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(54) **Title**: METHODS FOR PRODUCING CORN PLANTS WITH DOWNY MILDEW RESISTANCE AND COMPOSITIONS THEREOF

(57) **Abstract**: The present disclosure is in the field of plant breeding and disease resistance. The disclosure provides methods for breeding corn plants having downy mildew (DM) resistance using marker-assisted selection. The disclosure further provides corn germplasm resistant to DM. The disclosure also provides markers associated with DM resistance loci for introgressing these loci into elite germplasm in a breeding program, thus producing novel DM resistant germplasm.

METHODS FOR PRODUCING CORN PLANTS WITH DOWNY MILDEW RESISTANCE AND COMPOSITIONS THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit and priority of U.S. Provisional Application No. 62/216,593, filed on September 10, 2015 which is incorporated by reference in its entirety herein.

FIELD

[0002] The present disclosure relates to the field of agricultural biotechnology. More specifically, this disclosure relates to methods for producing corn plants or seeds with improved downy mildew resistance.

INCORPORATION OF SEQUENCE LISTING

[0003] A sequence listing contained in the file named P34336US01_SEQ.txt which is 251,070 bytes (measured in MS-Windows®) and created on September 8, 2016, comprises 570 nucleotide sequences, is filed electronically herewith and incorporated by reference in its entirety.

BACKGROUND

[0004] Corn (*Zea mays* L.) is one of the most important commercial crops in the world. Like many commercial crops, corn is subjected to numerous potentially detrimental environmental conditions (*e.g.*, moisture availability, temperature stresses, soil conditions, pests, disease) that can reduce, or entirely eliminate, crop yield. Crop disease alone accounted for the loss of more than 1.3 billion bushels of corn in the United States and Ontario, Canada in 2012. *See* Mueller, Corn Disease Loss Estimates from the United States and Ontario, Canada - 2012. *Purdue Extension Publication* BP-96-12--W (2014).

[0005] Downy mildew (DM) is a crop disease caused by several oomycete pathogens of the genera *Peronosclerospora, Sclerophthora*, and *Sclerospora*. Some DM pathogens are known to be host-species specific. For instance, *Sclerospora graminicola* infects *Setaria* sp., but not pearl millet (*Pennisetum glaucum*). Young corn plants infected by DM often die prematurely. Plants that do not die prematurely from DM infection are often stunted in growth. Corn plants infected by DM often exhibit leaf chlorosis, and leaves that are more

narrow and erect than is typical. DM infected fields routinely see yield reductions of about 40-60%, but up to 100% yield loss has been documented. Yield loss in surviving plants is primarily due to a failure to form cobs, which hold the seed, and replacement of parts of the pollen-bearing tassel with vegetative tissues (*e.g.,* leaves). *See* Jeger *et al*, The epidemiology, variability and control of the downy mildews of pearl millet and sorghum, with particular reference to Africa. *Plant Pathology*, 47:544-569 (1998).

[0006] Currently, there are few effective control measures to combat DM infection in corn fields. The fungicide metalaxyl can be used in reducing DM infection for about 42 days, but it can be prohibitively expensive and it is most useful when applied to seed prior to planting. Additionally, at least some oomycetes that cause DM infection show signs of being resistant to fungicides, including metalaxyl. *See* Dalmacio, Importance of and Growing Concerns for Maize Diseases in the Asian Region. In: Vasal *et al.* eds. (2000) *Proceedings of 7th Asian Regional Maize Workshop. The 7th Asian Regional Maize Workshop: Strengthening hybrid maize technology and public-private partnership to accelerate maize production in the Asian region*. Los Baños, Philippines, 23-27 February 1998, Laguna, Philippines: PCARRD, p267-276.

[0007] Genetic resistance to DM presents an attractive option for combating DM infection. Studies describing DM resistance quantitative trait loci (QTLs) have been reported, although commercialization of these genetic resistance has been lacking. *See* Agrama *et al.*, Mapping of QTL for downy mildew resistance in maize. *Theoretical and Applied Genetics*, 99:519-523 (1999); Nair *et al.*, Identification and validation of QTLs conferring resistance to sorghum downy mildew (*Peronosclerospora sorghi*) and Rajasthan downy mildew (*P. heteropogoni*) in maize. *Theoretical and Applied Genetics*, 110:1384-1392 (2005); Sabry *et al.* A region of maize chromosome 2 affects response to downy mildew pathogens. *Theoretical and Applied Genetics*, 113:321-330 (2006); Singh *et al.* Graphical Genotyping of Genomic Resources (QTL-NILs and RILs) and Transcriptome Profiling of Maize Genotypes in Response to Sorghum Downy Mildew (*Peronosclerospora sorghi*) in India. In: Zaidi *et al.* eds. (2010) *Maize for Asia: Emerging Trends and Technologies. Proceedings of The 10th Asian Regional Maize Workshop*. Makassar, Indonesia, 20-23 October 2008, Mexico D.F.: CIMMYT, p220-223; Jampatong *et al.*, QTL mapping for downy mildew (*Peronosclerospora sorghi*) resistance in maize. In: Zaidi *et al.* eds. (2010) *Maize for Asia: Emerging Trends and Technologies. Proceedings of The 10th Asian Regional Maize Workshop*. Makassar, Indonesia, 20-23 October 2008, Mexico D.F.: CIMMYT, p291-298;

Jampatong *et al.*, Mapping of QTL affecting resistance against sorghum downy mildew (*Peronosclerospora sorghi*) in maize (*Zea mays* L). *Maydica*, 58:119-126 (2013).

[0008] There is a need in corn breeding to identify corn germplasm that provides resistance to DM infection. There is also a need to develop polymorphic markers for monitoring and introgressing DM resistance alleles, and further develop agronomically elite corn lines comprising DM resistance for enhancing plant productivity.

SUMMARY

[0009] The present disclosure identifies genetic loci conferring downy mildew (DM) resistance in corn, and provides molecular markers linked to these resistance loci. This disclosure further provides methods for introgressing resistance alleles of genetic loci conferring DM resistance into plant varieties previously lacking such alleles, thereby providing plants with DM resistance. The genetic loci, markers, and methods provided herein therefore allow for production of new varieties with enhanced DM resistance.

[0010] In an aspect, this disclosure provides a method of creating a population of corn plants or seeds, where the method comprises the steps of: (a) genotyping a first population of corn plants or seeds at one or more marker loci associated with and within about 20 cM of a DM resistance QTL selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; (b) selecting from the first population one or more corn plants or seeds comprising one or more DM resistance alleles of the marker loci; and (c) producing from the selected one or more corn plants or seeds a second population of corn plants or seeds comprising one or more DM QTLs.

[0011] In an aspect, this disclosure provides a method of creating a population of corn plants or seeds comprising at least one allele associated with DM resistance, where the method comprises the steps of: (a) genotyping a first population of corn plants, the population comprising at least one allele associated with DM resistance, wherein the at least one DM resistance allele is associated with a marker selected from the group consisting of SEQ ID NOs: 1-114; (b) selecting from the first population one or more corn plants or seeds comprising the at least one DM resistance allele; and (c) producing from the selected corn plants or seeds a second population of corn plants or seeds comprising the at least one DM resistance allele.

[0012] In an aspect, this disclosure provides a method for introgressing a resistance allele of a locus conferring DM resistance, where the method comprises the steps of: (a) crossing a first corn plant with a second corn plant, wherein the first corn plant comprises the resistance allele wherein the at least one DM resistance allele is associated with a marker selected from the group consisting of SEQ ID NOs: 1-114; (b) genotyping a progeny corn plant or seed from the cross using a marker associated with the resistance allele; and (c) selecting a progeny plant or seed comprising the resistance allele.

[0013] In an aspect, this disclosure provides a method of introgressing a DM resistance QTL, where the method comprises the steps of: (a) crossing a first corn plant comprising a DM resistance QTL selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01, with a second corn plant of a different genotype to produce one or more progeny plants or seeds; (b) assaying the one or more progeny plants or seeds at a marker locus associated with the DM resistance QTL; and (c) selecting a progeny plant or seed comprising the DM resistance QTL.

