. No. 5,596,838 to Greaves). The seeds produced by the inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 pollinated with the preserved pollen can be harvested. The hybrid seed produced by the hybrid combination of plants of inbred corn seed designated TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and plants of another inbred line or produced by the plants of inbred corn seed designated TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 pollinated by preserved pollen are included in the present invention. This invention further encompasses hybrid plants and plant parts thereof including but not limited to the grain and pollen of the plant grown from this hybrid seed.
(147) In two alternative embodiments, the method is provided for producing an hybrid maize seed, the method comprising crossing a plant of maize variety plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with a different maize variety (e.g., a different inbred line), wherein the pollen of the maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 pollinates the different maize variety, or in the alternative the pollen of the different maize variety pollinates maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, and the resultant hybrid maize seed is harvested.
(148) In particular embodiments, this invention is directed to the unique combination of traits that combine in corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684. Also encompassed within this invention is an F1 hybrid maize seed comprising an inbred maize plant cell of inbred maize plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684.
(149) The invention further relates to methods for producing other maize breeding lines derived from the corn inbred of this invention by crossing the maize inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 with a second maize plant and growing the progeny seed to yield a inbred TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684-derived maize plant. Thus, in some embodiments of this invention, a method is provided for producing a maize plant derived from the inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, the method comprising the steps of: (a) growing a hybrid progeny plant wherein the maize variety of this invention is a parent (b) crossing the hybrid progeny plant with itself or a different plant to produce a seed of a progeny plant; (c) growing the progeny plant from said seed and crossing the progeny plant with itself or a different plant; and (d) repeating steps (c) for an additional generation to produce a maize plant derived from the inbred plant TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684. The present invention also provides a maize seed produced by crossing the plant of this invention with itself or a different maize plant.
(150) Thus, other aspects of this invention include a method for developing a maize plant in a

maize plant breeding program, comprising applying plant breeding techniques comprising recurrent selection, backcrossing, pedigree breeding, marker enhanced selection, haploid/double haploid production, or transformation to the maize plant of this invention, or its parts, wherein application of said techniques results in development of a maize plant.

(151) B. Transfer of Additional Traits into Inbred Corn Line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684

(152) A specific location on a chromosome can be referred to as a locus. Trait conversion refers to a variety that has been modified such that the variety retains its physiological and morphological characteristics except for those changed by the introduction of the trait. Thus, a variety undergoing a herbicide resistance trait conversion will evidence the additional trait of resisting damage by the herbicide. The variety will after trait conversion have one or more loci with a specific desired trait. Such a variety modification may be through mutant genes, transgenes, or native traits. A maize line and any minor genetic modifications which may include a trait conversion, a mutation, or a variant is a variety.

(153) The use of an inbred maize plant, such as the inbred of the present invention, as a recurrent parent in a breeding program is referred to as backcrossing. Backcrossing is often employed to introduce an additional trait (e.g., targeted trait or trait of interest) or trait(s), either transgenic or nontransgenic, into a recurrent parent. A plant with a desired trait or locus is crossed into a recurrent maize parent usually in one or more backcrosses. If markers are employed to assist in selection of progeny that have the desired trait and recurrent parent background genetics, then the number of backcrosses needed to recover the recurrent parent with the desired trait or locus can be relatively few, e.g., two or three. However, 3, 4, 5 or more backcrosses are often required to produce the desired inbred with the gene or locus conversion in place. The number of backcrosses needed for a trait introduction is often linked to the genetics of the line carrying the trait and the recurrent parent and the genetics of the trait. Multigenic traits, recessive alleles and unlinked traits can affect the number of backcrosses that may be necessary to achieve the desired backcross conversion of the inbred.

(154) Basic maize crossing techniques, as well as other corn breeding methods including recurrent, bulk or mass selection, pedigree breeding, open pollination breeding, marker assisted selection/breeding, double haploids development and selection breeding are well known in the art (see, e.g., Hallauer, *Corn and Corn Improvement*, Sprague and Dudley, 3rd Ed. 1998). Dominant, single gene traits or traits with obvious phenotypic changes are particularly well managed in backcrossing programs, as are well known in the art. A backcross conversion or locus conversion both refer to a product of a backcrossing program.

(155) A backcrossing program is more complicated when the trait is a recessive gene. A determination of the presence of the recessive gene requires the use of some testing to determine if the trait has been transferred. Use of markers to detect the gene reduces the complexity of trait identification in the progeny. A marker specific for a recessive trait, such as a single nucleotide polymorphism (SNP), can increase the efficiency and speed of tracking the recessive trait within a backcrossing program.

(156) The last backcross generation can be selfed, if necessary, to give pure breeding progeny for the nucleic acid(s) being transferred. The resulting plants generally have essentially all of the morphological and physiological characteristics of the inbred corn line of interest, in addition to the transferred trait(s) (e.g., one or more gene traits). The exact backcrossing protocol will depend on the trait being altered to determine an appropriate testing protocol.

(157) Thus, in some embodiments, one or more additional traits can be introduced into a plant of this invention using any method known in the art for introducing traits into plants. Nucleotide sequences encoding traits of interest can all be located at the same genomic locus in the donor, non-recurrent parent, and in the case of transgenes, can be part of a single DNA construct integrated into the donor's genome or into additional chromosomes integrated into the donor's genome.

Alternatively, if the nucleotide sequences of interest are located at different genomic loci in the donor, non-recurrent parent, backcrossing can be carried out to establish all of the morphological and physiological characteristics of the plant of the invention in addition to the nucleotide sequences encoding the traits of interest in the resulting maize inbred line.

(158) Accordingly, the present invention provides a method of introducing or introgressing at least one additional trait into the maize inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, comprising the steps of: (a) crossing a plant grown from the seed of the maize inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 (which is the recurrent parent, representative seed of which has been deposited), with a donor plant of another maize line that comprises at least one additional trait to produce F1 plants; (b) selecting F1 plants having the at least one additional trait to produce the selected F1 progeny plants; (c) crossing the F1 plants of (b) with the recurrent parent to produce backcrossed progeny plants having the at least one additional trait; (d) selecting for backcrossed progeny plants that have at least one of the additional traits and physiological and morphological characteristics of maize inbred line of the recurrent parent to produce selected backcrossed progeny plants; and (e) repeating the crossing of the selected backcrossed progeny to the recurrent parent of step (c) and the selecting of step (d) in succession to produce a plant that comprises at least one additional trait and all of the physiological and morphological characteristics of the maize inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 when grown in the same environmental conditions (e.g., essentially the recurrent parent having the at least one additional trait).

(159) In some embodiments of this invention, the at least one additional trait comprises the trait of male sterility, herbicide resistance, insect resistance, disease resistance, altered starch, modified amylase starch, amylose starch, waxy starch, or any combination thereof. In other embodiments of this invention, the at least one desired trait is conferred by a nucleic acid molecule encoding an enzyme that includes, but is not limited to, a phytase, a stearyl-ACP desaturase, a fructosyltransferase, a levansucrase, an amylase, an invertase, a starch branching enzyme, or any combination thereof.

(160) In some embodiments, the selecting and crossing steps of (e) are repeated at least 3 times in order to produce a plant that comprises the at least one desired trait and all of the physiological and morphological characteristics of the maize inbred line of the recurrent parent in the present invention (listed in Table 1) when grown under the same environmental conditions (as determined at the 5% significance level). In other embodiments, the selecting and crossing steps of (e) are repeated from 0 to 2 times, from 0 to 3 times, from 0 to 4 times, 0 to 5 times, from 0 to 6 times, from 0 to 7 times, from 0 to 8 times, from 0 to 9 times or from 0 to 10 times, in order to produce a plant that comprises the at least one additional trait and all of the physiological and morphological characteristics of the maize inbred line of the recurrent parent in the present invention. In other embodiments, the crossing and growing steps of (a) and (b) in step (c) are repeated from 0 to n times (wherein n can be any number) in order to produce a plant that comprises the at least one additional trait and all of the physiological and morphological characteristics of the maize inbred line of the recurrent parent in the present invention.

(161) Another aspect of the invention provides a maize plant having essentially all the physiological and morphological characteristics of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and further comprising an additional trait, wherein the additional trait is selected from the group consisting of increased water stress resistance, waxy starch, male sterility or restoration of male fertility, modified carbohydrate metabolism, modified protein metabolism, modified fatty acid metabolism, altered starch, thermotolerant amylase, herbicide resistance, insect resistance, nematode resistance, bacterial disease resistance, fungal disease resistance, and viral disease resistance. In some embodiments, the additional trait is conferred by introducing a transgene. Some embodiments of the invention provide a seed produced

by the maize plant having essentially all the physiological and morphological characteristics of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and further comprising an additional trait.

(162) The method of introducing traits as described herein can be done with fewer back-crossing events if the trait and/or the genotype of the present invention is selected for or identified through the use of markers. SSR, microsatellites, single nucleotide polymorphisms (SNPs) and the like decrease the amount of breeding time required to locate a line with the desired trait or traits and the characteristics of the present invention. Backcrossing in two or even three traits (for example the glyphosate resistance, Europe corn borer resistance, corn rootworm resistance) is routinely done with the use of marker assisted breeding techniques and or selection pressure testing. Introduction of transgenes or mutations into a maize line is known as single gene conversion. More than one gene and, in particular, transgenes and/or mutations that are readily tracked with markers, can be moved during the same "single gene conversion" process. This single gene conversion process results in a line comprising more desired or targeted traits than just the one but still having the characteristics of the plant line of the present invention plus those characteristics added by the desired/targeted traits.

(163) In some aspects, the present invention provides a converted seed, plant, plant part or plant cell of inbred maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, representative seed of the maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 having been deposited, wherein the converted seed, plant, plant part or plant cell comprises a locus conversion, and wherein the plant or a plant grown from the converted seed, plant part or plant cell comprises the locus conversion and otherwise comprises the phenotypic characteristics of maize variety TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 listed in Table 1 when grown under the same environmental conditions.

(164) 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 one or more loci with a specific desired trait, such as male sterility, Insect resistance, disease resistance or herbicide tolerance or resistance. Examples of single locus conversions include mutant genes, transgenes and native traits finely mapped to a single locus. One or more locus conversion traits may be introduced into a single corn variety.

(165) Genetic variants of inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 that are naturally-occurring or created through traditional breeding methods using inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 are also intended to be within the scope of this invention. In particular embodiments, the invention encompasses plants of this invention and parts thereof further comprising one or more additional traits, in particular, specific, single gene transferred traits. Examples of traits that may be transferred include, but are not limited to, herbicide resistance, disease resistance (e.g., bacterial, fungal or viral disease), nematode resistance, tolerance to abiotic stresses (e.g., drought, temperature, salinity), yield enhancement, improved nutritional quality (e.g., oil starch and protein content or quality), modified metabolism (e.g. protein, carbohydrates, starch, amylase,) altered reproductive capability (e.g., male sterility) or other agronomically important traits.

(166) Such traits may be introduced into a plant of this invention from another corn line or through direct transformed into a plant of this invention (discussed below). One or more new traits can be transferred to a plant of this invention, or, alternatively, one or more traits of a plant of this invention are altered or substituted. The introduction of the trait(s) into a plant of this invention may be achieved by any method of plant breeding known in the art, for example, pedigree breeding, backcrossing, doubled-haploid breeding, and the like.

(167) C. Nucleic Acids for Introduction into Maize Plants of the Present Invention

(168) As would be appreciated by one of skill in the art, any nucleotide sequence of interest can be

introduced into the plants and/or parts thereof of the present invention. Some exemplary nucleotide sequences and traits that may be used with the present invention are provided herein.
(169) Methods and techniques for introducing and/or introgressing a trait or nucleotide sequence into a plant of the present invention through breeding, transformation, site specific insertion, mutation and the like, are well known and understood by those of ordinary skill in the art. Nonlimiting examples of such techniques include, but are not limited to, anther culturing, haploid/double haploid production, (including, but not limited to, stock six, which is a breeding/selection method using color markers), transformation, irradiation to produce mutations, and chemical or biological mutation agents.
(170) 1. Male Sterility
(171) As described herein, the inbred and hybrid lines plants of this invention can comprise male sterility. Male sterility and/or CMS (cytoplasmic male sterility) systems for maize parallel the CMS type systems, were first used in maize in the seventies but were to widely embraced; however, CMS has have been routinely used in hybrid production in sunflower plants. A number of methods are available to generate male sterile plants including, but not limited to, introduction into the plant of nucleotide sequences that confer male sterility, by chemicals, and/or by a mixture of nucleotide sequences conferring male sterility, natural or induced sterility mutations, and/or chemicals.
(172) As described herein, the inbred and hybrid plants of this invention can comprise the trait of male sterility. Male sterility is useful, for example, in hybrid production for elimination of pollen shed from the seed producing parent. Sterility can be produced by pulling or cutting tassels from the plant, i.e., detasseling, use of gametocides, or use of genetic material to render the plant sterile using a CMS type of genetic control or a nuclear genetic sterility, use of chemicals, for example herbicides that inhibit or kill pollen. The seed producing parent can be grown in isolation from other pollen sources except for the pollen source, which is the male fertile inbred, which serves as the male parent in the hybrid. To facilitate pollination of the seed producing (female) parent, the male fertile inbreds can be planted in rows near the male sterile (female) inbred.
(173) In hybrid seed production using the standard CMS system, three different maize lines are employed. The first line is cytoplasmic male-sterile. This line will be the seed producing parent line. The second line is a fertile inbred that is the same as or isogenic with the seed producing inbred parent but lacking the trait of male sterility. This is a maintainer line used to make new inbred seed of the seed producing male sterile parent. The third line is a different inbred which is fertile, has normal cytoplasm and carries a fertility restoring gene. This line is called the restorer line in the CMS system. The CMS cytoplasm is inherited from the maternal parent (or the seed producing plant); therefore, in order for the hybrid seed produced on such a plant to be fertile, the pollen used to fertilize this plant must carry the restorer gene. The positive aspect of this process is that it allows hybrid seed to be produced without the need for detasseling the seed parent. However, this system does require breeding of all three types of lines: 1) a male sterile line-to carry the CMS, 2) a maintainer line; and 3) a line carrying the fertility restorer gene.
(174) Accordingly, in some embodiments of the present invention, sterile hybrids are produced and the pollen necessary for the formation of grain on these hybrids is supplied by interplanting of fertile inbreds in the field with the sterile hybrids.
(175) A number of additional techniques exist that are designed to avoid detasseling in maize hybrid production. Nonlimiting examples of such techniques include switchable male sterility, lethal genes in the pollen or anther, inducible male sterility and/or male sterility genes with chemical restorers. Additional examples include, but are not limited to, U.S. Pat. No. 6,025,546, which describes the use of tapetum-specific promoters and the barnase gene to produce male sterility, and U.S. Pat. No. 6,627,799, which describes modifying stamen cells to provide male sterility. Therefore, one aspect of the present invention provides a corn plant of this invention comprising one or more nucleotide sequences that restore male fertility to male-sterile maize inbreds or hybrids and/or one or more nucleotide sequences or traits to produce male sterility in