[0014] In an aspect, this disclosure provides a method for creating a population of corn plants or seeds with DM resistance, where the method comprises the steps of: (a) concurrently detecting in a first population of corn plants or seeds the presence of a combination of two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more introgressed DM resistance loci selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; (b) selecting from the first population one or more corn plants or seed comprising the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more introgressed DM resistance QTLs; and (c) producing a population of offspring from the selected one or more corn plants or seeds.

[0015] In an aspect, this disclosure provides a method of producing a corn plant with enhanced DM resistance, where the method comprises the steps of: (a) crossing a first corn plant comprising a DM resistance QTL with a second corn plant of a different genotype to produce one or more progeny plants or seeds; and (b) selecting a progeny plant or seed comprising a DM resistance allele of a polymorphic locus linked to the DM resistance QTL, wherein the polymorphic locus is in a chromosomal segment flanked by: any two of marker

loci SEQ ID NOs: 1 to 11; any two of marker loci SEQ ID NOs: 12 to 22; any two of marker loci SEQ ID NOs: 23 to 28; any two of marker loci SEQ ID NOs: 29 to 32; any two of marker loci SEQ ID NOs: 33 to 38; any two of marker loci SEQ ID NOs: 39 to 45; any two of marker loci SEQ ID NOs: 46 to 55, and 57; any two of marker loci SEQ ID NOs: 56, and 58 to 62; marker loci SEQ ID NOs: 63 and 64; any two of marker loci SEQ ID NOs: 65 to 90; or any two of marker loci SEQ ID NOs: 91 to 114.

[0016] In an aspect, this disclosure provides a method of obtaining a corn plant or seed with enhanced DM resistance, where the method comprises the steps of: (a) detecting in a population of corn plants or seeds a plant or seed comprising a DM resistance allele at a polymorphic locus in a chromosomal segment flanked by: any two of marker loci SEQ ID NOs: 1 to 11; any two of marker loci SEQ ID NOs: 12 to 22; any two of marker loci SEQ ID NOs: 23 to 28; any two of marker loci SEQ ID NOs: 29 to 32; any two of marker loci SEQ ID NOs: 33 to 38; any two of marker loci SEQ ID NOs: 39 to 45; any two of marker loci SEQ ID NOs: 46 to 57; any two of marker loci SEQ ID NOs: 54 to 62; marker loci SEQ ID NOs: 63 and 64; any two of marker loci SEQ ID NOs: 65 to 90; or any two of marker loci SEQ ID NOs: 91 to 114; and (b) selecting the plant or seed from the population based on the presence of the DM resistance allele.

[0017] In an aspect, this disclosure provides a method of obtaining a corn plant or seed with enhanced DM resistance, where the method comprises the steps of: (a) detecting in a population of corn plants or seeds a plant or seed comprising a DM resistance allele at a polymorphic locus in a chromosomal segment flanked by: any two of marker loci SEQ ID NOs: 1 to 11; any two of marker loci SEQ ID NOs: 12 to 22; any two of marker loci SEQ ID NOs: 23 to 28; any two of marker loci SEQ ID NOs: 29 to 32; any two of marker loci SEQ ID NOs: 33 to 38; any two of marker loci SEQ ID NOs: 39 to 45; any two of marker loci SEQ ID NOs: 46 to 55, and 57; any two of marker loci SEQ ID NOs: 56, and 58 to 62; marker loci SEQ ID NOs: 63 and 64; any two of marker loci SEQ ID NOs: 65 to 90; or any two of marker loci SEQ ID NOs: 91 to 114; and (b) selecting the plant or seed from the population based on the presence of the DM resistance allele.

[0018] In an aspect, this disclosure provides a method of producing a corn plant with enhanced DM resistance, where the method comprises the steps of: (a) crossing a first corn plant comprising a DM resistance haplotype with a second corn plant of a different genotype to produce one or more progeny plants or seeds; and (b) selecting a progeny plant or seed based on the presence of the DM resistance haplotype, wherein the haplotype comprises

resistance alleles of two or more polymorphic loci in a chromosomal interval flanked by: any two marker loci selected from the group consisting of SEQ ID NOs: 1 to 11; any two marker loci selected from the group consisting of SEQ ID NOs: 12 to 22; any two marker loci selected from the group consisting of SEQ ID NOs: 23 to 28; any two marker loci selected from the group consisting of SEQ ID NOs: 29 to 32; any two marker loci selected from the group consisting of SEQ ID NOs: 33 to 38; any two marker loci selected from the group consisting of SEQ ID NOs: 39 to 45; any two marker loci selected from the group consisting of SEQ ID NOs: 46 to 57; any two marker loci selected from the group consisting of SEQ ID NOs: 54 to 62; SEQ ID NOs: 63 and 64; any two marker loci selected from the group consisting of SEQ ID NOs: 65 to 90; or any two marker loci selected from the group consisting of SEQ ID NOs: 91 to 114.

[0019] In an aspect, this disclosure provides a method of producing a corn plant with enhanced DM resistance, where the method comprises the steps of: (a) crossing a first corn plant comprising a DM resistance haplotype with a second corn plant of a different genotype to produce one or more progeny plants or seeds; and (b) selecting a progeny plant or seed based on the presence of the DM resistance haplotype, wherein the haplotype comprises resistance alleles of two or more polymorphic loci in a chromosomal interval flanked by: any two marker loci selected from the group consisting of SEQ ID NOs: 1 to 11; any two marker loci selected from the group consisting of SEQ ID NOs: 12 to 22; any two marker loci selected from the group consisting of SEQ ID NOs: 23 to 28; any two marker loci selected from the group consisting of SEQ ID NOs: 29 to 32; any two marker loci selected from the group consisting of SEQ ID NOs: 33 to 38; any two marker loci selected from the group consisting of SEQ ID NOs: 39 to 45; any two marker loci selected from the group consisting of SEQ ID NOs: 46 to 55, and 57; any two marker loci selected from the group consisting of SEQ ID NOs: 56, and 58 to 62; SEQ ID NOs: 63 and 64; any two marker loci selected from the group consisting of SEQ ID NOs: 65 to 90; or any two marker loci selected from the group consisting of SEQ ID NOs: 91 to 114.

[0020] In an aspect, this disclosure provides a method of obtaining a corn plant or seed with enhanced DM resistance, where the method comprises the steps of: (a) detecting in a population of corn plants or seeds a plant or seed comprising a DM resistance haplotype, wherein the haplotype comprises resistance alleles of two or more polymorphic loci in a chromosomal interval flanked by: any two marker loci selected from the group consisting of SEQ ID NOs: 5 to 8; SEQ ID NOs: 7 and 8; any two marker loci selected from the group

consisting of SEQ ID NOs: 12 to 14; any two marker loci selected from the group consisting of SEQ ID NOs: 18 to 20; any two marker loci selected from the group consisting of SEQ ID NOs: 25 to 27; any two marker loci selected from the group consisting of SEQ ID NOs: 29 to 31; any two marker loci selected from the group consisting of SEQ ID NOs: 34 to 36; any two marker loci selected from the group consisting of SEQ ID NOs: 39 to 45; any two marker loci selected from the group consisting of SEQ ID NOs: 49 to 51; SEQ ID NOs: 58 and 59; SEQ ID NOs: 63 and 64; any two marker loci selected from the group consisting of SEQ ID NOs: 77 to 80; or any two marker loci selected from the group consisting of SEQ ID NOs: 99 to 106; and (b) selecting the plant or seed from the population based on the presence of the DM resistance haplotype.

[0021] In an aspect, this disclosure provides a method for selecting a corn plant or seed comprising the steps of: (a) genotyping a population of corn plants or seeds at a polymorphic locus associated with a marker selected from the group consisting of SEQ ID NOs: 1-114; and (b) selecting a corn plant or seed comprising a DM resistance allele at the polymorphic locus.

[0022] In an aspect, this disclosure provides a method for selecting a corn plant or seed comprising the steps of: (a) isolating nucleic acids from a corn plant or seed; (b) analyzing the nucleic acids to detect a polymorphic marker associated with a DM resistance QTL selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; and (c) selecting a corn plant or seed comprising the DM resistance QTL.

[0023] In an aspect, this disclosure provides a method for selecting a corn plant or seed comprising the steps of: (a) detecting in a population of corn plants or seeds a corn plant or seed comprising a DM resistance allele of a marker locus associated with a DM resistance QTL selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; and (b) selecting the corn plant or seed comprising the DM resistance allele.

[0024] In an aspect, this disclosure provides a method for evaluating a collection of corn germplasm comprising the steps of: (a) obtaining a collection of corn germplasm; (b) isolating nucleic acids from each germplasm; (c) assaying the nucleic acids for one or more markers linked to a DM resistance QTL selected from the group consisting of DM_1.01,

DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; and (d) selecting germplasm comprising a DM resistance QTL based on the marker assay.

[0025] In an aspect, this disclosure provides a method comprising providing a set of corn seeds comprising one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01, to a person desirous of planting the set of corn seeds in a field plot.

[0026] In an aspect, this disclosure provides a method of growing a population of corn plants in a field plot, wherein the method comprises planting a population of corn seeds comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more introgressed DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 in the field plot.

[0027] In an aspect, this disclosure provides a corn plant or seed comprising DM resistance and one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more introgressed DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

BRIEF DESCRIPTION OF THE SEQUENCES

[0028] SEQ ID NOs: 1-114 list sequences of exemplary SNP marker loci associated with a DM resistance QTL. Example resistant and susceptible alleles of these marker loci are listed in Table 8. SEQ ID NOs: 115 to 570 list the sequences of exemplary primers and probes which can be used to detect the SNP marker loci of SEQ ID NOs: 1-114.

DETAILED DESCRIPTION

[0029] Unless defined otherwise herein, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art. Examples of resources describing many of the terms related to molecular biology used herein can be found in Alberts *et al.*, Molecular Biology of The Cell, 5th Edition, Garland Science Publishing, Inc.: New York, 2007; Rieger *et al.*, Glossary of Genetics: Classical and Molecular, 5th edition,

Springer-Verlag: New York, 1991; King *et al*, A Dictionary of Genetics, 6th ed., Oxford University Press: New York, 2002; and Lewin, Genes IX, Oxford University Press: New York, 2007. The nomenclature for DNA bases as set forth at 37 C.F.R. § 1.822 is used.

[0030] As used herein, terms in the singular and the singular forms "a," "an," and "the," for example, include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "plant," "the plant," or "a plant" also includes a plurality of plants; also, depending on the context, use of the term "plant" can also include genetically similar or identical progeny of that plant; use of the term "a nucleic acid" optionally includes, as a practical matter, many copies of that nucleic acid molecule; similarly, the term "probe" optionally (and typically) encompasses many similar or identical probe molecules.

[0031] As used herein, "plant" refers to a whole plant, any part thereof, or a cell or tissue culture derived from a plant, comprising any of: whole plants, plant components or organs (*e.g.*, leaves, stems, roots, etc.), plant tissues, seeds, plant cells, and/or progeny of the same. A progeny plant can be from any filial generation, *e.g.*, F_1, F_2, F_3, F_4, F_5, F_6, F_7, etc. A plant cell is a biological cell of a plant, taken from a plant or derived through culture from a cell taken from a plant.

[0032] As used herein, a "corn plant" or "maize plant" refers to a plant of species *Zea mays* L and includes all plant varieties that can be bred with corn, including wild maize species.

[0033] As used herein, "germplasm" refers to living sources of genetic material. The germplasm can be part of an organism or cell, or can be separate from the organism or cell. In general, germplasm provides genetic material with a specific molecular makeup that provides a physical foundation for some or all of the hereditary qualities of an organism or cell culture. As used herein, germplasm includes cells, seed, or tissues from which new plants may be grown, or plant parts, such as leaves, stems, pollen, or cells that can be cultured into a whole plant.

[0034] As used herein, the phrase "associated with" or "linked to" refers to a recognizable and/or assayable relationship between two entities. For example, the phrase "associated with DM resistance" refers to a trait, locus, gene, allele, marker, phenotype, etc., or the expression thereof, the presence or absence of which can influence an extent, degree, and/or rate at which a plant or a part of interest thereof that has a DM resistance trait. As such, a marker is "associated with" a trait when it is linked to it and when the presence of the marker is an indicator of whether and/or to what extent the desired trait or trait form will

occur in a plant/germplasm comprising the marker. Similarly, a marker is "associated with" an allele when it is linked to it and when the presence of the marker is an indicator of whether the allele is present in a plant/germplasm comprising the marker. For example, "a marker associated with a resistance allele" refers to a marker whose presence or absence can be used to predict whether and to what extent a plant will display a DM resistance phenotype.

[0035] As used herein, a centimorgan ("cM") is a unit of measure of recombination frequency and genetic distance between two loci. One cM is equal to a 1% chance that a marker at one genetic locus will be separated from a marker at, a second locus due to crossing over in a single generation.

[0036] As used herein, "closely linked" means that the marker or locus is within about 20 cM, 15 cM, 10 cM, 5 cM, 4 cM, 3 cM, 2 cM, 1 cM, 0.5 cM or less than 0.5 cM of another marker or locus. For example, 20 cM means that recombination occurs between the marker and the locus with a frequency of equal to or less than about 20%.

[0037] As used herein, "locus" is a chromosome region or chromosomal region where a polymorphic nucleic acid, trait determinant, gene, or marker is located. A locus may represent a single nucleotide, a few nucleotides or a large number of nucleotides in a genomic region. The loci of this disclosure comprise one or more polymorphisms in a population; *e.g.*, alternative alleles are present in some individuals. A "gene locus" is a specific chromosome location in the genome of a species where a specific gene can be found.

[0038] As used herein, "allele" refers to an alternative nucleic acid sequence at a particular locus. The length of an allele can be as small as one nucleotide base. For example, a first allele can occur on one chromosome, while a second allele occurs on a second homologous chromosome, *e.g.*, as occurs for different chromosomes of a heterozygous individual, or between different homozygous or heterozygous individuals in a population.

[0039] As used herein, "crossed" or "cross" means to produce progeny via fertilization (*e.g.* cells, seeds or plants) and includes crosses between plants (sexual) and self-fertilization (selfing).

[0040] As used herein, "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 introgressed. 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 introgressed. For example, *see* Ragot *et al.,* Marker-assisted Backcrossing: A Practical Example, in *Techniques*

Et Utilisations Des Marqueurs Moleculaires Les Colloques, 72:45-56 (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 F_1 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. In an aspect, a backcross is performed repeatedly, with a progeny individual of each successive backcross generation being itself backcrossed to the same parental genotype.

[0041] As used herein, "agronomically elite background" means any line that has resulted from breeding and selection for superior agronomic performance. Similarly, an "elite germplasm" or elite strain of germplasm is an agronomically superior germplasm. Numerous elite lines are available and known to those of skill in the art of corn breeding.

[0042] As used herein, "genotype" is the genetic constitution of an individual (or group of individuals) at one or more genetic loci, as contrasted with the observable trait (phenotype). Genotype is defined by the allele(s) of one or more known loci that the individual has inherited from its parents. The term genotype can be used to refer to an individual's genetic constitution at a single locus, at multiple loci, or, more generally, the term genotype can be used to refer to an individual's genetic make-up for all the genes in its genome. The term genotype can also refer to determining the genetic constitution of an individual (or group of individuals) at one or more genetic loci.

[0043] As used herein, a "haplotype" is the genotype of an individual at a plurality of genetic loci. Typically, the genetic loci described by a haplotype are physically and genetically linked, *e.g.*, in the same chromosome interval. A haplotype can also refer to a combination of SNP alleles located within a single gene.

[0044] As used herein, "marker assay" means a method for detecting a polymorphism at a particular locus using a particular method, *e.g.* measurement of at least one phenotype (such as seed color, flower color, or other visually detectable traits), restriction fragment length polymorphism (RFLP), single base extension, electrophoresis, sequence alignment, allelic specific oligonucleotide hybridization (ASO), random amplified polymorphic DNA (RAPD), microarray-based technologies, and nucleic acid sequencing technologies, *etc.*

[0045] As used herein, "marker assisted selection" (MAS) is a process by which phenotypes are selected based on marker genotypes. "Marker assisted selection breeding" refers to the process of selecting a desired trait or traits in a plant or plants by detecting one or

more nucleic acids from the plant, where the nucleic acid is linked to the desired trait, and then selecting the plant or germplasm possessing those one or more nucleic acids.