maize inbreds or hybrids.
(176) Furthermore, methods for genetic male sterility are disclosed in EPO Publication No. 89/3010153.8, PCT Publication No. WO 90/08828 and U.S. Pat. Nos. 4,654,465, 4,727,219, 3,861,709, 5,432,068 and 3,710,511. Gametocides, some of which are taught in U.S. Pat. No. 4,735,649 (incorporated by reference) can be employed to make the plant male sterile. Gametocides, including, but not limited to, glyphosate, and its derivatives are chemicals or substances that negatively affect the pollen or at least the fertility of the pollen and provide male sterility to the seed producing parent.
(177) It is noted that hybrid production employing any most forms of male sterility including mechanical emasculation can have a small occurrence of self pollinated female inbred seeds along with the intended F1 hybrid seeds. Great measures are taken to avoid the inbred seed production in a hybrid seed production field; but inbred seed can occur during F1 seed production and it gets harvested with the hybrid seed harvest.
(178) Inbred seed in a sample of hybrid seed may be detected using molecular markers. Alternatively, the seed sample can be planted and an inbred capture process can be used to isolate inbred seed from the hybrid F1 seed sources. The inbred plants tend to be readily distinguished from the hybrid plants due to the inbreds having a stunted appearance, i.e., shorter plant, smaller ear, etc. Self pollination of the stunted plants grown from these identified putative inbred plants produces either the female inbred seed, if it was an inbred plant or if it was a weak hybrid than the hybrid kernel will be F2 seed. The resultant plants are observed for size or they can be tested by markers to identify any inbred plants. The identified inbred plants can be selected and self-pollinated to form the inbred seed.
(179) 2. Additional Traits of Interest
(180) As discussed above, backcrossing of recessive traits has allowed known mutant traits to be moved into elite germplasm. Mutations can be introduced in germplasm by the plant breeder. Mutations can also result from plant or seed or pollen exposure to temperature alterations, culturing, radiation in various forms, chemical mutagens like EMS and like, as are well known in the art. Non-limiting examples of mutant genes that have been identified and introduced into elite maize useful with this invention include the genotypes numerous sterility and partial sterility genes, herbicide resistant mutants, phytic acid mutants, waxy (wx), amylose extender (ae), dull (du), horny (h), shrunken (sh), brittle (bt), floury (fl), opaque (o), and sugary (su). Some of the bracketed nomenclature for these mutant genes is based on the effect these mutant genes have on the physical appearance and phenotype of the kernel.
(181) Additional mutations useful with this invention include, but are not limited to, those that result in the production of starch with markedly different functional properties even though the phenotypes of the seed and plant remain the same. Such genotypes include, but are not limited to, sugary-1 (su1), sugary-2 (su2); shrunken 1 (sh1) and shrunken 2 (sh2).
(182) Additional, exemplary nucleic acid molecules that can be introduced into a plant of the present invention include, but are not limited to, nucleotide sequences that confer insect resistance including, but not limited to, resistance to Corn Rootworm in the event DAS-59122-7, Mir604 Modified Cry3A event, Event 5307 Syngenta, MON 89034, MON 88017 *Bacillus thuringiensis* (Cry genes) Cry34/35Ab1, CrylA.105, CrylF, Cry2Ab2, CrylA, CrylAB, CrylAc Cry3Bb1, or any combination thereof. Thus, for example, in some embodiments, an insecticidal gene that can be introduced into a plant of the present invention is a CrylAb gene or a portion thereof, for example, introduced into a plant of the present invention from a maize line comprising a Bt-11 event as described in U.S. Pat. No. 6,114,608, (incorporated herein by reference) or from a maize line comprising a 176 Bt event as described in Koziel et al. (Biotechnology 11:194-200 (1993)).
(183) In other embodiments of this invention, nucleotide sequences that confer disease resistance are introduced and/or transformed into the inbred line. Non-limiting examples of such nucleotide sequences include, but are not limited to, a nucleotide sequence encoding Mosaic virus resistance, a

nucleotide sequence encoding an MDMV strain B coat protein whose expression confers resistance to mixed infections of maize dwarf mosaic virus and maize chlorotic mottle virus (Murry et al. *Biotechnology* (1993) 11:1559-64, a nucleotide sequence conferring resistance to Northern corn leaf blight, and a nucleotide sequence conferring resistance to Southern corn leaf blight, or any combination thereof.

(184) In additional embodiments, nucleotide sequences that confer herbicide resistance/tolerance are useful with the present invention, non-limiting examples of which comprise nucleotide sequences conferring resistance to herbicides for example imazethapyr, glyphosate, dicamba, and the like, and nucleotide sequences encoding Pat (phosphinothricin-N-acetyltransferase), Bar (bialophos), altered acetohydroxyacid synthase (AHAS) (confers tolerance to various imidazolinone or sulfonamide herbicides) (U.S. Pat. No. 4,761,373), or any combination thereof.

(185) Additional, non-limiting examples of nucleotide sequences conferring herbicide resistance/tolerance that are useful with the present invention, include nucleotide sequences conferring tolerance to imidazolinones (e.g., a “IT” or “IR” trait). U.S. Pat. No. 4,975,374 (incorporated herein by reference), relates to plant cells and plants containing a gene encoding a mutant glutamine synthetase (GS) having resistance to inhibition by herbicides that are known to inhibit GS, e.g., phosphinothricin and methionine sulfoximine. Also, expression of a *Streptomyces* bar gene encoding a phosphinothricin acetyl transferase in maize plants confers tolerance to the herbicide phosphinothricin or glufosinate (U.S. Pat. No. 5,489,520). U.S. Pat. No. 5,013,659, (incorporated herein by reference), is directed to plants that express a mutant acetolactate synthase (ALS) that renders the plants resistant to inhibition by sulfonylurea herbicides. U.S. Pat. No. 5,162,602 discloses nucleotide sequences that confer resistance to cyclohexanedione and aryloxyphenoxypropanoic acid herbicides. The tolerance is conferred by an altered acetyl coenzyme A carboxylase (ACCase). U.S. Pat. No. 5,554,798 discloses transgenic glyphosate tolerant maize plants, which tolerance is conferred by an altered 5-enolpyruvyl-3-phosphoshikimate (EPSP) synthase gene. U.S. Pat. No. 5,804,425 discloses transgenic glyphosate tolerant maize plants, which tolerance is conferred by an EPSP synthase gene derived from *Agrobacterium tumefaciens* CP-4 strain. Also, tolerance to a protoporphyrinogen oxidase inhibitor is achieved by expression of a protoporphyrinogen oxidase enzyme in plants as disclosed in U.S. Pat. Nos. 5,767,373, 6,282,837, or WO 01/12825. Another trait transferable to the plant of the present invention confers a safety effect or additional tolerance to an inhibitor of the enzyme hydroxyphenylpyruvate dioxygenase (HPPD) and transgenes conferring such trait are, for example, described in PCT Publication Nos. WO 9638567, WO 9802562, WO 9923886, WO 9925842, WO 9749816, WO 9804685 and WO 9904021. Any of the above described nucleotide sequences identified to confer herbicide resistance/tolerance can be used to confer such resistance/tolerance to the plants of the present invention. These nucleotide sequences can be introduced or transformed into the plants of the present invention alone or in any thereof.

(186) Additional embodiments of this present invention include nucleotide sequences conferring altered traits. Such altered traits include, but are not limited to, lignin composition and production (including but not limited to nucleotide sequences conferring the brown mid-rib trait), flowering, senescence, and the like, or any combination thereof.

(187) The present invention also encompasses methods for the introduction into a plant of this invention, one or more traits that have an effect on products or by-products of the corn plant such as the sugars, oils, protein, ethanol, biomass and the like. Such traits can include those that result in the formation of an altered carbohydrate or altered starch. An altered carbohydrate or altered starch can be formed as a result of expression of one or more introduced nucleotide sequences that affect synthases, branching enzymes, pullanases, debranching enzymes, isoamylases, alpha amylases, beta amylases, AGP, ADP and other enzymes which affect amylose and/or amylopectin ratio or content, or the branching pattern of starch.

(188) Introduced fatty acid modifying nucleotide sequences can also affect starch content and

therefore can be employed in the methods and plants of this invention. Additionally, introduced nucleotide sequences that are associated with or affect starch and carbohydrates can be adapted so that the nucleotide sequence or its enzyme product does not necessarily alter the form or formation of the starch or carbohydrate of the seed or plant but instead the introduced nucleotide sequence or its RNA, polypeptide, protein or enzyme can be adapted to degrade, alter, or otherwise change the formed starch or carbohydrate. Examples of this technology are shown, for example, in U.S. Pat. Nos. 7,033,627, 5,714,474, 5,543,570, 5,705,375, 7,102,057, each of which are incorporated by reference. An example of the use of an alpha amylase adapted in this manner in maize is described in U.S. Pat. No. 7,407,677, the content of which is also incorporated herein by reference.

(189) By way of example only, specific events (followed by their APHIS petition numbers) that can be introduced into maize plants by backcross breeding techniques include Monsanto's Drought Tolerant/MON 87460 (09-055-01p); Male Sterile, Fertility Restored, Visual Marker/DP-32138-1 (08-338-01p); (07-253-01p) Syngenta Lepidopteran Resistant/MIR 162; (07-152-01p) Pioneer's Corn Glyphosate & Imidazolinone Tolerant/98140; (04-362-01p) Syngenta Corn Corn Rootworm Protected/MIR604; (04-229-01p) Monsanto Corn High Lysine/LY038; 04-125-01p Monsanto Corn Corn Rootworm Resistant/MON 88017; 03-353-01p Dow Corn Corn Rootworm Resistant/59122; (03-181-01p) Dow Corn Lepidopteran Resistant & Phosphinothricin Tolerant/6275; (01-137-01p) Monsanto Corn Corn Rootworm Resistant/MON 863; (00-136-01p) Mycogen c/o Dow & Pioneer Corn Lepidopteran Resistant Phosphinothricin Tolerant/1507; (97-099-01p) Monsanto Corn Glyphosate Tolerant/NK603; (98-349-01p) AgrEvo Corn Phosphinothricin Tolerant and Male Sterile/MS6; (97-342-01p) Pioneer Corn Male Sterile and Phosphinothricin Tolerant/676, 678, 680; (97-265-01p) AgrEvo Corn Phosphinothricin Tolerant and Lepidopteran Resistant/CBH-351; (96-017-01p) Monsanto Corn European Corn Borer Resistant/MON 809, MON 810; (09-233-01p) Dow Corn 2,4-D and ACCase-Inhibitor Tolerant/DAS-40278-9; (11-244-01p) Pioneer Corn Insect Resistant and Glufosinate Tolerant/DP-ØØ4114-3; (10-336-01p) Syngenta Corn Rootworm Resistant/5307; (10-281-01p) Monsanto Corn Male Sterile/MON 87427; (11-342-01p) Genective Corn Glyphosate Tolerant/VCO-Ø1981-5; glyphosate tolerant event GA21 (97-09901p), the glyphosate tolerant event NK603 (00-011-01p), the glyphosate tolerant/Lepidopteran insect resistant event MON 802 (96-31701p) Mon810, the Lepidopteran insect resistant event DBT418 (96-29101p), the male sterile event MS3 (95-22801p), the Lepidopteran insect resistant event Bt11 (95-19501p), the phosphinothricin tolerant event B16 (95-14501p), the Lepidopteran insect resistant events MON 80100 (95-09301p) and MON 863 (01-137-01p), the phosphinothricin tolerant events T14, T25 (94-35701p), the Lepidopteran insect resistant event 176 (94-31901p), Western corn rootworm (04-362-01p), the phosphinothricin tolerant and Lepidopteran insect resistant event CBH-351 (92-265-01p), the transgenic corn event designated 3272 (05-280-01p) Syngenta's Corn Thermostable Alpha-amylase/3272 as described in US Patent Publication No. 20060230473 (hereby incorporated by reference) and the like, or any combination thereof. Additionally, the genes, promoters, transit peptides, targeting sequence and other genetic material used to form these various transgenic events can be used in to form a new transgene, promoter, targeting, etc. or to configure a synthetic gene for use in transformation, and after this genetic material is transformed into a line, which is stable. The new event can be backcrossed into germplasm of the present invention.

(190) In some embodiments, a combination of traits can be transformed or introduced into the plants of the present invention. This in some embodiments, a transgene can be introduced into a plant of a present invention which comprises a nucleotide sequence conferring tolerance to a herbicide and at least another nucleotide sequence encoding another trait, such as for example, an insecticidal protein. Such a combination of single traits can be, for example, a CrylAb gene and a bar gene. The introduction of a Bt11 event into a maize line, such as the line of the present invention, by backcrossing is exemplified in U.S. Pat. No. 6,114,608, and the present invention includes methods of introducing a Bt11 event into a plant of the present invention and to progeny

thereof using, e.g., markers as described in U.S. Pat. No. 6,114,608.

(191) D. Transformation of Corn Inbred TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 Plants and/or Parts Thereof

(192) The term transgenic plant refers to a plant having one or more genetic sequences that are introduced into the genome of a plant by a transformation method and the progeny thereof. With the advent of molecular biological techniques that have allowed the isolation and characterization of nucleic acids that encode 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 nucleic acids, or additional, or modified versions of native or endogenous nucleic acids (perhaps driven by different promoters) in order to alter the traits of a plant in a specific manner. Such foreign, additional and/or modified nucleic acids are referred to herein collectively as “transgenes.” The term “transgene,” as used herein, is not necessarily intended to indicate that the foreign nucleic acid is from a different plant species. For example, the transgene may be a particular allele derived from another corn line or may be an additional copy of an endogenous gene. Over the last twenty to twenty-five years several methods for producing transgenic plants have been developed. Therefore, in particular embodiments, the present invention also encompasses transformed plants and/or parts thereof (e.g., cells, seeds, anthers, ovules, and the like) of inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684.

(193) Transformation methods are techniques for integrating new nucleotide sequence(s) into the genome of a plant by recombinant nucleic acid technology, rather than by standard breeding practices. However, once a transgene is introduced into plant material and stably integrated, standard breeding practices can be used to move the transgene into other germplasm.

(194) Plant transformation generally involves the construction of an expression vector that will function in plant cells. Such a vector comprises DNA or RNA comprising a nucleic acid under control of, or operatively linked to, a regulatory element (for example, a promoter). The expression vector may contain one or more such operably linked nucleic acid/regulatory element combinations. The vector(s) may be in the form of, for example, a plasmid or a virus, and can be used, alone or in combination with other vectors, to provide transformed maize plants, using transformation methods as described below to incorporate transgenes into the genetic material of the maize plant(s).

(195) Any transgene(s) known in the art may be introduced into a maize plant, tissue, cell or protoplast according to the present invention, e.g., to improve commercial or agronomic traits, herbicide resistance, disease resistance (e.g., to a bacterial fungal or viral disease), insect resistance, nematode resistance, yield enhancement, nutritional quality (e.g., oil starch and protein content or quality), altered reproductive capability (e.g., male sterility), and the like or any combination thereof. Alternatively, a transgene may be introduced for the production of recombinant proteins (e.g., enzymes) or metabolites.

(196) A recombinant nucleic acid molecule of the invention can be introduced into a plant cell in a number of art-recognized ways. Suitable methods of transforming plant cells include microinjection (Crossway et al. *BioTechniques* 4:320-334 (1986)), electroporation (Riggs et al. *Proc. Natl. Acad. Sci. USA* 83:5602-5606 (1986)), *Agrobacterium*-mediated transformation (Hinchee et al. *Biotechnology* 6:915-921 (1988)), direct gene transfer (Paszkowski et al. *EMBO J.* 3:2717-2722 (1984)), ballistic particle acceleration using devices available, e.g., from Agracetus, Inc., Madison, Wis. and Dupont, Inc., Wilmington, Del. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al. *Biotechnology* 6:923-926 (1988)), protoplast transformation/regeneration methods (see U.S. Pat. No. 5,350,689, issued Sep. 27, 1994 to Ciba-Geigy Corp.), Whiskers technology (See U.S. Pat. Nos. 5,464,765 and 5,302,523) and pollen transformation (see U.S. Pat. No. 5,629,183). See also Weissinger et al. *Annual Rev. Genet.* 22:421-477 (1988); Sanford et al. *Particulate Science and Technology* 5:27-37 (1987) (onion); Christou et al. *Plant Physiol.* 87:671-674 (1988) (soybean); McCabe et al. *Bio/Technology* 6:923-926 (1988)

(soybean); Datta et al. *Bio/Technology* 8:736-740 (1990) (rice); Klein et al. *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (1988) (maize); Klein et al. *Bio/Technology* 6:559-563 (1988) (maize); Klein et al. *Plant Physiol.* 91:440-444 (1988) (maize); Fromm et al., *Bio/Technology* 8:833-839 (1990); Gordon-Kamm et al. *Plant Cell* 2:603-618 (1990) (maize); and U.S. Pat. Nos. 5,591,616 and 5,679,558 (rice).

(197) A vector or nucleic acid construct of this invention can comprise leader sequences, transit polypeptides, promoters, terminators, genes or nucleotide sequences of interest, introns, nucleotide sequences encoding genetic markers, etc., and any combination thereof. The nucleotide sequence(s) of the vector or nucleic acid construct can be in sense, antisense, partial antisense, or partial sense orientation in any combination and multiple gene or nucleotide sequence copies can be used. The transgene or nucleotide sequence can come from a plant as well as from a non-plant source (e.g., bacteria, yeast, animals, and viruses)

(198) A vector or nucleic acid construct comprising a transgene that is to be introduced into a plant of this invention can comprise the transgene and/or encoding nucleotide sequence under the control of a promoter appropriate for the expression of the transgene and/or nucleotide sequence at the desired time and/or in the desired tissue or part of the plant. Constitutive or inducible promoters can be used, as are well known in the art. The vector or nucleic acid construct carrying the transgene and/or encoding nucleotide sequence can also comprise other regulatory elements such as, e.g., translation enhancers or termination signals. In some embodiments, the transgene or encoding nucleotide sequence is transcribed and translated into a protein. In other embodiments, the vector or nucleic acid construct can comprise a nucleotide sequence that encodes an antisense RNA, a sense RNA that is not translated or only partially translated, a mRNA, a tRNA, a rRNA and/or a snRNA, as are well known in the art.

(199) In general, methods to transform, modify, edit or alter plant endogenous genomic DNA include altering the plant native DNA sequence or a pre-existing transgenic sequence including regulatory elements, coding and non-coding sequences. These methods can be used, for example, to target nucleic acids to pre-engineered target recognition sequences in the genome. Such pre-engineered target sequences may be introduced by genome editing or modification. As an example, a genetically modified plant variety is generated using “custom” or engineered endonucleases such as meganucleases produced to modify plant genomes (see e.g., WO 2009/114321; Gao et al. (2010) Plant Journal 1:176-187). Another site-directed engineering method is through the use of zinc finger domain recognition coupled with the restriction properties of restriction enzyme. See e.g., Urnov, et al., (2010) Nat Rev Genet. 11 (9): 636-46; Shukla, et al., (2009) Nature 459 (7245): 437-41. A transcription activator-like (TAL) effector-DNA modifying enzyme (TALE or TALEN) is also used to engineer changes in plant genome. See e.g., US20110145940, Cermak et al., (2011) Nucleic Acids Res. 39 (12) and Boch et al., (2009), Science 326 (5959): 1509-12. Site-specific modification of plant genomes can also be performed using the bacterial type II CRISPR (clustered regularly interspaced short palindromic repeats)/Cas (CRISPR-associated) system. See e.g., Belhaj et al., (2013), Plant Methods 9:39; The Cas9/guide RNA-based system allows targeted cleavage of genomic DNA guided by a customizable small noncoding RNA in plants.

(200) E. Plant Tissue Culture and Regeneration

(201) Plant cells, which have been transformed by any method known in the art, can also be regenerated to produce intact plants using known techniques. Plant regeneration from cultured protoplasts is described in Evans et al., Handbook of Plant Cell Cultures, Vol. 1: (MacMilan Publishing Co. New York, 1983); and Vasil I. R. (ed.), Cell Culture and Somatic Cell Genetics of Plants, Acad. Press, Orlando, Vol. I, 1984, and Vol. II, 1986). It is known that practically all plants can be regenerated from cultured cells or tissues.

(202) Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing transformed explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently root. Alternatively,

somatic embryo formation can be induced in the callus tissue. These somatic embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and plant hormones, such as auxin and cytokinins. A large number of plants have been shown capable of regeneration from transformed individual cells to obtain transgenic whole plants. Patents and patent publications cited as exemplary for the processes for transforming plant cells and regenerating plants are the following: U.S. Pat. Nos. 4,459,355, 4,536,475, 5,464,763, 5,177,010, 5,187,073, 4,945,050, 5,036,006, 5,100,792, 5,371,014, 5,478,744, 5,179,022, 5,565,346, 5,484,956, 5,508,468, 5,538,877, 5,554,798, 5,489,520, 5,510,318, 5,204,253 and 5,405,765; European Patent Nos. EP 267,159, EP 604 662, EP 672 752, EP 442 174, EP 486 233, EP 486 234, EP 539 563 and EP 674 725, and PCT Publication Nos. WO 91/02071 and WO 95/06128.

(203) The use of pollen, cotyledons, zygotic embryos, meristems and ovum as the target tissue for transformation can eliminate or minimize the need for extensive tissue culture work. Generally, cells derived from meristematic tissue are useful. The method of transformation of meristematic cells of cereal is taught in PCT Publication No. WO96/04392. Any number of various cell lines, tissues, calli and plant parts can and have been transformed by those having knowledge in the art. Methods of preparing callus or protoplasts from various plants are well known in the art. Cultures can be initiated from most of the above-identified tissues. The only requirement of the plant material to be transformed is that it can ultimately be used to produce a transformed plant.

(204) In Duncan et al. (*Planta* 165:322-332 (1985)) studies were conducted that demonstrated that 97% of plants cultured that produced callus were capable of plant regeneration. Subsequent experiments with both inbreds and hybrids showed that 91% appeared capable of producing regenerable callus. In a further study (Songstad et al. *Plant Cell Reports* 7:262-265 (1988)), several media additions were identified that enhanced regenerability of callus of two inbred lines. Other published reports indicated that “nontraditional” tissues are capable of producing somatic embryogenesis and plant regeneration. Rao et al. (*Maize Genetics Cooperation Newsletter* 60:64-65 (1986)) describes somatic embryogenesis from glume callus cultures and Conger et al. (*Plant Cell Reports* 6:345-347 (1987)) describes 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 from callus are, and were, “conventional” in the sense that they are routinely used and have a very high rate of success.

(205) Tissue culture procedures of maize are described in Green and Rhodes (“Plant Regeneration in Tissue Culture of Maize” in *Maize for Biological Research* (Plant Molecular Biology Association, Charlottesville, VA at 367 372 (1987)) and in Duncan, et al. (“The Production of Callus Capable of Plant Regeneration from Immature Embryos of Numerous *Zea mays* Genotypes” *Planta* 165:322-332 (1985)). Thus, another aspect of this invention is to provide cells that upon growth and differentiation produce maize plants having the physiological and morphological characteristics of the plants of the present invention.

(206) Accordingly, in some embodiments, the present invention provides a tissue culture of regenerable cells of TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, wherein the cells of the tissue culture regenerate plants that express the genotype of TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684. The tissue culture can be but is not limited to tissue culture derived from leaf, pollen, embryo, root, root tip, guard cell, ovule, seed, anther, silk, flower, kernel, ear, cob, husk and stalk, cell and protoplast thereof. In some aspects of this invention, additionally provided is a tissue culture of regenerable cells of hybrid plants produced from TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 germplasm. A corn plant regenerated from TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 or any part thereof is also included in the present invention. The present invention additionally provides regenerated corn plants that express the genotype of TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and/or manifest its phenotype, as well as mutants and/or variants thereof.

(207) F. Transgenic Plants and/or Parts Thereof of Inbred Corn Line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684

(208) The inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 comprising at least one transgene adapted to give TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 additional and/or altered phenotypic traits is a further aspect of the invention. Such transgenes are often associated with regulatory elements (promoters, enhancers, terminators and the like). As described above, transgenes that can be incorporated into a plant of this invention include, but are not limited to, insect resistance, herbicide resistance, disease resistance, increased or decreased starch or sugars or oils, lengthened or shortened life cycle or other altered trait, in any combination.

(209) In some embodiments, the present invention provides inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 expressing at least one transgene or nucleotide sequence adapted to give TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 modified starch traits. Further provided is the inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 expressing at least one mutant gene adapted to give modified starch, fatty acid or oil traits, i.e., amylase, waxy, amylose extender or amylose.

(210) The present invention additionally provides the inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 and at least one transgenic gene, which can be, but is not limited to, a nucleotide sequence or a synthetic sequence encoding a *Bacillus thuringiensis* toxin, a nucleotide sequence encoding phosphinothricin acetyl transferase (e.g., bar or pat), a nucleotide sequence encoding Gdha, a nucleotide sequence encoding GOX, a nucleotide sequence encoding VIP (vegetative insect protein), a nucleotide sequence encoding a phosphomannose isomerase, nucleotide sequence encoding a FR8a (the active insecticidal principle), a nucleotide sequence encoding EPSP synthase, a nucleotide sequence encoding for low phytic acid production, or a nucleotide sequence encoding zein, and any combination thereof. In further embodiments, the present invention provides the inbred corn line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 expressing at least one transgenic gene useful as a selectable marker or a screenable marker, as are well known in the art.

(211) G. Genotyping and Genetic Marker Profiles

(212) A number of well-known methods can be employed to identify the genotype of a maize plant. One of the oldest methods is the use of isozymes, which provides a generalized footprint of the genetic material. Other approaches adapted to provide a higher definition profile include restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLPs), random amplified polymorphic DNAs (RAPDs), amplification methods such as the polymerase chain reaction (PCR), which can employ different types of primers or probes, microsatellites (SSRs), single nucleotide polymorphisms (SNPs), sequence selection markers, etc. as are well known in the art and can be found in standard textbooks such as *Breeding Field Crops*, Milton et. al. Iowa State University Press and *Genetic Mapping and Marker Assisted Selection: Basics, Practice and Benefits*, N. Manikanda Boopathi Springer India 2013.

(213) The marker profile of the inbred of this invention should be close to homozygous for alleles. A marker profile produced with any of the locus identifying systems known in the industry will identify a particular allele at a particular locus. An F1 hybrid made from the inbred of this invention will comprise a marker profile of the sum of both of the profiles of its inbred parents. At each locus, the allele for the inbred of the present invention and the allele for the other inbred parent should be present. Thus, the profile of the inbred of the present invention allows for identification of hybrids as containing the inbred parent of the present invention. To identify the female portion of any hybrid, the hybrid seed material from the pericarp, which is maternally inherited, is employed in a marker technique. The resultant profile, therefore, is of the maternal parent. A comparison of this maternal profile with the hybrid profile will allow the identification of the paternal profile.

Accordingly, some embodiments of the present invention provide an inbred or hybrid plant, plant part thereof, including but not limited to a seed or an embryo, and/or a cell thereof having the allele marker profile of the inbred plant of the this invention, TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684.

(214) Marker profiles of plants of this invention can be employed to identify essentially derived varieties or progeny developed with the inbred in its ancestry. The progeny of the inbred line of this invention, TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, can be identified by identifying in the progeny the molecular marker profile of the inbred line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, as measured by either percent identity or percent similarity.

(215) Different nucleotide sequences or polypeptide sequences having homology are referred to herein as "homologues." The term homologue includes homologous sequences from the same and other species and orthologous sequences from the same and other species. "Homology" refers to the level of similarity between two or more nucleotide sequences and/or amino acid sequences in terms of percent of positional identity (i.e., sequence similarity or identity). Therefore, as used herein "sequence identity" refers to the extent to which two optimally aligned polynucleotide or polypeptide sequences are invariant throughout a window of alignment of components, e.g., nucleotides or amino acids. "Identity" can be readily calculated by known methods including, but not limited to, those described in: *Computational Molecular Biology* (Lesk, A. M., ed.) Oxford University Press, New York (1988); *Biocomputing: Informatics and Genome Projects* (Smith, D. W., ed.) Academic Press, New York (1993); *Computer Analysis of Sequence Data, Part I* (Griffin, A. M., and Griffin, H. G., eds.) Humana Press, New Jersey (1994); *Sequence Analysis in Molecular Biology* (von Heinje, G., ed.) Academic Press (1987); and *Sequence Analysis Primer* (Gribskov, M. and Devereux, J., eds.) Stockton Press, New York (1991).

(216) As described herein, marker systems are not just useful for identification of the plants of this invention but can also be used for breeding and trait conversion techniques. Polymorphisms in maize permit the use of markers for linkage analysis. If SSR are employed with flanking primers, the marker profile can be developed with PCR, and therefore Southern blots can often be eliminated. Use of flanking markers, PCR and amplification to genotype maize is well known in the art. Primer sequences for SSR markers and maize genome mapping information are publicly available on the USDA website at the Maize Genomics and Genetic Database (Maize GDB).

(217) H. Production of Treated Seed

(218) The present invention encompasses a method of producing treated hybrid or inbred seed of the plants of the present invention and the resultant treated seed. The method includes obtaining seed and treating the seed to improve its performance. Hybrid and inbred seed is often treated with one or more of the following including, but not limited to, fungicides, herbicides, herbicidal safeners, fertilizers, insecticides, acaricides, nematocides, bactericides, virus resistant material and/or other biocontrol agents. Pyrethrins, synthetic pyrethroids, oxadizine derivatives, chloronicotinyls, nitroguanidine derivatives and triazoles, organophosphates, pyrrols, pyrazoles, phenyl pyrazoles, diacylhydrazines, biological/fermentation products, carbamates and the like are used as pesticidal seed treatments. Additionally, fludioxonil, mefenoxam, azoxystrobin, thiamethoxam, clothianidin and the like are frequently used to treat maize seed. Methods for treating seed include but are not limited to the use of a fluidized bed, a roller mill, a rotostatic seed treater. a drum coaster, misting, soaking, filming coating and the like, in any combination. These methods of seed treatment are well known in the industry.

(219) I. Maize as Human Food and Livestock Feed

(220) Maize is used as human food, livestock feed and as raw material in industry. Sweet corn kernels having a relative moisture of approximately 72% are consumed by humans and may be processed by canning or freezing. 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.