[0046] As used herein, "polymorphism" means the presence of one or more variations in a population. A polymorphism may manifest as a variation in the nucleotide sequence of a nucleic acid or as a variation in the amino acid sequence of a protein. Polymorphisms include the presence of one or more variations of a nucleic acid sequence or nucleic acid feature at one or more loci in a population of one or more individuals. The variation may comprise but is not limited to one or more nucleotide base changes, the insertion of one or more nucleotides or the deletion of one or more nucleotides. A polymorphism may arise from random processes in nucleic acid replication, through mutagenesis, as a result of mobile genomic elements, from copy number variation and during the process of meiosis, such as unequal crossing over, genome duplication and chromosome breaks and fusions. The variation can be commonly found or may exist at low frequency within a population, the former having greater utility in general plant breeding and the latter may be associated with rare but important phenotypic variation. Useful polymorphisms may include single nucleotide polymorphisms (SNPs), insertions or deletions in DNA sequence (Indels), simple sequence repeats of DNA sequence (SSRs), a restriction fragment length polymorphism, and a tag SNP. A genetic marker, a gene, a DNA-derived sequence, a RNA-derived sequence, a promoter, a 5' untranslated region of a gene, a 3' untranslated region of a gene, microRNA, siRNA, a tolerance locus, a satellite marker, a transgene, mRNA, ds mRNA, a transcriptional profile, and a methylation pattern may also comprise polymorphisms. In addition, the presence, absence, or variation in copy number of the preceding may comprise polymorphisms.

[0047] As used herein, "SNP" or "single nucleotide polymorphism" means a sequence variation that occurs when a single nucleotide (A, T, C, or G) in the genome sequence is altered or variable. "SNP markers" exist when SNPs are mapped to sites on the genome.

[0048] As used herein, "marker," or "molecular marker," or "marker locus" is a term used to denote a nucleic acid or amino acid sequence that is sufficiently unique to characterize a specific locus on the genome. Any detectable polymorphic trait can be used as a marker so long as it is inherited differentially and exhibits linkage disequilibrium with a phenotypic trait of interest. A number of markers and integrated genetic maps have been developed for corn, *e.g.*, the UMC 98 map, the Nested Association Mapping (NAM) map, the

Intermated B73/Mo17 (IBM2) Neighbors 2008 genetic map, and the LHRF Gnp2004 map. *See* maizegdb.org/data_center/map for more. All markers are used to define a specific locus in corn genomes. Large numbers of these markers have been mapped. *See* maizegdb.org/data_center/marker. Each marker is therefore an indicator of a specific segment of DNA, having a unique nucleotide sequence. The map positions provide a measure of the relative positions of particular markers with respect to one another. When a trait is stated to be linked to a given marker it will be understood that the actual DNA segment whose sequence affects the trait generally co-segregates with the marker. More precise and definite localization of a trait can be obtained if markers are identified on both sides of the trait. By measuring the appearance of the marker(s) in progeny of crosses, the existence of the trait can be detected by relatively simple molecular tests without actually evaluating the appearance of the trait itself, which can be difficult and time-consuming because the actual evaluation of the trait requires growing plants to a stage and/or under environmental conditions where the trait can be expressed. Molecular markers have been widely used to determine genetic composition in corn. In an aspect, markers used herein exhibit LOD scores of 2 or greater, 3 or greater, 4 or greater, 5 or greater, 6 or greater, 7 or greater, 8 or greater, or 9 or greater with an associated trait of interest (*e.g.*, DM resistance), measuring using a method known in the art such as Qgene Version 2.23 (1996) and default parameters.

[0049] As used herein, "linkage disequilibrium" (LD) refers to a non-random segregation of genetic loci or traits (or both). In either case, linkage disequilibrium implies that the relevant loci are within sufficient physical proximity along a length of a chromosome so that they segregate together with greater than random (*i.e.*, non-random) frequency (in the case of co-segregating traits, the loci that underlie the traits are in sufficient proximity to each other). Linked loci co-segregate more than 50% of the time, *e.g.*, from about 51% to about 100% of the time. Linkage disequilibrium can be measured using any one of the methods provided in Hedrick, Gametic disequilibrium measures: proceed with caution. *Genetics*, 117:331–41(1987). The term "physically linked" is sometimes used to indicate that two loci, *e.g.*, two marker loci, are physically present on the same chromosome. Advantageously, the two linked loci are located in close proximity such that recombination between homologous chromosome pairs does not occur between the two loci during meiosis with high frequency, *e.g.*, such that linked loci co-segregate at least about 90% of the time, *e.g.*, 91 %, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.75%, or more of the time.

[0050] As used herein, a "genetic map" is the relationship of genetic linkage among loci on one or more chromosomes (or linkage groups) within a given species, generally depicted in a diagrammatic or tabular form. "Genetic mapping" is the process of defining the linkage relationships of loci through the use of genetic markers, populations segregating for the markers, and standard genetic principles of recombination frequency. A "genetic map location" is a location on a genetic map relative to surrounding genetic markers on the same linkage group where a specified marker can be found within a given species. In contrast, a "physical map" of the genome refers to absolute distances (for example, measured in base pairs or isolated and overlapping contiguous genetic fragments, *e.g.*, contigs). In general, the closer two markers or genomic loci are on the genetic map, the closer they lie to one another on the physical map. A physical map of the genome does not take into account the genetic behavior (*e.g.*, recombination frequencies) between different points on the physical map. A lack of precise proportionality between genetic distances and physical distances can exist due to the fact that the likelihood of genetic recombination is not uniform throughout the genome; some chromosome regions are cross-over "hot spots," while other regions demonstrate only rare recombination events, if any. Genetic mapping variability can also be observed between different populations of the same crop species. In spite of this variability in the genetic map that may occur between populations, genetic map and marker information derived from one population generally remains useful across multiple populations in identification of plants with desired traits, counter-selection of plants with undesirable traits and in MAS breeding. As one of skill in the art will recognize, recombination frequencies (and as a result, genetic map positions) in any particular population are not static. The genetic distances separating two markers (or a marker and a QTL) can vary depending on how the map positions are determined. For example, variables such as the parental mapping populations used, the software used in the marker mapping or QTL mapping, and the parameters input by the user of the mapping software can contribute to the QTL marker genetic map relationships. However, it is not intended that this disclosure be limited to any particular mapping populations, use of any particular software, or any particular set of software parameters to determine linkage of a particular marker or haplotypes with a desired phenotype. It is well within the ability of one of ordinary skill in the art to extrapolate the novel features described herein to any gene pool or population of interest, and using any particular software and software parameters. Indeed, observations regarding genetic markers and haplotypes in

populations in addition to those described herein are readily made using the teaching of the present disclosure.

[0051] As used herein, "selecting" or "selection" in the context of marker-assisted selection or breeding refer to the act of picking or choosing desired individuals, normally from a population, based on certain pre-determined criteria.

[0052] As used herein, "primer" refers to an oligonucleotide (synthetic or occurring naturally), which is capable of acting as a point of initiation of nucleic acid synthesis or replication along a complementary strand when placed under conditions in which synthesis of a complementary strand is catalyzed by a polymerase. Typically, primers are about 10 to 30 nucleotides in length, but longer or shorter sequences can be employed. Primers may be provided in double-stranded form, though the single-stranded form is more typically used. A primer can further contain a detectable label, for example a 5' end label.

[0053] As used herein, "probe" refers to an oligonucleotide (synthetic or occurring naturally) that is complementary (though not necessarily fully complementary) to a polynucleotide of interest and forms a duplex structure by hybridization with at least one strand of the polynucleotide of interest. Typically, probes are oligonucleotides from 10 to 50 nucleotides in length, but longer or shorter sequences can be employed. A probe can further contain a detectable label.

[0054] As used herein, a "population of plants," "population of seeds", "plant population", or "seed population" means a set comprising any number, including one, of individuals, objects, or data from which samples are taken for evaluation. Most commonly, the terms relate to a breeding population of plants from which members are selected and crossed to produce progeny in a breeding program. A population of plants can include the progeny of a single breeding cross or a plurality of breeding crosses, and can be either actual plants or plant derived material, or *in silico* representations of the plants or seeds. The population members need not be identical to the population members selected for use in subsequent cycles of analyses or those ultimately selected to obtain final progeny plants or seeds. Often, a plant or seed population is derived from a single biparental cross, but may also derive from two or more crosses between the same or different parents. Although a population of plants or seeds may comprise any number of individuals, those of skill in the art will recognize that plant breeders commonly use population sizes ranging from one or two hundred individuals to several thousand, and that the highest performing 5-20% of a

population is what is commonly selected to be used in subsequent crosses in order to improve the performance of subsequent generations of the population.