(221) The present invention further encompasses a hybrid plant with a plant part being the segregating grain formed on the ear of the hybrid. This grain is a commodity plant product as are the protein concentrate, protein isolate, starch, meal, flour or oil. A number of different industrial processes can be employed to extract or utilize these plant products, as are well known in the art.

(222) 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.

(223) The seed of the plant of the present invention can further comprise one or more single gene traits. The plant produced from the inbred seed of the maize line TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684, the hybrid maize plant produced from the crossing of said inbred, hybrid seed and various parts of the hybrid maize plant, can be utilized for human food, livestock feed, and as a raw material in industry.

(224) The present invention therefore also provides an agricultural product comprising a plant of the present invention or derived from a plant of the present invention. The present invention further provides an industrial product comprising a plant of the present invention or derived from a plant of the present invention. Additionally, provided herein are methods of producing an agricultural and/or industrial product, the methods comprising planting seeds of the present invention, growing plant from such seeds, harvesting the plants and/or processing them to obtain an agricultural or industrial product. In some embodiments, the present invention provides a method of producing a commodity plant product comprising growing the plant from the seed of this invention or a part thereof and producing said commodity plant product, wherein said commodity plant product includes, but is not limited to, a protein concentrate, a protein isolate, starch, meal, flour, oil, or any combination thereof.

Deposit Information

(225) Applicants are making a deposit of at least 625 2500 seeds of inbred corn line KFX6631 with the Bigelow Laboratory for Ocean Science 60 Bigelow Drive East Boothbay, ME 04544. The deposit number of the deposit is 202411015 The date of deposit is Nov. 14, 2024, and the seed is tested on Dec. 13, 2024 and found to be viable. Access to this deposit will be available during the pendency of the application to the Commissioner for Patents and persons determined by the Commissioner to be entitled thereto upon request. Upon granting of a patent on any claims in the application all restrictions upon availability to the public will be irrevocably removed. Additionally, Applicants will meet the requirements of 37 CFR § 1.801-1.809, including providing an indication of the viability of the sample when the deposit is made. The ATCC deposit will be maintained in that depository, which is a public depository, for a period of 30 years, or 5 years after the last request, or for the enforceable life of the patent, whichever is longer, and will be replaced if it becomes nonviable during that period.

(226) Additional public information on patent variety protection may be available from the PVP Office, a division of the U.S. Government.

(227) TABLE-US-00001 VARIETY DESCRIPTION INFORMATION TABLE 1 TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 VARIETY DESCRIPTION

INFORMATION #1 Type: Dent #2 Region Best Adapted: - Inbred Maturity Hybrid Area of Line MG Range RM Adaptation TPJC7638 7 111 EASTERN CORN BELT KFX6631 6 112 EASTERN CORN BELT KFX7481 7 113 EASTERN CORN BELT KFX5450 5 107 EASTERN CORN BELT KHI5609 5 109 WESTERN CORN BELT KFX6684 6 107 EASTERN CORN BELT KFX5474 5 107 EASTERN CORN BELT *MG = Maturity group **Maturity is the number of days from planting to physiological maturity (planting to black layer) ***RM = relative maturity #3. Inbred name TPJC7638 Inbred 1 Inbred 2 Days to 50% SLK from planting 65 63 64 HU to 50% Silk from planting 1544 1495 1520 Days to 50% plants pollen shedding 65 63 63 from planting HU to 50% Pollen Shed from 1544 1495 1495 planting Plant Height in CM 209.296 226 199.1 Ear Height CM 64.516 52.3 72.6 Tassel length from top leaf collar to 43 52.8 39.8 tassel tip CM Tassel Peduncle length in cm - top 15.8 19.8 10.4 node below flag; If to bottom tassel branch CM Tassel central spike length cm (From 26.8 25.2 21.6 top tassel branch to tassel tip) Anther color - Munsell value Yellow Yellow Green Anther Color - Munsell Code 10Y8.5/8 10Y8.5/9 2.5GY8/10 Glume color - Munsell value Green Green Green Glume Color - Munsell Code 5GY7/6 2.5GY6/4 5GY6/6 Silk color - Munsell value Green Green Green Silk Color - Munsell Code 2.5GY8/6 2.5GY8/6 2.5GY8/4 Ear length (cm) 16 16.6 15 Ear diameter at mid-point (mm) 49.49 42.5 50.1 Number of kernel rows 18.4 14 16 Hard endosperm Munsell value Yellow Yellow-Orange Yellow Hard endosperm Munsell code 2.5Y8/10 2.5Y7/10 2.5Y8/10 Cob color - Munsell PVP number Pink Red Pink value Cob Color - Munsell Code 2.5YR6/8 2.5YR4/6 2.5YR6/6 Inbred line KFX6631 Inbred 1 Inbred 2 Days to 50% SLK from planting 65 63 66 HU to 50% Silk from planting 1544 1495 1568 Days to 50% plants pollen shedding 65 64 67 from planting HU to 50% Pollen Shed from planting 1544 1520 1592 Plant Height in CM 195.1 220 188.5 Ear Height CM 71.6 77.7 59.4 Length of ear node leaf CM 71.6 78.2 85 Number of lateral tassel branches 3.4 1.6 9.2 Tassel length from top leaf collar to 27.2 38 43.4 tassel tip CM Tassel Peduncle length in cm - top 4.6 12 12.4 node below flag If to bottom tassel branch CM Tassel central spike length cm (From 17.4 24.6 19.8 top tassel branch to tassel tip) Anther color - Munsell value Pink Pink Pink Anther Color - Munsell Code 5R5/4 5R5/6 2.5YR6/6 Glume color - Munsell value Green Green Green and Purple Glume Color - Munsell Code 2.5GY6/4 2.5GY6/4 5GY6/6 and 5R4/4 Silk color - Munsell value Green Green Green Silk Color - Munsell Code 2.5GY8/6 2.5GY8/6 2.5GY8/6 Ear length (cm) 14.2 16.4 16.8 Ear diameter at mid-point (mm) 46 45.8 43.906 Number of kernel rows 18.4 17.2 15.2 Cob color - Munsell number value Red Pink Red Cob Color - Munsell Code 10R4/8 2.5YR6/8 10R4/8 Kernel color - Munsell value Yellow Yellow Yellow Kernel color - Munsell code 2.5Y7/10 2.5Y7/10 2.5Y7/10 Inbred line KFX7481 Inbred 1 Inbred 2 Days to 50% SLK from planting 66 63 66 HU to 50% Silk from planting 1568 1495 1568 Days to 50% plants pollen shedding 66 64 67 from planting HU to 50% Pollen Shed from planting 1568 1520 1592 Plant Height in CM 212.9 220 188.5 Ear Height CM 79.8 77.7 59.4 Length of ear node leaf CM 76.8 78.2 85 Number of lateral tassel branches 5.6 1.6 9.2 Tassel length from top leaf collar to 38.4 38 43.4 tassel tip CM Tassel Peduncle length in cm - top 14.4 12 12.4 node below flag If to bottom tassel branch CM Tassel central spike length cm (From 17 24.6 19.8 top tassel branch to tassel tip) Anther color - Munsell value Pink Pink Pink Anther Color - Munsell Code 5R5/6 5R5/6 2.5YR6/6 Glume color - Munsell value Green Green Green and Purple Glume Color - Munsell Code 2.5GY6/4 2.5GY6/4 5GY6/6 and 5R4/4 Silk color - Munsell value Green Green Green Silk Color - Munsell Code 2.5GY8/6 2.5GY8/6 2.5GY8/6 Ear length (cm) 14.8 16.4 16.8 Ear diameter at mid-point (mm) 47.1 45.8 43.906 Number of kernel rows 16 17.2 15.2 Cob color - Munsell number value Red Pink Red Cob Color - Munsell Code 10R4/8 2.5YR6/8 10R4/8 Kernel color - Munsell value Yellow Yellow Yellow Kernel color - Munsell code 2.5Y8/10 2.5Y7/10 2.5Y7/10 Inbred line KFX5450 Inbred 1 Inbred 2 Days to 50% SLK from planting 63 63 66 HU to 50% Silk from planting 1495 1495 1568 Days to 50% plants pollen shedding 63 64 67 from planting HU to 50% Pollen Shed from planting 1495 1520 1592 Plant Height in CM 198.1 220 188.5 Ear Height CM 63.5 77.7 59.4 Length of ear node leaf CM 76.8 78.2 85 Number of lateral tassel branches 2.2 1.6 9.2 Tassel length from top leaf collar to 34.2 38 43.4 tassel tip CM Tassel Peduncle length in cm - top 7.6 12 12.4 node below flag If to bottom tassel branch CM Tassel central spike length cm (From 23.6 24.6 19.8 top tassel branch to tassel tip) Anther color - Munsell value Pink Pink Pink Anther Color - Munsell Code 5R5/6 5R5/6 2.5YR6/6 Glume color - Munsell value Green Green Green and Purple Glume Color - Munsell Code 2.5GY6/4 2.5GY6/4 5GY6/6 and 5R4/4 Silk color - Munsell value Green Green Green Silk Color - Munsell Code 2.5GY8/6 2.5GY8/6 2.5GY8/6 Ear length (cm) 14.4 16.4 16.8 Ear diameter at mid-point (mm) 44.3 45.8 43.9 Number of kernel rows 15.6 17.2 15.2 Cob color - Munsell number value Pink Pink Red Cob Color - Munsell Code 2.5YR6/6 2.5YR6/8 10R4/8 Kernel color - Munsell value Yellow Yellow Yellow Kernel color - Munsell code 2.5Y7/10 2.5Y7/10 2.5Y7/10 Inbred name KHI5609 Inbred 1 Inbred 2 Days to 50% SLK from planting 62 64 63 HU to 50% Silk from planting 1469 1520 1495 Days to 50% plants pollen shedding 62 63 63 from planting HU to 50% Pollen Shed from 1469 1495 1495 planting Plant Height in CM 195.6 199.1 226 Ear Height CM 67.6 72.6 52.3 Tassel length from top leaf collar to 37 39.8 52.8 tassel tip CM Tassel Peduncle length in cm - top 10.2 10.4 19.8 node below flag If to bottom tassel branch CM Tassel central spike length cm 25.6 21.6 25.2 (From top tassel branch to tassel tip) Anther color - Munsell value Green and Green Yellow Pink Anther Color - Munsell Code 2.5GY8/10 2.5GY8/10 10Y8.5/8 and 7.5YR8/2 Glume color - Munsell value Green w/ Green Green red* Glume Color - Munsell Code 5GY6/6 5GY6/6 2.5GY6/4 Silk color - Munsell value Yellow Green Green Silk Color - Munsell Code 2.5Y8/6 2.5GY8/4 2.5GY8/6 Ear length (cm) 14.8 15 16.6 Ear diameter at mid-point (mm) 40.9 50.1 42.5 Number of kernel rows 13.2 16 14 Hard endosperm Munsell value Yellow Yellow Yellow Hard endosperm Munsell code 2.5Y7/10 2.5Y8/10 2.5Y7/10 Cob color - Munsell PVP number Red Pink Red value Cob Color - Munsell Code 10R4/8 2.5YR6/6 2.5YR4/6 *slight red; no Munsell code recorded for red Inbred name KFX6684 Inbred 1 Inbred 2 Anther color - Munsell value Purple Red Red Glume color - Munsell value Green and Green and Green and Red Red purple Silk color - Munsell value Pink Yellow Red/purple Cob color - Munsell value Red Red Pink Inbred line KFX5474 Inbred 1 Inbred 2 Days to 50% SLK from planting 62 63 66 HU to 50% Silk from planting 1469 1495 1568 Days to 50% plants pollen shedding 62 64 67 from planting HU to 50% Pollen Shed from 1469 1520 1592 planting Plant Height in CM 229.1 220 188.5 Ear Height CM 76.7 77.7 59.4 Length of ear node leaf CM 83.4 78.2 85 Number of lateral tassel branches 5.4 1.6 9.2 Tassel length from top leaf collar to 42 38 43.4 tassel tip CM Tassel Peduncle length in cm - top 14.6 12 12.4 node below flag If to bottom tassel branch CM Tassel central spike length cm 23.6 24.6 19.8 (From top tassel branch to tassel tip) Anther color - Munsell value Purple Pink Pink Anther Color - Munsell Code 5RP5/4 5R5/6 2.5YR6/6 Glume color - Munsell value Green Green Green and w/red* Purple red Glume Color - Munsell Code 5GY6/6 2.5GY6/4 5GY6/6 and 5R4/4 Silk color - Munsell value Red Green Green Silk Color - Munsell Code 5R4/6 2.5GY8/6 2.5GY8/6 Ear length (cm) 17.4 16.4 16.8 Ear diameter at mid-point (mm) 43.5 45.8 43.906 Number of kernel rows 14.4 17.2 15.2 Cob color - Munsell number value Red Pink Red Cob Color - Munsell Code 10R4/8 2.5YR6/8 10R4/8 Kernel color - Munsell value Yellow Yellow Yellow Kernel color - Munsell code 2.5Y7/10 2.5Y7/10 2.5Y7/10 *no Munsell code recorded for red

The data provided above is often a color. The Munsell code is a reference book of color, which is known and used in the industry and by persons with ordinary skill in the art of plant breeding. The purity and homozygosity of inbred TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 is constantly being tracked using genotypes.

(228) TABLE-US-00002 PAIRED INBRED COMPARISON DATA TABLE A HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats TPJC7638 37835 1519.3 1554.4 171.3 76.5 4 11.1 13.9 Inbred1 1531.3 1596.1 187.2 76.3 Diff 11.9 41.7 17.9 2.4 # Expts 18 18 3 3 Prob 0.382 0.000*** 0.043** 0.706 % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count TPJC7638 5.5 0.4 4 2.9 4.9 6.2 0 0 136 Inbred1 153.8 Diff 25 # Expts 1 Prob

HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX6631 271.9 1507 1509 168 81.5 0.3 0 0 Inbred1 183.2 35323 1491.9 1486.5 186 94.9 4.8 29.5 27.8 Diff 40.3 15.1 22.5 17.4 6.4 3.5 14.8 8.2 # Expts 4 16 16 6 5 3 5 5 Prob 0.302 0.343 0.136 0.096* 0.229 0.056* 0.029** 0.022** % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX6631 0 0 0 0 0 0 0 0 Inbred1 10.5 13.6 10.1 8.3 7.7 4.8 0 0 Diff 0 0.4 2.8 0.5 11.3 6.9 0 0 # Expts 5 5 5 5 5 5 5 5 Prob 0.096* 0.074* 0.107 0.028** 0.027** HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX7481 299 1474.5 1479.3 203.9 103.8 0.3 0 0 Inbred1 183.2 35323 1491.9 1486.5 186 94.9 4.8 29.5 27.8 Diff 67.4 17.4 7.2 18.5 15.8 3.5 14.8 8.2 # Expts 4 16 16 6 5 3 5 5 Prob 0.110 0.139 0.442 0.308 0.035** 0.056* 0.029** 0.022** % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX7481 0 0 0 0 0 0 0 0 Inbred1 10.5 13.6 10.1 8.3 7.7 4.8 0 0 Diff 0 0.4 2.8 0.5 11.3 6.9 0 0 # Expts 5 5 5 5 5 5 5 5 Prob 0.096* 0.074* 0.107 0.028** 0.027** HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX5450 160.1 38076.2 1427.3 1451.7 177.8 78.4 1.6 45.3 46.4 Inbred1 173.1 37045.8 1464.3 1467.9 182.9 87.8 4.8 34.2 36.2 Diff 4.7 399.8 37 16.2 7.4 12.5 3.2 9.6 10.9 # Expts 9 6 24 24 9 9 9 10 10 Prob 0.685 0.800 0.001*** 0.041** 0.393 0.144 0.023** 0.175 0.051* % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX5450 1.6 5.6 25.2 26.9 17.9 13.2 2.8 0.2 80 Inbred1 6.1 14.4 15.4 11.5 11.3 8.7 0 0 53 Diff 5.9 6.1 9.2 12.5 7.2 5.2 3.6 0.2 27 # Expts 10 10 10 10 10 10 10 10 1 Prob 0.106 0.290 0.032** 0.001*** 0.076* 0.133 0.260 0.343 HeatUnits to HeatUnits to Plant Ear % Inbred Yield Stand P50 S50 Height Height Discard % Rounds % Flats KHI5609 37835 1376 1421 165.4 68.6 1.6 20.7 29.3 Inbred1 37835 1445.4 1540.8 167.5 86.4 5.6 13.3 24.2 Diff 0 67.2 118.4 8.5 4 4.4 4.4 # Expts 1 18 18 2 2 2 2 Prob 0.000*** 0.000*** 0.126 0.373 0.528 0.528 % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KHI5609 11.7 1.3 5.8 13.9 3.2 13.2 0 0 171.2 Inbred1 7.1 3.4 1 14.1 1.9 8.2 0 0 157 Diff 3.2 4.8 6.6 7.4 1.1 3.3 0 0 6.6 # Expts 2 2 2 2 2 2 2 2 9 Prob 0.708 0.275 0.044** 0.123 0.427 0.746 0.571 HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX6684 143.7 35834.8 1444.8 1500.2 177.8 81.3 4.5 44.2 55.8 Inbred1 135.9 36332.5 1509.5 1502.5 167.9 83.5 2.8 44.8 55.2 Diff 7.7 497.7 64.8 2.3 9.8 2.2 1.7 0.6 0.6 # Expts 5 5 16 16 4 4 5 5 5 Prob 0.626 0.723 0.000*** 0.885 0.130 0.581 0.465 0.891 0.891 % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX6684 28.9 28.2 7.6 5 2.8 15.7 0 1 Inbred1 7.5 6.6 22.4 39.2 13.6 7.8 0 0.5 Diff 21.5 21.5 14.9 34.2 10.8 7.8 0 0.5 # Expts 5 5 5 5 5 5 5 5 Prob 0.000*** 0.021** 0.001*** 0.000*** 0.049** 0.150 0.704 HeatUnits to HeatUnits Plant Ear % Inbred Yield Stand P50 to S50 Height Height Discard % Rounds % Flats KFX5474 136.8 36242 1371.1 1415.7 203.2 98.2 1.7 44.4 55.6 Inbred1 158.7 35572 1455.3 1468.9 178.6 87.9 3.6 46 46.5 Diff 6.7 844.3 76.6 47.2 8.9 3.8 1.6 0.2 0.2 # Expts 3 3 21 21 2 2 3 3 3 Prob 0.396 0.623 0.000*** 0.000*** 0.257 0.210 0.091* 0.886 0.886 % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX5474 15.2 9.3 23.3 42.5 5.1 2.9 0 0 61 Inbred1 12.4 19.6 20.3 16.6 11.6 8.7 0 0 53 Diff 7.6 22.6 7.1 23.8 1.4 0.2 0 0 8 # Expts 3 3 3 3 3 3 3 3 1 Prob 0.295 0.023** 0.076* 0.014** 0.570 0.940 *.05 < Prob <= .10 **.01 < Prob <= .05 ***.00 < Prob <= .01

(229) In Paired Inbred Comparison Data Table B TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 shows a comparison for traits like yield, pollination, heat and silking heat units when compared with the other inbred.

(230) TABLE-US-00003 HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats TPJC7638 37835 1522.2 1558.7 171.3 76.5 4 9.8

12.4 Inbred2 37835 1490.5 1575.4 170.5 88.3 4.2 8.9 16.1 Diff 0 31.7 16.7 3.9 7.7 1.5 0.1 5.5 # Expts 1 19 19 7 1 2 9 9 Prob 0.059* 0.132 0.399 0.599 0.990 0.413 % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count TPJC7638 4.9 0.3 3.6 2.6 4.3 5.5 0 0 138.8 Inbred2 3.2 4.5 2.8 7.6 1.5 4.3 0 0 158.2 Diff 1.4 4.7 0.5 5.8 2.7 0.7 0 0 8.4 # Expts 9 9 9 9 9 9 9 6 6 Prob 0.333 0.073* 0.885 0.083* 0.384 0.688 0.578 HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX6631 152.3 36703.6 1506.1 1510.3 168 81.5 2.9 24.7 25.3 Inbred2 135.2 36999 1507.6 1507.3 164.1 76.1 2.6 37.5 47.3 Diff 12.2 1052 1.4 3.1 3.6 4.4 0.5 12.3 8.9 # Expts 14 10 19 19 6 5 13 10 10 Prob 0.304 0.143 0.918 0.841 0.461 0.392 0.270 0.042** 0.065* % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX6631 0 0 0 0 0 0 1.3 0 Inbred2 4.2 7.5 14.2 14 13.7 12.2 0 0.1 Diff 0 2.2 8.7 2.8 14.8 13 1.3 0.1 # Expts 5 5 5 5 5 5 15 15 Prob 0.374 0.143 0.091* 0.189 0.021** 0.020** 0.334 0.334 HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX7481 168.1 37536.3 1475.2 1479.3 203.9 103.8 2.7 25.7 18.8 Inbred2 139 37425.6 1506.9 1506.6 164.1 76.1 2.3 37.1 46.9 Diff 22.7 816.6 31.7 27.3 39.5 26.7 0.6 10.3 13.2 # Expts 13 10 19 19 6 5 13 9 9 Prob 0.117 0.543 0.003*** 0.011** 0.006*** 0.007*** 0.364 0.158 0.009*** % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX7481 0 0 0 0 0 0 8.4 0.7 Inbred2 4.2 7.5 14.2 14 13.7 12.2 0.1 0.2 Diff 0 2.2 8.7 2.8 14.8 13 8.3 0.4 # Expts 5 5 5 5 5 5 15 15 Prob 0.374 0.143 0.091* 0.189 0.021** 0.020** 0.239 0.109 HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX5450 147 37728.4 1413.5 1437.8 177.8 78.4 2.3 46.8 46.9 Inbred2 143.8 37035.2 1478.9 1482.3 162.2 74.9 2.2 37.4 48.2 Diff 1.6 437.7 65.5 44.5 15.1 2.7 0.3 6.3 4.4 # Expts 16 14 31 31 9 9 17 12 12 Prob 0.820 0.697 0.000*** 0.000*** 0.041** 0.388 0.570 0.138 0.151 % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX5450 1.4 5.2 23.5 24 20.8 16.3 1.8 0.1 123.3 Inbred2 6 11.8 16.6 14.9 11.5 14.6 0.1 0.2 149.3 Diff 4.7 3.6 7.7 7.7 6.8 0.2 2.3 0.1 26 # Expts 10 10 10 10 10 10 18 18 2 Prob 0.007*** 0.217 0.016** 0.003*** 0.000*** 0.926 0.193 0.622 0.684 HeatUnits to HeatUnits to Plant Ear % Inbred Yield Stand P50 S50 Height Height Discard % Rounds % Flats KHI5609 37835 1384.2 1415.5 163.9 68.6 1.6 20.7 29.3 Inbred2 1501.9 1571.2 187.2 76.3 Diff 116.1 150.3 # Expts 15 15 Prob 0.000*** 0.000*** % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KHI5609 11.7 1.3 5.8 13.9 3.2 13.2 0 0 170.8 Inbred2 153.8 Diff 9.7 # Expts 3 Prob 0.734 HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX6684 136.6 35990.8 1444.4 1487.5 174 79.1 5 42.9 57.1 Inbred2 110.2 30431 1503.4 1529.1 195.7 92.2 6.6 48.2 51.8 Diff 25.1 5419.8 52.1 33.3 22.6 15.6 1.5 8.1 8.1 # Expts 19 19 27 27 7 7 19 14 14 Prob 0.001*** 0.001 0.000*** 0.000*** 0.002*** 0.002*** 0.250 0.004*** 0.004*** % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX6684 18.2 32.6 15.8 12.1 3.2 10.7 0 0.3 130 Inbred2 14.6 21.2 22.1 28.5 4.2 6.6 0 0 64.7 Diff 2.4 11.4 5.1 15.5 0.6 3.6 0 0.3 12.7 # Expts 9 9 9 9 9 9 19 19 1 Prob 0.184 0.032** 0.092* 0.044** 0.636 0.426 0.331 HeatUnits HeatUnits Plant Ear % Inbred Yield Stand to P50 to S50 Height Height Discard % Rounds % Flats KFX5474 116.9 34903.7 1363.6 1411.1 203.2 98.2 4 55.3 44.7 Inbred2 127.1 36530.6 1473.2 1485.4 158.3 72.9 2.5 43.1 54.8 Diff 2.9 3112.3 102.6 67.7 39.1 13.4 2 11.4 11.4 # Expts

11 11 24 24 2 2 11 6 6 Prob 0.672 0.077* 0.000*** 0.000*** 0.144 0.181 0.101 0.038** 0.038** % Large % Large % Med. % Med. % Small % Small % Shed Pollen Inbred Rounds Flats Rounds Flats Rounds Flats Lodging % Snap Duration Count KFX5474 15.2 9.3 23.3 42.5 5.1 2.9 0 0.5 61 Inbred2 8.9 13.2 20.9 22.7 11.4 15.5 0 0.1 58 Diff 7.7 4.7 3.5 11.5 7.8 8 0 0.5 3 # Expts 3 3 3 3 3 3 11 11 1 Prob 0.323 0.175 0.217 0.001*** 0.132 0.105 0.242

(231) The General Combining Ability Table shows the GCA (General Combining Ability) estimates of TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 compared with the GCA estimates of the other inbreds. The estimates show the general combining ability is weighted by the number of experiment/location combinations in which the specific hybrid combination occurs. The interpretation of the data for all traits is that a positive comparison is a practical advantage. A negative comparison is a practical disadvantage. The general combining ability of an inbred is clearly evidenced by the results of the general combining ability estimates. This data compares the inbred parent in a number of hybrid combinations to a group of “checks”. The check data is from our company's and other companies' hybrids which are commercial products and pre-commercial hybrids, which were grown in the same sets and locations.

(232) TABLE-US-00004 % % Late % Early % Stay Test % Stalk Push Root Root Dropped Final Green Line N Yield Moisture Weight Lodging Test Lodging Lodging Ears Stand % TPJC7638 2 7.64 0.01 0.61 0.03 −1.29 3.04 0.51 TPJC7638 1 −6.15 1.23 0.75 3.46 −1.42 −38.75 TPJC7638 1 1.11 0.21 −2.61 3.37 −0.42 −13.75 TPJC7638 1 1.16 0.33 1.45 7.85 −3.09 −13.75 TPJC7638 1 2.93 −0.39 −1.74 10.64 0.21 TPJC7638 1 0.98 1.48 −0.63 40.78 −2.09 TPJC7638 1 19.12 −0.57 0.05 31.91 −0.12 TPJC7638 1 0.85 0.52 0.14 0.16 TPJC7638 1 14.33 0.16 −0.04 10.64 0.05 TPJC7638 1 3.67 −4.55 0.2 0.09 −11.25 XR= 11 4.84 −0.14 −0.11 0.03 13.42 3.04 −0.51 −19.38 XH= 10 4.56 −0.16 −0.18 0.03 13.42 3.04 −0.61 −19.38 XT= 1 7.64 0.01 0.61 0.03 −1.29 3.04 0.51 % Green Emergence Vigor Heatunits Heatunits Ear Plant Line Snap % Barren Rating Rating to S50 to P50 Height Height TPJC7638 −1.76 −0.6 1.07 1.2 0.88 −2.2 −7.08 TPJC7638 −4.68 TPJC7638 −6.09 TPJC7638 −10.26 TPJC7638 −3.02 TPJC7638 4.4 TPJC7638 −9.1 TPJC7638 −8.15 TPJC7638 −13.55 TPJC7638 −11.26 XR= −1.76 −0.6 1.07 1.2 0.88 −6.01 −7.08 XH= −1.76 −0.6 1.07 1.2 0.88 −6.39 −7.08 XT= −1.76 −0.6 1.07 1.2 0.88 −2.2 −7.08 % % Late % Early % Stay Test % Stalk Push Root Root Dropped Final Green Line N Yield Moisture Weight Lodging Test Lodging Lodging Ears Stand % KFX6631 1 −1.39 1.06 −0.15 2.91 0.58 3.15 0 −3.72 −8 KFX6631 1 −16.26 −0.99 2.48 0.37 0 −1.25 −0.7 KFX6631 4 2.64 −1.08 −0.71 0.91 0.73 19.12 0 −1.72 KFX6631 1 −15.28 1.76 1.86 −7.04 0 −68.18 0 −0.15 KFX6631 1 −21.96 2.77 1.99 −4.42 1.97 2.03 0 −5.36 −8.33 KFX6631 1 8.96 0.80 2.74 −0.32 0 11.36 0 0 KFX6631 1 −4.27 1.44 0.26 −52.69 8 20.45 0.14 XR= 10 −3.96 0.25 1.21 −8.61 1.61 −1.9 0 −1.67 −8.17 XH= 7 −6.79 0.82 1.21 −8.61 1.61 −1.9 0 −1.64 −8.17 XT= % Green Emergence Vigor Heatunits Heatunits Plant Line Snap % Barren Rating Rating to S50 to P50 Ear Height Height KFX6631 −1.22 −0.8 1 −0.4 −5.51 KFX6631 14.19 KFX6631 0.15 0.57 −0.83 31.4 8.95 −12.33 8.23 KFX6631 −22.85 KFX6631 −1 0.08 −0.52 KFX6631 3.51 KFX6631 10.83 XR= −1.22 0.15 −0.41 0.08 31.4 8.95 −1 0.73 XH= −1.22 0.15 −0.41 0.08 31.4 8.95 −1 0.73 XT= % % Late % Early % Stay Test % Stalk Push Root Root Dropped Final Green Line N Yield Moisture Weight Lodging Test Lodging Lodging Ears Stand % KFX7481 1 5.09 1.06 −0.43 −3.23 6.49 12.08 −6.98 KFX7481 1 7.25 1.07 −2.81 1.28 −1.48 8.18 0 −5.26 −5.83 KFX7481 1 −1.36 1.68 −1.27 −0.99 2.97 4.55 0.11 −6.49 −15 KFX7481 1 8.87 −0.99 −2.99 0.19 −0.75 2.53 0 −4.45 −0.83 KFX7481 1 −0.13 −1.75 −1.26 0.42 −16.25 0 −0.52 KFX7481 1 12.22 −1.9 −3 0.42 1.25 0 −0.52 KFX7481 1 5.34 1.13 0.16 0.42 −16.25 −7.29 −0.73 KFX7481 1 23.51 −0.04 −1.91 0.09 0.92 −1.71 KFX7481 1 5.49 −0.73 −0.17 0.74 −12.83 −2.52 −1.54 −1.33 XR= 9 7.37 −0.05 −1.52 −0.07 −3.99 2.19 0.04 −3.13 −5.75 XH= 9 7.37 −0.05 −1.52 −0.07 −3.99 2.19 0.04 −3.13 −5.75 XT= % Green Emergence Vigor Heatunits Heatunits Ear Plant Line Snap % Barren Rating Rating to S50 to P50 Height Height KFX7481 0.34 0.33 1.83 6.23 −19.68 KFX7481 0.17 7.93 −11.1 KFX7481 0.5 16.72 8.74 KFX7481 0.17 11.57