[0055] As used herein, "cultivar" and "variety" are used synonymously and mean a group of plants within a species (*e.g.*, *Z. mays* L.) that share certain genetic traits that separate them from other possible varieties within that species. Corn cultivars can be inbreds or hybrids, though commercial corn cultivars are mostly hybrids to take advantage of hybrid vigor. Individuals within a corn hybrid cultivar are homogeneous, nearly genetically identical, with most loci in the heterozygous state.

[0056] As used herein, the term "inbred" means a line that has been bred for genetic homogeneity.

[0057] As used herein, the term "hybrid" means a progeny of mating between at least two genetically dissimilar parents. Without limitation, examples of mating schemes include single crosses, modified single cross, double modified single cross, three-way cross, modified three-way cross, and double cross wherein at least one parent in a modified cross is the progeny of a cross between sister lines.

[0058] As used herein, "introgression" refers to the transmission of a desired allele of a genetic locus from one genetic background to another.

[0059] As used herein, the term "chromosome interval" or "chromosomal interval" designates a contiguous linear span of genomic DNA that resides on a single chromosome.

[0060] As used herein, "flanked by," when used to describe a chromosomal interval, refers to two loci physically surrounding the chromosomal interval, with one locus on each side of the chromosomal interval. As referenced herein, a chromosomal interval flanked by two marker loci includes the two marker loci.

[0061] As used herein, a "resistant allele" is an allele at a particular locus that confers, or contributes to, DM resistance, or alternatively, is an allele that allows the identification of plants that comprise DM resistance. A resistant allele of a marker is a marker allele that segregates with DM resistance, or alternatively, segregates with DM susceptibility, therefore providing the benefit of identifying plants having DM susceptibility. A resistant allelic form of a chromosome interval is a chromosome interval that includes a nucleotide sequence that contributes to DM resistance at one or more genetic loci physically located in the chromosome interval.

[0062] As used herein, "genetic element" or "gene" refers to a heritable sequence of DNA, *e.g.*, a genomic sequence, with functional significance. The term "gene" can also be

used to refer to, *e.g.*, a cDNA and/or an mRNA encoded by a genomic sequence, as well as to that genomic sequence.

[0063] As used herein, the terms "phenotype," or "phenotypic trait," or "trait" refers to one or more detectable characteristics of a cell or organism which can be influenced by genotype. The phenotype can be observable to the naked eye, or by any other means of evaluation known in the art, *e.g.*, microscopy, biochemical analysis, genomic analysis, an assay for a particular disease tolerance, etc. In some cases, a phenotype is directly controlled by a single gene or genetic locus, *e.g.*, a "single gene trait." In other cases, a phenotype is the result of several genes.

[0064] As used herein, "resistance" and "enhanced resistance" are used interchangeably herein and refer to any type of increase in resistance, or any type of decrease in susceptibility. A "resistant plant" or "resistant plant variety" need not possess absolute or complete resistance. Instead, a "resistant plant," "resistant plant variety," or a plant or plant variety with "enhanced resistance" will have a level of resistance which is higher than that of a comparable susceptible plant or variety. The level of downy mildew resistance can be determined based on disease ratings as determined in Example 1. Specifically, resistance to DM infection of corn plants is scored using a DM resistance scale, wherein DM resistance is measured by counting the percentage of plants infected by DM in a field plot 40 days after planting. A DM resistance scale comprises ratings of highly resistant (*e.g.,* fewer than 5% of plants infected); moderately resistant (*e.g.*, 5 to 15% of plants infected); intermediate (*e.g.,* 15-35% of plants infected); moderately susceptible (*e.g.,* 35-45% of plants infected); and highly susceptible (*e.g.,* greater than 45% of plants infected).

[0065] As used herein, "quantitative trait locus" (QTL) or "quantitative trait loci" (QTLs) refer to a genetic domain that effects a phenotype that can be described in quantitative terms and can be assigned a "phenotypic value" which corresponds to a quantitative value for the phenotypic trait.

[0066] As used herein, "adjacent", when used to describe a nucleic acid molecule that hybridizes to DNA containing a polymorphism, refers to a nucleic acid that hybridizes to DNA sequences that directly abut the polymorphic nucleotide base position. For example, a nucleic acid molecule that can be used in a single base extension assay is "adjacent" to the polymorphism.

[0067] As used herein, "downy mildew" refers to a plant disease caused by oomycete species in the genera *Peronosclerospora*, *Sclerophthora*, and *Sclerospora*.

[0068] As used herein, a "low downy mildew stress condition" refers to a condition where very few to no DM susceptible corn plants in a field plot (*e.g.*, fewer than 10%) exhibit signs of DM infection. Signs of DM infection can include: premature death, stunted growth, chlorotic leaves, narrow leaves, erect leaves, shredded leaves, failed cob formation, and vegetative tissue within the tassel.

[0069] As used herein, a "high downy mildew stress condition" refers to a condition where a plurality of DM susceptible corn plants in a field plot (*e.g.*, more than 30%) exhibit signs of DM infection.

[0070] As used herein, "field plot" refers to a location that is suitable for growing corn. The location may be indoors (*e.g.,* a greenhouse or growth chamber) or outdoors; irrigated or non-irrigated; in the ground or in a container that holds soil.

[0071] As used herein, a "planting season" is the length of time, typically about 90-120 days, in which corn may be grown from seed to maturity. One skilled in the art would recognize that a "planting season" could be significantly shorter or longer than about 90-120 days depending on the corn variety being grown and environmental conditions.

[0072] As used herein, "staggered planting" refers to planting a crop in a single field plot multiple times during the same planting season, with each planting separated by at least 1 day. For instance, planting corn seeds in a field plot on day 1 and again on day 15 would comprise a staggered planting.

[0073] As used herein, "transgenic" means a plant or seed whose genome has been altered by the stable integration of recombinant DNA. A transgenic line includes a plant regenerated from an originally-transformed plant cell and progeny transgenic plants from later generations or crosses of a transformed plant.

[0074] As used herein, "haploid" means a line that has had its normal chromosome complement reduced by half, typically by pollinating an ear with pollen from a haploid inducing line. In corn, haploid refers to an individual plant or seed that has a haploid chromosome complement where n=10, instead of the normal diploid chromosome complement where 2n=20. A "doubled haploid" refers to a haploid line (n=10) that has been induced, typically via chemical means, to double its chromosome complement and return to a diploid state (2n=20) that is homozygous at all loci within the genome.

[0075] As used herein, "yield penalty" refers to a reduction of seed yield in a line correlated with or caused by the presence of a DM resistance allele or DM resistance QTL as compared to a line that does not contain that DM resistance allele or DM resistance QTL.

[0076] As used herein, "seed yield" can refer to a measure of crop production such as test weight, seed number per plant, seed weight, seed number per unit area (*i.e.* seeds, or weight of seeds, per acre), bushels per acre, tons per acre, kilograms per hectare, or quintals per hectare.

[0077] Downy mildew is a plant disease caused by oomycete species of several genera, such as *Peronosclerospora*, *Sclerophthora*, and *Sclerospora*. Due to poor understanding of downy mildew systematics, it is not always possible to identify members of *Peronosclerospora*, *Sclerospora*, and *Sclerophthora* to species. However, species known to cause downy mildew include, but are not limited to: *P. eriochloae, P. graminicola, P. heteropogoni, P. maydis, P. miscanthi, P. philippinensis, P. sacchari, P. sorghi, P. spontanea, P. zeae, Sclerophthora macrospora, Scleropthora rayssiae* var. *zeae, and Sclerospora graminicola*. Downy mildew afflicts corn worldwide, with particularly devastating effects in Africa and Asia. About 29-31% of total areas growing tropical lowland, subtropical, mid-altitude, transition zone, and highland corn report economic losses due to downy mildew. *See* Jeffers *et al.* Status in Breeding for Resistance to Maize Diseases at CIMMYT. In: In: Vasal *et al.* eds. (2000) *Proceedings of 7th Asian Regional Maize Workshop. The 7th Asian Regional Maize Workshop: Strengthening hybrid maize technology and public-private partnership to accelerate maize production in the Asian region*. Los Baños, Philippines, 23-27 February 1998, Laguna, Philippines: PCARRD, p257-266.