13.21 KFX7481 −6.51 15.56 KFX7481 −7.65 19.79 KFX7481 9.4 13.02 KFX7481 −6.63 1.92 KFX7481 −0.48 −0.17 8.94 −2.73 XR= −1.92 0.29 0.83 11.3 −2.31 XH= −1.92 0.29 0.83 11.3 −2.31 % % % Early % Test % Stalk Push Late Root Root Dropped Final Line N Yield Moisture Weight Lodging Test Lodging Lodging Ears Stand KFX5450 1 −7.01 1.17 −1.25 −2.17 7.70 0.60 KFX5450 1 21.94 −1.46 −2.75 2.04 0.33 0.00 −0.41 KFX5450 1 −0.41 −2.85 −0.27 2.04 −12.77 0.24 KFX5450 1 9.16 −0.30 −1.98 1.02 −3.78 0.33 KFX5450 2 0.33 −1.23 1.82 −4.47 −5.05 1.53 2.05 KFX5450 1 −39.01 0.12 2.76 7.14 −1.49 KFX5450 1 −5.67 0.73 1.66 6.03 0.46 −0.37 KFX5450 1 8.62 0.46 0.90 20.92 0.46 −0.37 KFX5450 1 15.22 −0.15 0.44 5.36 −1.00 KFX5450 1 −14.18 0.76 0.85 −13.17 0.79 8.16 0.12 −5.03 KFX5450 1 4.84 −1.38 −1.12 0.34 9.58 0.00 −0.97 KFX5450 1 13.49 −3.13 −0.53 −1.40 −20.83 0.00 0.23 KFX5450 1 −1.05 −0.60 0.14 −1.03 −1.81 8.83 0.78 KFX5450 1 11.60 −0.94 −0.64 −6.36 0.00 2.55 3.38 KFX5450 1 −1.44 −1.20 0.37 −9.93 0.46 −1.83 KFX5450 1 2.85 −1.86 −1.07 16.67 0.46 −0.37 KFX5450 2 −0.21 −1.64 −0.97 −0.30 2.02 10.25 0.74 KFX5450 2 16.13 −1.37 1.26 −0.06 9.40 1.60 2.52 KFX5450 1 12.36 −1.01 1.73 −15.25 0.46 −0.37 KFX5450 1 5.71 −2.14 0.95 −9.93 0.46 −0.37 KFX5450 1 10.85 −2.27 0.99 −47.16 0.46 −0.37 KFX5450 1 −5.64 −3.07 1.64 16.67 0.46 −0.37 KFX5450 1 7.95 −3.16 0.08 6.03 0.46 −0.37 KFX5450 1 9.26 −1.60 −0.10 −47.16 0.46 −0.37 KFX5450 1 −16.07 −0.39 2.87 −1.24 −0.71 KFX5450 1 −13.44 −0.27 1.82 4.43 −0.71 KFX5450 1 3.20 −1.33 1.43 5.50 −1.20 KFX5450 1 5.21 0.81 1.84 6.78 −0.98 KFX5450 1 −8.63 −0.64 1.48 5.36 −0.31 KFX5450 1 −0.20 −0.00 0.65 8.38 −2.09 KFX5450 1 −1.58 0.80 −0.14 1.33 0.12 KFX5450 1 −8.26 1.61 0.67 −3.99 0.12 KFX5450 2 11.30 −0.36 −0.90 −0.42 4.07 0.00 −11.54 3.74 XR= 37 2.02 −0.88 0.43 −1.64 −0.53 1.76 −2.28 0.11 XH= 33 1.43 −0.85 0.44 −1.84 −0.98 1.39 −2.28 −0.16 XT= 2 5.54 −1.00 −0.93 −0.36 3.05 5.12 −11.54 2.24 Stay % Emer- Heat Heat Green Green % gence Vigor units units Plant Line % Snap Barren Rating Rating to S50 to P50 Ear Height Height KFX5450 1.87 KFX5450 −1.62 KFX5450 −6.55 2.59 KFX5450 13.61 KFX5450 −3.83 −5.01 −4.38 KFX5450 −21.75 −4.12 KFX5450 −4.81 −5.46 KFX5450 −4.81 −0.19 KFX5450 −3.75 −2.85 KFX5450 −13.00 −0.28 −0.80 0.60 −1.12 3.63 KFX5450 19.83 KFX5450 6.83 KFX5450 0.00 4.30 26.48 KFX5450 −2.91 21.21 8.87 KFX5450 −3.53 −11.51 KFX5450 −4.81 −13.31 KFX5450 −0.77 0.50 2.33 −3.54 −8.29 KFX5450 −3.59 3.32 8.86 KFX5450 −4.81 5.25 KFX5450 −4.81 4.75 KFX5450 −4.81 −7.87 KFX5450 −4.81 −8.64 KFX5450 −4.81 1.25 KFX5450 −4.81 0.23 KFX5450 10.00 4.64 KFX5450 0.00 −7.42 KFX5450 0.00 5.28 KFX5450 −8.75 10.49 KFX5450 −3.75 −3.48 KFX5450 −13.75 −9.83 KFX5450 −3.22 KFX5450 −5.76 KFX5450 6.17 −1.17 2.83 50.12 39.33 6.52 21.37 XR= −4.86 −3.42 −0.15 1.92 50.12 39.33 0.49 7.74 XH= −4.86 −3.66 −0.15 1.92 50.12 39.33 0.52 8.08 XT= 6.17 −0.97 0.50 2.58 50.12 39.33 1.49 6.54 % % Late % Early % Stay Test % Stalk Push Root Root Dropped Final Green Line N Yield Moisture Weight Lodging Test Lodging Lodging Ears Stand % KHI5609 1 2.52 −0.42 0.01 0.67 −3.48 5 −2.24 KHI5609 5 0.06 0.55 −0.51 1.67 1.86 2.54 1.78 −1.2 −6 KHI5609 1 8.83 −2.86 −0.65 0 0.80 −0.29 KHI5609 1 −1.97 −0.99 −0.28 18.88 8.24 −0.02 KHI5609 2 −0.21 −1.64 −0.97 −0.3 2.02 10.25 0.74 KHI5609 1 −5.2 −0.47 1.22 15.96 1.15 −0.98 KHI5609 1 −3.47 2.94 −1.1 −1.53 0.81 6.93 0 5.82 −9 KHI5609 1 −1.31 −0.16 1.21 0.23 0.69 5.49 −1.74 KHI5609 1 −7.37 −0.74 0.25 −1.01 0.69 5.49 2.85 XR= 14 −0.58 −0.23 −0.27 0.28 3.92 5.1 1.19 −0.08 −7 XH= 9 −0.9 −0.42 −0.09 −0.04 4.68 5.1 0.89 0.33 −7.5 XT= 2 −0.08 −0.54 −0.74 0.69 1.94 6.39 1.78 −0.23 −6 Emer- % Green % gence Vigor Heatunits Heatunits Ear Plant Line Snap Barren Rating Rating to S50 to P50 Height Height KHI5609 −2.09 1.5 −0.67 12.07 6.17 KHI5609 −0.58 0.07 −0.5 0.75 −39.94 −32.79 −1.04 −14.32 KHI5609 2.1 KHI5609 −0.64 9.21 KHI5609 −0.77 0.5 2.33 −3.54 −8.29 KHI5609 −2.24 −5.54 KHI5609 −1.14 0.2 −0.3 7.69 6.81 KHI5609 −0.09 6.73 −8.83 KHI5609 −0.09 2.54 5 XR= −0.85 0.07 0.12 0.53 −39.94 −32.79 2.05 −5.6 XH= −0.96 0.07 0.43 0.53 −39.94 −32.79 3.36 −2.24 XT= −0.68 0.07 0 1.54 −39.94 −32.79 −2.29 −11.3 % % Late % Early % Stay Test % Stalk Push Root Root Dropped Final Green Line N Yield Moisture Weight Lodging Test Lodging Lodging Ears Stand % KFX6684 1 −1.8 −1.75 0.25 0.74 7.58 0 KFX6684 1 6.79 −1.78 −1.49 −0.26 −0.22 0 0.51 KFX6684 1 26.04 −1.07 −1.22 0.89 −1.27 0 1.14 KFX6684 1 −5.86 0.05 2.21 −1.7 4.79 −2.2 1.02 KFX6684 4 −0.53

−0.93 0.3 0.63 0.62 10.5 −12.22 2.83 KFX6684 1 −0.82 −1.65 0.75 −1.05 37.5 0.22 2.07 0.08 10.53 21.5 KFX6684 2 8.09 −0.64 −0.55 −4.35 −0.33 −4.27 −1.37 KFX6684 1 −17.5 −0.41 1.87 20.48 9.58 −1.2 KFX6684 1 −2.98 0.04 1.48 9.58 −0.45 KFX6684 1 12.5 −1.9 −1.02 0.43 1.6 4.95 0.52 KFX6684 1 0.63 −1.26 1.93 21.01 0.80 0.2 KFX6684 1 −17.83 1.24 3.41 −14.41 −2.63 −18.75 KFX6684 1 3.48 −0.86 2.03 −1.24 −1.47 6.25 KFX6684 1 0.65 −0.64 1.04 0 −14.56 0.02 KFX6684 1 −3.85 0.64 2.22 −1.18 11.35 17.12 −0.92 KFX6684 1 −4.76 −1.25 1.07 −0.42 −3.13 KFX6684 1 13.14 −1.54 0.75 0 0 6.32 0 KFX6684 1 11.97 2.32 −0.17 −11.27 −5.55 5.5 −11.17 KFX6684 1 −2.37 −0.3 −0.11 −2.17 1.96 0.22 0.01 KFX6684 1 −10.43 −0.25 2.25 20.48 9.58 −0.03 KFX6684 1 2.2 −0.96 1.99 −16.13 −1.47 11.25 KFX6684 1 9.18 −1.99 1.54 −19.68 −1.47 11.25 KFX6684 1 −4.73 −0.72 3.18 −14.63 0.12 16.25 KFX6684 1 −1.31 −0.16 1.21 0.23 0.69 5.49 −1.74 KFX6684 1 −1.45 −2 1.62 0.33 −0.83 KFX6684 1 20.83 0.88 0.79 1.01 2.95 0 1.62 KFX6684 1 −9.95 −0.18 2.7 −20.39 −1.47 −18.75 KFX6684 1 −1.96 −1.32 3.02 −10.82 −1.47 1.25 KFX6684 1 −12.52 −1.15 2.94 −2.3 −1.47 1.25 KFX6684 1 −6.18 −0.64 2.73 −33.87 −1.47 −13.75 KFX6684 1 −4.39 −2.01 2.31 −5.5 −1.47 6.25 KFX6684 1 3.35 −2.18 1.51 −2.13 −1.89 21.25 KFX6684 1 3.47 2.09 0.65 −1.89 6.77 0.14 −1.32 KFX6684 1 −9.92 −0.35 2.96 −4.43 −1.45 1.25 KFX6684 1 −4.27 −2.25 1.92 −14.36 −1.89 16.25 KFX6684 1 11.45 −1.84 −0.28 0.42 −26.25 0 1.38 KFX6684 2 10.65 −0.61 1.17 0.42 −6.47 −3.13 2.73 KFX6684 1 13.1 0.39 0.01 0.95 7.91 0.14 −0.52 KFX6684 1 6.37 0.03 1.19 2.65 6.77 0.14 −1.52 KFX6684 1 −4.09 4.37 0.71 2.65 3.74 0.14 0.21 KFX6684 1 −19.69 −2.35 3.53 −26.77 −1.45 16.25 KFX6684 1 −9.48 −1.7 1.58 −3.72 −1.89 6.25 KFX6684 1 7.76 −0.23 −0.54 0.42 −26.25 −3.13 −1.44 KFX6684 1 0.68 −1.15 0.22 0.42 −2.08 0 1.87 KFX6684 1 11.52 −0.82 −0.4 0.42 −0.42 0 0 KFX6684 1 −21.8 3.12 −0.98 2.65 −9.89 −0.99 0.48 KFX6684 1 12.23 0 0.06 0.42 −17.08 0 0 KFX6684 1 3.03 0.5 1.63 0.42 −10.42 0 −0.15 KFX6684 1 −0.74 −2.24 1.49 0.89 −1.96 1.25 KFX6684 1 −14.03 −0.15 1.19 0.48 −6.06 −1.26 KFX6684 1 −15.76 −0.07 1.71 0.48 −5.8 −4.59 KFX6684 1 −3.34 0.12 1 0.48 6.51 1.66 XR= 57 0.03 −0.55 1.1 −0.3 37.5 −3.88 1.89 0.03 −1.41 4.96 XH= 52 −0.29 −0.53 1.18 −0.23 37.5 −4.09 1.82 0.03 −0.86 4.96 XT= 3 6.07 −0.73 0.31 −1.1 −2.06 1.03 −3.62 2.83 % Emer- Green % gence Vigor Heatunits Heatunits Ear Plant Line Snap Barren Rating Rating to S50 to P50 Height Height KFX6684 4.2 KFX6684 20.38 KFX6684 3.88 KFX6684 −19.05 KFX6684 −0.6 0.55 0.43 −0.08 −14.09 11.08 17.94 KFX6684 −0.83 −0.56 0.48 24.29 0.25 0.77 0.76 KFX6684 18.85 1.93 15.66 KFX6684 −2.01 −13.41 KFX6684 −2.01 4.13 KFX6684 −4.54 KFX6684 −0.32 −5.01 KFX6684 16.75 KFX6684 2.91 KFX6684 −14.18 KFX6684 −7.25 KFX6684 1.16 −1.36 KFX6684 7.89 KFX6684 −0.57 −0.6 −1 12.61 11.94 KFX6684 3.87 KFX6684 −2.01 −3.95 KFX6684 4.18 KFX6684 −4.07 KFX6684 6.03 KFX6684 −0.09 6.73 −8.83 KFX6684 −3.99 2.7 KFX6684 19.01 KFX6684 6.09 KFX6684 4.82 KFX6684 −4.07 KFX6684 10.53 KFX6684 12.44 KFX6684 4.18 KFX6684 −2.29 −3.53 KFX6684 9.9 KFX6684 0.58 KFX6684 −5.99 15.56 KFX6684 −2.48 8.87 9.03 KFX6684 −3.42 9.17 KFX6684 −3.42 −0.99 KFX6684 −1.15 1.55 KFX6684 4.82 KFX6684 6.51 KFX6684 −6.51 16.19 KFX6684 −4.29 3.7 KFX6684 −4.38 6.67 KFX6684 0.55 12.56 KFX6684 −5.99 25.08 KFX6684 20.76 13.02 KFX6684 1.01 KFX6684 −0.49 2.12 −1.41 KFX6684 −1.33 −9.31 4.94 KFX6684 −1.33 −5.5 7.9 XR= −0.62 −0.02 0.08 8.04 −9.31 4.18 7.59 XH= −0.55 −0.21 −0.03 12.11 −6.92 4 6.44 XT= 5.26 0.55 0.43 −0.08 −14.09 7.3 14.21 % % Late % Early % Stay Test % Stalk Push Root Root Dropped Final Green Line N Yield Moisture Weight Lodging Test Lodging Lodging Ears Stand % KFX5474 1 14.67 0.43 0.49 10.64 0.08 KFX5474 1 11.81 1.74 0.63 21.28 0.33 KFX5474 1 18.49 0.39 −0.35 −1.07 1.87 0 1.66 KFX5474 1 5.5 −3.13 −0.57 2.04 −6.38 0.24 KFX5474 1 1.48 −1.46 −2.21 −0.85 −2.31 −0.38 KFX5474 1 −0.67 −2.3 −0.03 0.21 2.88 20 0.87 KFX5474 1 −4.31 1.02 2.92 2.79 −1.14 KFX5474 2 −1.13 −1.82 0 −3.34 13.59 −4.27 −7.98 −2.2 KFX5474 1 2.62 0.52 0.15 −2.14 −57.5 0.57 8.32 0.08 3.12 −36 KFX5474 1 11.6 −4.21 −1.49 0.82 0.78 −4.23 KFX5474 1 −11.86 −0.08 0.01 1.13 3.85 0 −3.92 KFX5474 1 −9.38 −3.98 −0.29 1.17 1.17 2.68 KFX5474 1 13.61 −2.91 −2.44 0.57 0.46 0 1.98 KFX5474 1 −12.98 −2.96 −1.26 0.36 1.7 −7.36 KFX5474 1 7.68 −0.49 0.99 −6.63 0 2.74 1.9 KFX5474 1 3.37 1.3 2.74 −5.31 −32.68 0 −0.24 KFX5474 1 15.19 −0.71 1.48 −5.32 0.80

KFX5474 2 4.16 −0.36 0.92 0.74 19.95 2.79 0 −0.11 KFX5474 1 −8.3 0.19 1.53 0.34 9.58 0 −0.5 KFX5474 1 −6.14 −0.91 1 −4.13 0.11 0 1.14 KFX5474 1 19.56 −5.06 −3.35 0.80 0.98 KFX5474 1 8.55 −2.29 −0.87 0.57 −0.6 0 0.38 KFX5474 1 32.02 −1.74 −1.32 0.57 0.46 0 −0.62 KFX5474 1 15.52 −5.47 −0.59 −0.25 −9.84 0 0.12 KFX5474 1 4.4 −0.97 0.25 2.79 0.78 −5.06 KFX5474 1 −16.31 1.17 2.64 3.03 −1.49 KFX5474 1 −13.16 −0.74 1.33 3.03 −1.49 KFX5474 1 −10.31 −0.96 0.84 3.03 −2.49 KFX5474 1 −16.99 −1.49 1.47 3.03 −1.91 KFX5474 1 −10.89 −2.41 1.48 3.03 −1.42 KFX5474 1 13.21 −1.41 1.12 −1.03 −4.4 0 −0.14 KFX5474 1 12.84 −0.49 −0.25 0.99 −17.94 0 0.02 KFX5474 1 6.61 0.98 0.02 0.48 13.29 −9.78 1.6 KFX5474 1 1.13 0.05 2.87 −5.27 −1 −3.75 KFX5474 1 −7.58 0.94 0.4 9.75 −1.8 −20 KFX5474 1 10.28 −2.48 −0.85 −2.1 8.24 0 −0.14 KFX5474 1 5.63 −2.42 −0.11 5.32 1.15 −1.91 KFX5474 1 3.18 −0.62 1.87 −2.79 −6.54 4.95 2.09 KFX5474 1 −12.49 −2.73 −0.14 0.53 3.06 −0.55 −0.28 KFX5474 1 −7.43 −1.43 0.02 −0.65 4.04 −2.34 KFX5474 1 17.55 0.49 0.41 0.41 2.58 1.46 KFX5474 1 14.26 −0.93 −0.72 −0.12 4.04 0.31 KFX5474 1 9.63 −0.48 −0.57 0.41 3.31 0.31 KFX5474 1 2.22 −2.54 −0.46 −19.03 −0.4 KFX5474 1 7.71 −3.64 −0.95 2.74 8.24 0.76 KFX5474 1 2.83 −1.24 −1.36 −1.18 −2.16 0.31 KFX5474 1 10.34 −0.01 −0.26 −1.06 6.87 0.55 2.17 KFX5474 1 3.74 −2.58 −1.15 −2.52 3.55 0 −0.57 KFX5474 1 5.68 −1.78 −0.08 1.17 1.17 0.08 KFX5474 1 4.85 −3.73 1.62 1.17 −0.96 0 0.08 KFX5474 1 12.31 −2.6 −2.64 0 0.80 0.03 KFX5474 2 −6.17 −0.66 2.01 1.7 1.6 −11.18 −0.44 KFX5474 1 −0.3 −2.18 0.07 −0.23 −3.08 0 1.67 KFX5474 1 2.89 −0.31 −1.63 3.99 3.99 9.62 1 KFX5474 1 −3.94 −1.27 1.55 11.7 0.80 KFX5474 1 15.73 −2.95 −1.06 2.79 0.78 −10.43 KFX5474 2 5.06 −2.62 1.72 −3.12 11.17 1.48 0.23 −0.19 KFX5474 1 6.36 −2.68 −0.69 0.41 4.04 −0.04 KFX5474 1 19.91 −1.58 −0.5 0.41 −11.29 −0.04 KFX5474 1 −0.79 −1.04 0.41 0.06 2.37 0 1.28 KFX5474 2 15.27 −1.92 1.18 0.57 −12.37 −38 0 −0.73 −3.75 KFX5474 1 8.55 −2.43 0.58 −15.21 7.58 0.92 KFX5474 1 13.58 −0.52 −1.37 −0.23 −6.9 −1.15 −0.92 KFX5474 1 17.33 −2.15 −0.7 2.18 −0.43 −7.88 KFX5474 1 13.56 −3.38 −1.06 0 1.96 −0.31 KFX5474 1 21 −5.16 −1.05 0 −3.04 0 −1.12 KFX5474 1 15.83 −4.92 −0.14 0 −10.54 0 −1.12 KFX5474 1 11.71 −3.71 −1.18 0 6.96 0 −1.63 KFX5474 1 12.27 −5.35 −1.86 0 −0.54 −2.45 KFX5474 1 5.77 −0.9 −1.09 2.79 0.78 −3.85 KFX5474 1 16.03 −1.29 −2.91 −1.66 6.21 0 −0.57 KFX5474 1 20.15 −4.04 −1.61 0 −5.54 −2.08 −1.12 KFX5474 1 12.75 −4.66 −0.94 0 −0.45 KFX5474 1 −0.63 −1.78 −0.16 0 4.46 −1.85 KFX5474 1 3.54 −2.19 −1.73 2.79 −0.55 −1.68 KFX5474 1 3.91 −3.28 −1.69 −7.15 1.15 0 0.23 KFX5474 1 0.15 −1.72 −1.16 0.68 6.94 −0.8 1.03 KFX5474 1 −5.56 1.81 1.71 5.32 −0.24 KFX5474 1 13.06 0.39 0.16 21.28 0.3 KFX5474 1 −7.92 −1.75 −0.9 2.79 −6.42 −8.26 KFX5474 1 −6.35 1.54 0.53 −0.32 −25.93 −1.32 KFX5474 4 21.15 −0.78 1.58 −1.03 1.46 0.72 −0.79 −0.09 0.1 KFX5474 2 −6.55 −0.17 2.37 0.99 1.38 2.24 −9.9 KFX5474 1 7.69 0.88 −0.15 0 0.94 KFX5474 1 −12.03 0.54 0.52 −4.38 −31.29 −7.35 XR= 8 8.4 −0.26 1.43 −0.92 1.46 −3.77 0.72 −0.09 −3.22 XH= 4 2.57 0.12 1.08 −1.48 1.46 −7.3 0.72 −0.09 −4.05 XT= Emer- % Green % gence Vigor Heatunits Heatunits Ear Plant Line Snap Barren Rating Rating to S50 to P50 Height Height KFX5474 −1.75 KFX5474 −3.65 KFX5474 −0.49 −12.83 0.57 KFX5474 −6.55 5.09 KFX5474 4.47 KFX5474 3.28 KFX5474 −4.55 KFX5474 3.81 −0.45 0.80 −23.33 −30.97 −0.5 12.18 KFX5474 −0.83 −0.56 1.48 −47.04 −57.62 −12.69 10.51 KFX5474 0.41 31.2 21.96 KFX5474 −0.64 3.42 −0.56 KFX5474 9.1 KFX5474 15.41 KFX5474 3.93 8.37 KFX5474 −2.38 −8.9 3.07 KFX5474 0.87 KFX5474 −0.2 KFX5474 −0.32 −0.06 KFX5474 5.16 KFX5474 8.6 KFX5474 −1.24 KFX5474 15.91 KFX5474 4.91 KFX5474 7.83 KFX5474 2.9 1.77 21.92 KFX5474 8.3 KFX5474 1.66 KFX5474 3.52 KFX5474 −4.5 KFX5474 −22.3 KFX5474 −2.93 KFX5474 1.07 KFX5474 6.94 KFX5474 3.5 KFX5474 −2.34 KFX5474 29.07 KFX5474 −2.24 −9.47 KFX5474 −1.88 KFX5474 −0.88 KFX5474 3.72 KFX5474 12.72 KFX5474 2.39 KFX5474 −3.94 KFX5474 −0.17 KFX5474 −2.93 KFX5474 2.06 KFX5474 −12.5 KFX5474 12.16 KFX5474 18.6 KFX5474 −0.07 KFX5474 6.26 KFX5474 −2.24 −9.66 KFX5474 3.43 KFX5474 0.88 KFX5474 −2.74 KFX5474 −1.05 21.12 22.65 KFX5474 −6.55 −1.06 KFX5474 0.06 KFX5474 11.72 KFX5474 11.24 KFX5474 10.21 KFX5474 −5.47 KFX5474 19.16 KFX5474 4.39 17.7 28.63 KFX5474 −4.34 −11.25 KFX5474 −2.63 0.82 KFX5474 −4.34 −7.44 KFX5474 −3.79 0.82 KFX5474 −3.2

2.72 KFX5474 −0.37 9.2 1.82 KFX5474 15.49 KFX5474 −3.22 1.45 KFX5474 −3.2 4.26 KFX5474 −4.34 −9.34 KFX5474 3.82 9.02 9.77 KFX5474 15.16 KFX5474 10.46 KFX5474 13.71 KFX5474 6.93 KFX5474 3 −0.85 2.54 KFX5474 0.80 KFX5474 11.66 −0.53 0.65 −32.68 −44.96 3.37 3.48 KFX5474 0.15 1.33 0.22 −62.19 −53.05 −10.89 13.14 KFX5474 0 −1.35 −1.86 KFX5474 1 1.27 9.45 XR= 5.18 0.4 0.43 −47.43 −49 −1.9 6.05 XH= 3.2 0.4 0.43 −47.43 −49 −1.9 6.05 XT=

The Paired Hybrid Comparison Data Table A shows the inbred TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 in hybrid combination, in comparison with another hybrid, which is adapted for the same region of the Corn Belt.

(233) TABLE-US-00005 PAIRED HYBRID COMPARISON DATA TABLE A Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 231.1 19.9 55.5 1.8 0.7 3.5 227.8 w/ TPJC7638 Hybrid2 225.3 19.2 53.8 8.1 0.3 4.9 230.1 ′#Expts 33 33 25 3 7 6 33 ′Diff 5.8 0.7 1.7 6.4 0.3 1.4 2.3 ′Prob 0.161 0.001*** 0.000*** 0.184 0.551 0.635 0.326 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Pltht Earht Hybrid1 0 4 3.3 1388 1395 242.6 122.4 w/ TPJC7638 Hybrid2 1.2 5 3.8 1396 1376 244.9 126.6 ′#Expts 4 1 4 4 4 8 8 ′Diff 1.2 1 0.5 7.6 19.8 2.3 4.2 ′Prob 0.306 0.391 0.602 0.207 0.594 0.257 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 202.9 19.3 55.9 2.6 0.5 0.4 0 134.8 w/ KFX6631 Hybrid2 204.8 21 55.5 9.2 1.4 0.4 0 136.8 ′#Expts 54 54 37 3 15 6 1 54 ′Diff 1.9 1.7 0.5 6.5 0.9 0 0 2 ′Prob 0.506 0.000*** 0.070* 0.268 0.222 0.951 0.165 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Pltht Earht Hybrid1 0 4.6 4.7 1374 1365 252.2 108.1 w/ KFX6631 Hybrid2 0 4.9 4.5 1378 1378 270.2 134.5 ′#Expts 3 10 6 6 6 6 6 ′Diff 0 0.3 0.2 4 13.2 18 26.4 ′Prob 0.081* 0.741 0.609 0.289 0.079* 0.003*** Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 202 24.1 54.3 2.6 0.6 11.2 86.1 w/ KFX7481 Hybrid2 185.8 23.2 54.9 21.5 1.1 7.3 86.1 ′#Expts 9 9 7 3 2 2 9 ′Diff 16.1 0.9 0.5 18.9 0.6 3.9 0 ′Prob 0.167 0.172 0.265 0.300 0.500 0.688 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Pltht Earht Hybrid1 5.7 253.5 132.1 w/ KFX7481 Hybrid2 2.3 266.2 130.8 #Expts 2 3 3 ′Diff 3.4 12.6 1.3 ′Prob 0.742 0.290 0.184 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 221.4 20.8 56.9 0 5.3 9.7 203 w/ KFX5450 Hybrid2 220.3 20.7 54.8 0 0.6 2.6 201.2 ′#Expts 61 61 54 4 18 7 61 ′Diff 1.1 0.1 2.1 0 4.7 7.1 1.8 ′Prob 0.704 0.834 0.000*** 0.038** 0.228 0.283 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Pltht Earht Hybrid1 2.4 2.6 3 1347 1341 270.4 123.5 w/ KFX5450 Hybrid2 6.9 2.2 3 1379 1412 266.3 122.5 ′#Expts 5 5 1 3 3 6 10 ′Diff 4.5 0.4 0 32 71 4.1 1.1 ′Prob 0.396 0.477 0.025** 0.006*** 0.550 0.830 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 212.4 19.1 55.1 0 0.4 0 0 199.6 w/ KHI5609 Hybrid2 219 19.5 54.9 10.1 0.7 9.8 0.8 202.8 ′#Expts 107 107 61 4 17 10 2 107 ′Diff 6.6 0.4 0.2 10.1 0.3 9.8 0.8 3.1 ′Prob 0.001*** 0.032** 0.076* 0.195 0.371 0.041** 0.500 0.005*** Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Pltht Earht Hybrid1 30 0 1.7 3.3 3 1378 1382 169 87 w/ KHI5609 Hybrid2 33 0.7 0.9 4 3 1427 1390 181.5 87.9 ′#Expts 5 12 10 3 2 7 7 15 15 ′Diff 3 0.7 0.9 0.7 0 48.7 7.4 12.5 0.9 ′Prob 0.607 0.252 0.084* 0.529 0.000*** 0.173 0.029** 0.759 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 225.2 21.8 53.9 1.6 2.6 7.7 0 155 w/ KFX6684 Hybrid2 221.8 21.2 53.8 0 1 6.9 0 161.9 ′#Expts 17 17 16 2 4 2 1 17 ′Diff 3.3 0.7 0.2 1.6 1.6 0.8 0 6.9 ′Prob 0.579 0.062* 0.587 0.500 0.482 0.623 0.032** Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Pltht Earht Hybrid1 2 1.5 1395 1416 259 116.3 w/ KFX6684 Hybrid2 1 3.5 1416 1439 272 125.7 #Expts 2 2 1 1 1 3 ′Diff 1 2 21 23 13 9.3 ′Prob 0.500 0.393 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 209 19.4 57.8 6.7 7.4 44.3 0.4 0.4 196.5 w/ KFX5474 Hybrid2 212.9 19.5 56.1 3.3 2.5 31.4 3.7 0.1 204.7 ′#Expts 228 228