[0078] Corn plants are at risk of contracting downy mildew infection as they emerge from the ground as seedlings; downy mildew oospores can persist in soil for at least up to 10 years. If corn plants are infected at the seedling stage they often die prematurely. Older corn plants may be infected by wind-blown downy mildew spores. Typical symptoms of corn afflicted by downy mildew include stunted growth, chlorotic leaves, narrow leaves, and erect leaves. More rarely, infected corn leaves exhibit a shredded phenotype. Corn seed yields are reduced by downy mildew due to a failure of cob formation and a replacement of tassels by vegetative structures such as leaves. *See* Jeger *et al*, The epidemiology, variability and control of the downy mildews of pearl millet and sorghum, with particular reference to Africa. *Plant Pathology*, 47:544-569 (1998). Varieties of corn that are highly susceptible to downy mildew can experience up to 50-100% yield loss, although up to 40-60% yield loss is more typical. When staggered planting is used, late-plantings suffer the greatest yield losses.

[0079] Several systemic fungicides, including metalaxyl, fosetyl-Al, furalaxyl, Patafol, and benalaxyl are used to combat downy mildew. *See* Dalmacio, Importance of and

Growing Concerns for Maize Diseases in the Asian Region. In: Vasal *et al.* eds. (2000) *Proceedings of 7th Asian Regional Maize Workshop. The 7th Asian Regional Maize Workshop: Strengthening hybrid maize technology and public-private partnership to accelerate maize production in the Asian region.* Los Baños, Philippines, 23-27 February 1998, Laguna, Philippines: PCARRD, p267-276. However, reliance on chemical agents to reduce DM incidence is unreliable, because DM may develop resistance to the chemical agents. Indeed, incidences of DM occurring in fields planted with metalaxyl-treated seeds and causing yield loss have been reported. *Id.* A corn plant or seed disclosed herein possesses one or more DM resistance QTLs and/or DM resistance alleles that confer enhanced resistance to downy mildew compared to a corn plant or seed that lacks the one or more DM resistance QTLs or DM resistance alleles. Further, a corn plant or seed disclosed herein provides increased yield in high DM pressure conditions, while suffering no yield penalties in low DM pressure conditions.

[0080] In an aspect, a corn plant or seed provided in this disclosure is *Zea mays* L. In another aspect, a corn plant or seed provided in this disclosure is *Zea mays* ssp. *mays*. In yet another aspect, a corn plant or seed provided herein is a domesticated line or variety. In an aspect, a corn plant or seed provided herein is not *Zea diploperennis.* In an aspect, a corn plant or seed provided herein is not *Zea perennis.* In an aspect, a corn plant or seed provided herein is not *Zea luxurians.* In an aspect, a corn plant or seed provided herein is not *Zea nicaraguensis.* In an aspect, a corn plant or seed provided herein is not *Zea mays* ssp. *huehuetenangensis.* In an aspect, a corn plant or seed provided herein is not *Zea mays* ssp. *mexicana.* In an aspect, a corn plant or seed provided herein is not *Zea mays* ssp. *parviglumis*.

[0081] In an aspect, this disclosure provides quantitative trait loci (QTLs) that exhibit significant co-segregation with DM resistance. The QTLs of this disclosure can be tracked during plant breeding or introgressed into a desired genetic background in order to provide plants exhibiting enhanced DM resistance and one or more other beneficial traits. In an aspect, this disclosure identifies QTL intervals that are associated with DM resistance in corn varieties CV357626 and CV368354.

[0082] In an aspect, this disclosure provides molecular markers linked to the QTLs disclosed herein and methods of using these markers for detection of and selection for DM resistance. An aspect of this disclosure includes specific markers and their resistance alleles, chromosome intervals comprising the markers, and methods of detecting markers genetically linked to DM resistance to identify plant lines with enhanced DM resistance. For example,

one aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 5 to 8. Another aspect of this disclosure provides a chromosome interval associated with DM resistance, where the interval is flanked by marker loci SEQ ID NOs: 7 and 8. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 12 to 14. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 18 to 20. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 25 to 27. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 29 to 31. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 34 to 36. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 39 to 45. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 49 to 51. Another aspect of this disclosure provides a chromosome interval associated with DM resistance, where the interval is flanked by marker loci SEQ ID NOs: 58 and 59. Another aspect of this disclosure provides a chromosome interval associated with DM resistance, where the interval is flanked by marker loci SEQ ID NOs: 63 and 64. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 77 to 80. Another aspect of this disclosure provides a chromosome interval associated with DM resistance which is flanked by any two of marker loci SEQ ID NOs: 99 to 106. Also provided herein are markers, *e.g.*, SEQ ID NOs: 1-114, that are useful for tracking DM resistant alleles and can be used in marker assisted selection (MAS) breeding programs to produce plants with enhanced DM resistance.

[0083] This disclosure further provides methods of using the markers identified herein to introgress loci associated with DM resistance into DM susceptible plants. Thus, one skilled in the art can use this disclosure to create a novel corn plant or seed with DM resistance by crossing a donor line comprising a QTL disclosed herein with any desired recipient line, with or without MAS.

[0084] In another aspect, this disclosure further provides methods for introgressing multiple DM resistance QTLs identified herein to generate an enhanced DM resistant population of corn plants or seeds.

[0085] In an aspect, this disclosure provides a method of creating a population of corn plants or seeds, where the method comprises the steps of: (a) genotyping a first population of corn plants or seeds at one or more marker loci associated with one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; (b) selecting from the first population one or more corn plants or seeds comprising one or more DM resistance alleles of the one or more marker loci; and (c) producing from the selected one or more corn plants or seeds a second population of corn plants or seeds comprising one or more DM QTLs.

[0086] In an aspect, this disclosure provides a method of creating a population of corn plants or seeds, which method comprising the steps of: (a) genotyping a first population of corn plants, the population comprising at least one allele associated with DM resistance, wherein the DM resistance allele is associated with a marker selected from the group consisting of SEQ ID NOs: 1-114; (b) selecting from the first population one or more corn plants or seeds comprising the DM resistance allele; and (c) producing from the selected corn plants or seeds a second population of corn plants or seeds comprising the at least one DM resistance allele.

[0087] In an aspect, this disclosure provides a method for introgressing a resistance allele of a locus conferring DM resistance, which method comprising the steps of: (a) crossing a first corn plant with a second corn plant, wherein the first corn plant comprises the resistance allele, wherein the DM resistance allele is associated with a marker selected from the group consisting of SEQ ID NOs: 1-114; (b) genotyping a progeny corn plant or seed from the cross using a marker associated with the resistance allele; and (c) selecting a progeny plant or seed comprising the resistance allele.

[0088] In an aspect, this disclosure provides a method for introgressing a DM resistance QTL, which method comprising the steps of: (a) crossing a first corn plant comprising a DM resistance QTL selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01, with a second corn plant of a different genotype to produce one or more progeny plants or seeds; (b) assaying the one or

more progeny plants or seeds at a marker locus associated with the DM resistance QTL; and (c) selecting a progeny plant or seed comprising the DM resistance QTL.

[0089] In an aspect, this disclosure provides a method for creating a population of corn plants or seeds with DM resistance, which method comprising the steps of: (a) concurrently detecting in a first population of corn plants or seeds the presence of a combination of two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more introgressed DM resistance loci selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; (b) selecting from the first population one or more corn plants or seed comprising the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more introgressed DM resistance QTLs; and (c) producing a population of offspring from the selected one or more corn plants or seeds. In an aspect, a method comprises concurrent detection of one or more molecular markers located in at least one chromosome interval flanked by any two of marker loci SEQ ID NOs: 1 to 11, any two of marker loci SEQ ID NOs: 12 to 22, any two of marker loci SEQ ID NOs: 23 to 28, any two of marker loci SEQ ID NOs: 29 to 32, any two of marker loci SEQ ID NOs: 33 to 38, any two of marker loci SEQ ID NOs: 39 to 45, any two of marker loci SEQ ID NOs: 46 to 57, any two of marker loci SEQ ID NOs: 54 to 62, any two of marker loci SEQ ID NOs: 65 to 90, or any two of marker loci SEQ ID NOs: 91-114. In another aspect, a method comprises concurrent detection of one or more molecular markers located in at least one chromosome interval flanked by any two of marker loci SEQ ID NOs: 5 to 8, marker loci SEQ ID NOs: 7 and 8, any two of marker loci SEQ ID NOs: 12 to 14, any two of marker loci SEQ ID NOs: 18 to 20, any two of marker loci SEQ ID NOs: 25 to 27, any two of marker loci SEQ ID NOs: 29 to 31, any two of marker loci SEQ ID NOs: 34 to 36, any two of marker loci SEQ ID NOs: 39 to 45, any two of marker loci SEQ ID NOs: 49 to 51, marker loci SEQ ID NOs: 58 and 59, marker loci SEQ ID NOs: 63 and 64, any two of marker loci SEQ ID NOs: 77 to 80, or any two of marker loci SEQ ID NOs: 99 to 106.