192 9 37 7 22 10 228 ′Diff 3.9 0.1 1.7 3.4 4.8 12.9 3.3 0.3 8.2 ′Prob 0.005*** 0.425 0.000*** 0.381 0.067* 0.211 0.352 0.343 0.000*** Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Plttht Earht Hybrid1 17.9 5.1 3.3 2.6 1299 1298 252.5 115.7 w/ KFX5474 Hybrid2 11.4 1.9 4.5 4.2 1356 1355 237.3 110.1 ′#Expts 7 23 43 27 14 14 17 17 ′Diff 6.4 3.2 1.2 1.6 57.6 57.6 15.2 5.6 ′Prob 0.412 0.024** 0.000*** 0.000*** 0.000*** 0.000*** 0.006*** 0.155 *.05 < Prob <= .10 **.01 < Prob <= .05 ***.00 < Prob <= .01

(234) TABLE-US-00006 PAIRED HYBRID COMPARISON DATA TABLE B Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 230.7 19.9 55.5 1.8 0.3 3.5 226.5 w/ TPJC7638 Hybrid3 227.9 22.1 54.6 3.1 0.7 6.2 221.8 ′#Expts 32 32 25 3 6 6 32 ′Diff 2.8 2.2 0.9 1.3 0.4 2.7 4.8 ′Prob 0.516 0.000*** 0.002*** 0.423 0.255 0.363 0.108 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Plttht Earht Hybrid1 0 4 3.3 1388 1395 242.6 122.4 w/ TPJC7638 Hybrid3 1.2 4 4.5 1409 1402 260.9 136.4 ′#Expts 4 1 4 4 4 8 8 ′Diff 1.2 0 1.3 20.6 7 18.3 14 ′Prob 0.391 0.194 0.212 0.391 0.024** 0.002*** Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 186.6 19.4 55.9 2.6 0.5 0.4 0 112 w/ KFX6631 Hybrid3 182 18.8 55.7 5.1 0.5 0 0 113.5 ′#Expts 81 81 49 3 14 6 1 81 ′Diff 4.6 0.6 0.2 2.5 0 0.4 0 1.5 ′Prob 0.061* 0.007*** 0.415 0.544 0.972 0.287 0.164 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Plttht Earht Hybrid1 0 0.2 4.6 4.3 1361 1352 257.6 111.6 w/ KFX6631 Hybrid3 1.3 0.6 3.6 3.7 1338 1353 240.8 112.6 ′#Expts 3 10 10 6 6 6 6 6 ′Diff 1.3 0.4 1 0.7 23 1 16.8 1 ′Prob 0.423 0.194 0.008*** 0.465 0.334 0.937 0.148 0.895 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 204.4 23.3 54.8 1.9 0.6 11.2 85.7 w/ KFX7481 Hybrid3 195.1 22.5 55.7 1.7 0 0 85.7 ′#Expts 10 10 8 4 2 2 10 ′Diff 9.3 0.8 0.8 0.3 0.6 11.2 0 ′Prob 0.428 0.167 0.049** 0.391 0.500 0.500 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Plttht Earht Hybrid1 3.8 253.5 132.1 w/ KFX7481 Hybrid3 4.9 249 121.7 ′#Expts 3 3 3 ′Diff 1.1 4.5 10.4 ′Prob 0.423 0.798 0.110 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 204.2 19.2 57.4 6.5 9.9 250.4 w/ KFX5450 Hybrid3 200.1 18.4 56.8 25.4 13.4 258.8 ′#Expts 36 36 35 14 6 36 ′Diff 4.2 0.8 0.6 18.8 3.5 8.3 ′Prob 0.252 0.001*** 0.000*** 0.046** 0.432 0.004*** Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Plttht Earht Hybrid1 3.2 2.6 3 1355 1337 277.2 133.9 w/ KFX5450 Hybrid3 0.8 2.8 3 1296 1276 263.2 117.7 ′#Expts 4 5 1 4 4 3 3 ′Diff 2.5 0.2 0 59.4 61 14 16.2 ′Prob 0.307 0.621 0.010** 0.009*** 0.169 0.170 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 216.6 19.1 55 0 0.6 0 0 212 w/ KHI5609 Hybrid3 211.9 18 55.9 0 0.7 0.8 0.5 215.2 ′#Expts 86 86 51 3 9 7 1 86 ′Diff 4.7 1.1 0.9 0 0.1 0.8 0.5 3.2 ′Prob 0.025** 0.000*** 0.000*** 0.833 0.356 0.019** Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Plttht Earht Hybrid1 35 0 1.3 2.5 3 1378 1382 176.8 91.2 w/ KHI5609 Hybrid3 40 2.1 1.1 3 2 1393 1423 194.3 98.4 ′#Expts 4 12 7 2 2 7 7 10 10 ′Diff 5 2.1 0.2 0.5 1 14.7 40.7 17.5 7.2 ′Prob 0.182 0.233 0.760 0.500 0.500 0.099* 0.003*** 0.001*** 0.181 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL PCTDE Stand Hybrid1 225.2 21.8 53.9 1.6 2.6 7.7 0 155 w/ KFX6684 Hybrid3 220.4 20.8 56 1.6 10.6 15.4 0 166.7 ′#Expts 17 17 16 2 4 2 1 17 ′Diff 4.7 1.1 2 0 8 7.7 0 11.7 ′Prob 0.323 0.004*** 0.000*** 0.206 0.572 0.006*** Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Plttht Earht Hybrid1 2 1.5 1395 1416 259 116.3 w/ KFX6684 Hybrid3 1.5 3 1302 1286 277 112.7 ′#Expts 2 2 1 1 1 3 ′Diff 0.5 1.5 93.6 130.1 18 3.7 ′Prob 0.795 0.205 0.624 Hybrid Yield Moist TWT PCTERL PCTSL PCTPUSH PLTLRL

PCTDE Stand Hybrid1 209.1 19.8 57.7 5.9 7.5 45 0.4 0.5 207.5 w/ KFX5474 Hybrid3 215.9 20 55.5 0 0.6 58.3 6.6 0.2 217.2 ′#Expts 186 186 151 6 33 6 22 9 186 ′Diff 6.8 0.2 2.2 5.9 6.8 13.3 6.2 0.3 9.7 ′Prob 0.000*** 0.104 0.000*** 0.282 0.026** 0.443 0.179 0.347 0.000 Hybrid PCTSG PCTGS PctBarren Emerge Vigor HUS50 HUP50 Pltht Earht Hybrid1 24 5.3 3.3 2.6 1305 1304 244.3 117.2 w/ KFX5474 Hybrid3 40 3.3 3.6 2.8 1370 1392 242.6 119.7 #Expts 5 22 37 21 10 10 13 16 ′Diff 16 2 0.3 0.1 65 88 1.7 2.5 ′Prob 0.078* 0.051* 0.108 0.614 0.000*** 0.000*** 0.790 0.441 *.05 < Prob <= . 10 **.01 < Prob <= . 05 ***.00 < Prob <= . 01

The Yield by Environment Response Table shows the yield response of Hybrid 1 w/TPJC7638, KFX6631, KFX7481, KFX5450, KHI5609, KFX5474, and KFX6684 as a parent in comparison with two other hybrids and the plants in the environment around it at the same location.

(235) TABLE-US-00007 Yield By Environment Response Table Research Plots Environment Yield Hybrid Error # Plots 75 100 125 150 175 200 Hybrid1 w/TPJC7638 16.2 33 73 101 129 157 185 213 Hybrid2 21.8 4390 91 114 137 160 183 206 Hybrid1 w/KFX6631 19.7 62 79 105 130 156 182 207 Hybrid2 20.6 4002 81 105 130 154 178 203 Hybrid1 w/KFX7481 19.9 10 106 125 144 163 183 202 Hybrid2 21.6 1996 79 104 129 154 179 204 Hybrid1 w/KFX5450 18.3 64 70 97 124 151 179 206 Hybrid2 20.3 6190 92 115 138 161 184 207 Hybrid1 w/KHI5609 17.2 103 96 118 140 162 184 206 Hybrid2 21.8 4390 91 114 137 160 183 206 Hybrid1 w/KFX6684 16.3 17 19 56 94 131 168 206 Hybrid2 20.3 6190 92 115 138 161 184 207 Hybrid1 w/KFX5474 20.1 244 83 107 131 155 178 202 Hybrid2 20.1 1914 99 120 141 162 182 203 Hybrid1 w/TPJC7638 16.2 33 73 101 129 157 185 213 Hybrid3 20.6 4002 81 105 130 154 178 203 Hybrid1 w/KFX6631 19.7 62 79 105 130 156 182 207 Hybrid3 22 1979 86 108 131 153 175 198 Hybrid1 w/KFX7481 19.9 10 106 125 144 163 183 202 Hybrid3 20.7 711 88 112 135 159 182 205 Hybrid1 w/KFX5450 18.3 64 70 97 124 151 179 206 Hybrid3 23.7 1978 72 97 122 146 171 195 Hybrid1 w/KHI5609 17.2 103 96 118 140 162 184 206 Hybrid3 20.3 6190 92 115 138 161 184 207 Hybrid1 w/KFX6684 16.3 17 19 56 94 131 168 206 Hybrid3 23.7 1978 72 97 122 146 171 195 Hybrid1 w/KFX5474 20.1 244 83 107 131 155 178 202 Hybrid3 20.3 6190 92 115 138 161 184 207

(236) Accordingly, the present invention has been described with some degree of particularity directed to the embodiment of the present invention. It should be appreciated, though that the present invention is defined by the following claims construed in light of the prior art so that modifications or changes may be made to the embodiment of the present invention without departing from the inventive concepts contained herein.

Claims

1. A seed of maize variety KFX6631, wherein representative seed of said maize variety KFX6631 has been deposited under Accession Number 202411015.
2. A plant of maize variety KFX6631, wherein representative seed of said maize variety variety KFX6631 has been deposited under ATCC Accession Number 202411015.
3. A plant part of the plant of claim 2.
4. The plant part of claim 3, wherein said part is a pollen grain, a silk, a protoplast, a cell, a tassel, an anther or an ovule.
5. A maize seed produced on the plant of claim 2.
6. A maize plant having all of the physiological and morphological characteristics of the plant according to claim 2 and further comprising an additional trait, wherein the additional trait is selected from the group consisting of water stress resistance, waxy starch, male sterility or restoration of male fertility, modified carbohydrate metabolism, modified protein metabolism, modified fatty acid metabolism, altered starch, thermotolerant amylase, herbicide resistance, insect resistance, nematode resistance, bacterial disease resistance, fungal disease resistance, and viral disease resistance.

7. The plant of claim 6 wherein the additional trait is conferred by introducing a transgene.
8. A converted seed, plant, plant part or plant cell of maize variety KFX6631, representative seed of the maize variety variety KFX6631 having been deposited under ATCG Accession Number 202411015, wherein the converted seed, plant, plant part or plant cell comprises a locus conversion, and wherein the plant or a plant grown from the converted seed, plant part or plant cell comprises the locus conversion and otherwise comprises the phenotypic characteristics of maize variety KFX6631 when grown under the same environmental conditions.
9. A process for producing maize seed, said process comprising crossing the maize plant of claim 2 with a different maize plant, and harvesting the seed.
10. An F1 maize seed produced by the process of claim 9.
11. An F1 maize plant produced by germinating the seed of claim 10.
12. A method of producing a genetic marker profile comprising extracting nucleic acids from the seed of claim 10 or the plant germinated from said seed and genotyping said nucleic acids at one or more genetic loci, thereby producing a genetic marker profile.
13. A method of plant breeding comprising a) isolating nucleic acids from the seed of claim 10, b) identifying one or more polymorphisms from the isolated nucleic acids, and c) selecting a plant obtained from said seed having said one or more polymorphisms, wherein the plant is used in a plant breeding method.
14. A method of plant breeding comprising a) isolating nucleic acids from the plant of claim 11, b) identifying one or more polymorphisms from the isolated nucleic acids, and c) selecting a plant having said one or more polymorphisms, wherein the plant is used in a plant breeding method.
15. A process of introducing an additional trait into maize plant KFX6631 comprising: (a) crossing KFX6631 plants grown from variety KFX6631 seeds, representative seeds deposited under Accession Number 202411015, with plants of another maize variety that comprise an additional trait to produce hybrid progeny plants, (b) selecting hybrid progeny plants that have the additional trait to produce selected hybrid progeny plants; (c) crossing the selected progeny plants with the KFX6631 plants to produce backcross progeny plants; (d) selecting for backcross progeny plants that have the additional trait to produce selected backcross progeny plants; and (e) repeating steps (c) and (d) at least three or more times to produce backcross progeny plants that comprise the additional trait and all of the physiological and morphological characteristics of maize inbred plant KFX6631 when grown in the same environmental conditions.
16. A plant produced by the process of claim 15.
17. A method of producing a maize plant derived from the inbred plant KFX6631, the method comprising the steps of (a) growing the plant of claim 11; (b) crossing said plant with itself or a different plant to produce a seed of a progeny plant; (c) repeating step (b) at least one or more times; and (d) growing said progeny plant from said seed and crossing the progeny plant with itself or a different plant to produce a maize plant derived from the inbred plant KFX6631.
18. A method for developing a second maize variety in a maize plant breeding program, comprising applying plant breeding techniques wherein said techniques comprise recurrent selection, backcrossing, pedigree breeding, marker enhanced selection, haploid/double haploid production, or transformation to the maize plant of claim 11, wherein application of said techniques results in development of a second maize variety.
19. A method of producing a commodity plant product comprising growing the plant from the seed of claim 10, and producing said commodity plant product comprising protein concentrate, protein isolate, starch, meal, flour or oil therefrom.
20. A method of producing a maize plant with doubled haploid chromosomes from the maize variety variety KFX6631 the method comprising: (a) crossing the plant of claim 11 with an inducer maize plant to produce a progeny with haploid chromosomes; and (b) doubling the haploid chromosomes in the progeny to produce a maize plant with doubled haploid chromosomes.