[0090] In an aspect, a method comprises concurrently detecting DM resistance QTLs DM_5.01, DM_6.02, and DM_7.01. In an aspect, a method comprises concurrently detecting DM resistance QTLs DM_5.01, DM_6.02, DM_7.01, and DM_8.01. In an aspect, a method comprises concurrently detecting DM resistance QTLs DM_5.01, DM_6.02, and DM_8.01.

In an aspect, a method comprises concurrently detecting DM resistance QTLs DM_6.02, DM_7.01, and DM_8.01. In an aspect, a method comprises concurrently detecting DM resistance QTLs DM_1.01, DM_2.03, and DM_6.01. In an aspect, a method comprises concurrently detecting DM resistance QTLs DM_1.01, DM_4.01, and DM_6.01.

[0091] In another aspect, a method comprises concurrently detecting DM resistance QTL 1.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0092] In another aspect, a method comprises concurrently detecting DM resistance QTL 1.02 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0093] In another aspect, a method comprises concurrently detecting DM resistance QTL 2.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_2.02, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0094] In another aspect, a method comprises concurrently detecting DM resistance QTL 2.02 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0095] In another aspect, a method comprises concurrently detecting DM resistance QTL 2.03 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01,

DM_2.02, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0096] In another aspect, a method comprises concurrently detecting DM resistance QTL 3.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02 DM_2.03, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0097] In another aspect, a method comprises concurrently detecting DM resistance QTL 4.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02 DM_2.03, DM_3.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0098] In another aspect, a method comprises concurrently detecting DM resistance QTL 5.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02 DM_2.03, DM_3.01, DM_4.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[0099] In another aspect, a method comprises concurrently detecting DM resistance QTL 6.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02 DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00100] In another aspect, a method comprises concurrently detecting DM resistance QTL DM_6.02 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_7.01, DM_8.01, and DM_9.01.

[00101] In another aspect, a method comprises concurrently detecting DM resistance QTL 7.01 and at least one or more, two or more, three or more, five or more, six or more,

seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02 DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_8.01, and DM_9.01.

[00102] In another aspect, a method comprises concurrently detecting DM resistance QTL 8.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02 DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, and DM_9.01.

[00103] In another aspect, a method comprises concurrently detecting DM resistance QTL 9.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs selected from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02 DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, and DM_8.01.

[00104] In an aspect, this disclosure provides a method of producing a corn plant with enhanced DM resistance, which method comprising the steps of: (a) crossing a first corn plant comprising a DM resistance QTL with a second corn plant of a different genotype to produce one or more progeny plants or seeds; (b) selecting a progeny plant or seed comprising a DM resistance allele of a polymorphic locus linked to a DM resistance QTL, wherein a polymorphic locus is in a chromosomal segment flanked by any two of marker loci SEQ ID NOs: 1 to 11, any two of marker loci SEQ ID NOs: 12 to 22, any two of marker loci SEQ ID NOs: 23 to 28, any two of marker loci SEQ ID NOs: 29 to 32, any two of marker loci SEQ ID NOs: 33 to 38, any two of marker loci SEQ ID NOs: 39 to 45, any two of marker loci SEQ ID NOs: 46 to 57, any two of marker loci SEQ ID NOs: 54 to 62, any two of marker loci SEQ ID NOs: 63 and 64, any two of marker loci SEQ ID NOs: 65 to 90, or any two of marker loci SEQ ID NOs: 91-114; (c) crossing the selected progeny plant with itself or the second corn plant to produce one or more further progeny plants or seeds; and (d) selecting a further progeny plant or seed comprising the DM resistance allele. In an aspect, the further progeny plant in step (d) is an F_2 to F_7 progeny plant. In another aspect, the further progeny plant in step (d) comprises 2 to 7 generations of backcrossing. In yet another aspect,

a method comprises using marker-assisted selection to select a DM resistance allele in at least one polymorphic locus selected from the group consisting of SEQ ID NOs: 1-114.

[00105] In an aspect, this disclosure provides a method of obtaining a corn plant or seed with enhanced DM resistance, which method comprises the steps of: (a) detecting in a population of corn plants or seeds a plant or seed comprising a DM resistance allele at a polymorphic locus in a chromosomal segment flanked by SEQ ID NOs: 1 to 11, any two of marker loci SEQ ID NOs: 12 to 22, any two of marker loci SEQ ID NOs: 23 to 28, any two of marker loci SEQ ID NOs: 29 to 32, any two of marker loci SEQ ID NOs: 33 to 38, any two of marker loci SEQ ID NOs: 39 to 45, any two of marker loci SEQ ID NOs: 46 to 57, any two of marker loci SEQ ID NOs: 54 to 62, any two of marker loci SEQ ID NOs: 63 and 64, any two of marker loci SEQ ID NOs: 65 to 90, or any two of marker loci SEQ ID NOs: 91-114; and (b) selecting the plant or seed from the population based on the presence of the DM resistance allele.

[00106] In an aspect, this disclosure provides a method of producing a corn plant with enhanced DM resistance, which method comprising the steps of: (a) crossing a first corn plant comprising a DM resistance haplotype with a second corn plant of a different genotype to produce one or more progeny plants or seeds; (b) selecting a progeny plant or seed based on the presence of the DM resistance haplotype, wherein the haplotype comprises resistance alleles of two or more polymorphic loci in a chromosomal interval flanked by: any two marker loci selected from the group consisting of SEQ ID NOs: 1 to 11; any two marker loci selected from the group consisting of SEQ ID NOs: 12 to 22; any two marker loci selected from the group consisting of SEQ ID NOs: 23 to 28; any two marker loci selected from the group consisting of SEQ ID NOs: 29 to 32; any two marker loci selected from the group consisting of SEQ ID NOs: 33 to 38; any two marker loci selected from the group consisting of SEQ ID NOs: 39 to 45; any two marker loci selected from the group consisting of SEQ ID NOs: 46 to 57; any two marker loci selected from the group consisting of SEQ ID NOs: 54 to 62; SEQ ID NO: 63 and SEQ ID NO: 64; any two marker loci selected from the group consisting of SEQ ID NOs: 65 to 90; or any two marker loci selected from the group consisting of SEQ ID NOs: 91-114.

[00107] In an aspect, this disclosure provides a method of obtaining a corn plant or seed with enhanced DM resistance, which method comprising the steps of: (a) detecting in a population of corn plants or seeds a plant or seed comprising a DM resistance haplotype, wherein the haplotype comprises resistance alleles of two or more polymorphic loci in a

chromosomal interval flanked by: any two marker loci selected from the group consisting of SEQ ID NOs: 5 to 8; SEQ ID NO: 7 and SEQ ID NO: 8; any two marker loci selected from the group consisting of SEQ ID NOs: 12 to 14; any two marker loci selected from the group consisting of SEQ ID NOs: 18 to 20; any two marker loci selected from the group consisting of SEQ ID NOs: 25 to 27; any two marker loci selected from the group consisting of SEQ ID NOs: 29 to 31; any two marker loci selected from the group consisting of SEQ ID NOs: 34 to 36; any two marker loci selected from the group consisting of SEQ ID NOs: 39 to 45; any two marker loci selected from the group consisting of SEQ ID NOs: 49 to 51; SEQ ID NO: 58 and SEQ ID NO: 59; SEQ ID NO: 63 and SEQ ID NO: 64; any two marker loci selected from the group consisting of SEQ ID NOs: 66 to 76; or any two marker loci selected from the group consisting of SEQ ID NOs: 99 to 106; and (b) selecting a plant or seed from the population based on the presence of the DM resistance haplotype. In yet another aspect, a DM resistance haplotype comprises resistance alleles of two or more polymorphic loci selected from the group consisting of SEQ ID NOs: 5-8, 12-14, 18-20, 25-27, 29-31, 34-36, 39-45, 49-51, 58, 59, 63, 64, 66-76, and 99-106.

[00108] In an aspect, this disclosure provides a method for selecting a corn plant or seed, which method comprising the steps of: (a) isolated nucleic acids from a corn plant or seed; (b) analyzing the nucleic acids to detect a polymorphic marker associated with a DM resistance QTL selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; and (c) selecting a corn plant or seed comprising the DM resistance QTL.

[00109] In an aspect, this disclosure provides a method for selecting a corn plant or seed, which method comprising the steps of: (a) detecting in a population of corn plants or seeds a corn plant or seed comprising a DM resistance allele of a marker locus associated with a DM resistance QTL selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; and (b) selecting a corn plant or seed comprising the DM resistance allele.

[00110] In an aspect, this disclosure provides a method for evaluating a collection of corn germplasm, which method comprising the steps of: (a) obtaining a collection of corn germplasm; (b) isolating nucleic acids from each germplasm; (c) assaying the nucleic acids for one or more markers linked to a DM resistance QTL selected from the group consisting of

DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01; and (d) selecting germplasm comprising a DM resistance QTL based on the marker assay.

[00111] In an aspect, a method disclosed herein comprises genotyping by a marker assay. In an aspect, a method disclosed herein comprises marker-assisted selection. In another aspect, a method disclosed herein comprises assaying a SNP marker. In yet another aspect, a method disclosed herein comprises the use of an oligonucleotide probe. In a further aspect, a method disclosed herein comprises using an oligonucleotide probe adjacent to a polymorphic nucleotide position in a marker locus being genotyped.

[00112] In an aspect, a corn plant or seed disclosed herein may be an inbred, a hybrid, a transgenic, a haploid, a doubled haploid, or in an agronomically elite background. These groups are not mutually exclusive, and a corn plant or seed could be in two or more groups (*e.g.*, a plant could be a transgenic hybrid, another plant could be an inbred doubled haploid, etc.).

[00113] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a polymorphic marker locus within about 20 cM, 15 cM, 10 cM, 5 cM, 4 cM, 3 cM, 2 cM, 1 cM, 0.5 cM or less than 0.5 cM of any one of marker loci SEQ ID NOs: 1-114. In an aspect, this disclosure provides a method comprising genotyping a polymorphic locus selected from the group consisting of SEQ ID NOs: 1-114.

[00114] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_1.01, which DM resistance QTL DM_1.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 1 to 8. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_1.01, which DM resistance QTL DM_1.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 5 to 8.

[00115] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_1.02 which DM resistance QTL DM_1.02 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 6 to 11. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with

DM resistance QTL DM_1.02 which DM resistance QTL DM_1.02 is located in a chromosomal interval flanked by marker loci SEQ ID NO: 7 and SEQ ID NO: 8.

[00116] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_2.01, which DM resistance QTL DM_2.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 12 to 22. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_2.01, which DM resistance QTL DM_2.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 18 to 20.

[00117] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_2.02, which DM resistance QTL DM_2.02 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 23 to 28. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_2.02, which DM resistance QTL DM_2.02 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 25 to 27.

[00118] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_2.03, which DM resistance QTL DM_2.03 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 12 to 14.

[00119] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_3.01, which DM resistance QTL DM_3.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 29 to 32. In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_3.01, which DM resistance QTL DM_3.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 29 to 31.

[00120] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_4.01, which DM resistance QTL DM_4.01 is located in a chromosomal interval flanked by any two of the marker loci

selected from the group consisting of SEQ ID NOs: 33 to 38. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_4.01, which DM resistance QTL DM_4.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 34 to 36.

[00121] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_5.01, which DM resistance QTL DM_5.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 39 to 45.

[00122] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_6.01, which DM resistance QTL DM_6.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 46 to 57. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_6.01, which DM resistance QTL DM_6.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 49 to 51.

[00123] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_6.02, which DM resistance QTL DM_6.02 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 54 to 62. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_6.02, which DM resistance QTL DM_6.02 is located in a chromosomal interval flanked by marker loci SEQ ID NO: 59 and SEQ ID NO: 59.

[00124] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_7.01 which DM resistance QTL DM_7.01 is located in a chromosomal interval flanked marker loci SEQ ID NO: 63 and SEQ ID NO: 64.

[00125] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_8.01, which DM resistance QTL DM_8.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 65 to 90. In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with

DM resistance QTL DM_8.01, which DM resistance QTL DM_8.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 66 to 76.

[00126] In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_9.01, which DM resistance QTL DM_9.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 91-114. In an aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus associated with DM resistance QTL DM_9.01, which DM resistance QTL DM_9.01 is located in a chromosomal interval flanked by any two of the marker loci selected from the group consisting of SEQ ID NOs: 99 to 106.

[00127] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 1 to 11. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 5 to 8. In yet another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NO: 7 and SEQ ID NO: 8.

[00128] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 12 to 22. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID Nos: 12 to 14. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 18 to 20.

[00129] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 23 to 28. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 25 to 27.

[00130] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 29 to 32. In another aspect, a method disclosed herein comprises

genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 29 to 31. In yet another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any marker loci SEQ ID NO: 30 and SEQ ID NO: 31.

[00131] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 33 to 38. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 34 to 36.

[00132] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 39 to 45.

[00133] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 46 to 57. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 49 to 51.

[00134] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 54 to 62. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NO: 58 and SEQ ID NO: 59.

[00135] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NO: 63 and SEQ ID NO: 64.

[00136] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 65 to 90. In another aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 66 to 76.

[00137] In a further aspect, a method disclosed herein comprises genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 91-114. In another aspect, a method disclosed herein comprises

genotyping a corn plant or seed at a marker locus located in a chromosomal interval flanked by any two of marker loci SEQ ID NOs: 99 to 106.

[00138] In another aspect, a method disclosed herein comprises genotyping a corn plant or seed by detecting a haplotype. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 1 to 11. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, or three or more of marker loci SEQ ID NO: 5 to 8. In an aspect, a haplotype comprises a DM resistance allele at one or more of marker loci SEQ ID NO: 7 and SEQ ID NO: 8. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 12 to 22. In an aspect, a haplotype comprises a DM resistance allele at one or more, or two or more of marker loci SEQ ID NO: 12 to 14. In an aspect, a haplotype comprises a DM resistance allele at one or more, or two or more of marker loci SEQ ID NO: 18 to 20. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 23 to 28. In an aspect, a haplotype comprises a DM resistance allele at one or more, or two or more of marker loci SEQ ID NO: 25 to 27. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, or three or more of marker loci SEQ ID NO: 29 to 32. In an aspect, a haplotype comprises a DM resistance allele at one or more, or two or more of marker loci SEQ ID NO: 29 to 31. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 33 to 38. In an aspect, a haplotype comprises a DM resistance allele at one or more, or two or more of marker loci SEQ ID NO: 34 to 36. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 39 to 45. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 46 to 57. In an aspect, a haplotype comprises a DM resistance allele at one or more, or two or more of marker loci SEQ ID NO: 49 to 51. In an aspect, a haplotype comprises a DM resistance allele at one or more of marker loci SEQ ID NO: 58 and SEQ ID NO: 59. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 54 to 62. In an aspect, a haplotype comprises a DM resistance allele at one or more of marker loci SEQ ID NO: 63 and SEQ ID NO: 64. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or

more, three or more, four or more, or five or more of marker loci SEQ ID NO: 65 to 90. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 66 to 76. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 91-114. In an aspect, a haplotype comprises a DM resistance allele at one or more, two or more, three or more, four or more, or five or more of marker loci SEQ ID NO: 99 to 106.

[00139] In an aspect, a corn plant or seed comprising DM resistance QTLs or DM resistant alleles disclosed herein exhibits intermediate resistance to DM infection from oomycetes from the group consisting of *Peronosclerospora*, *Sclerophthora*, and *Sclerospora*. In another aspect, a corn plant or seed comprising DM resistance QTLs or DM resistant alleles disclosed herein exhibits moderate resistance to DM infection from oomycetes from the group consisting of *Peronosclerospora*, *Sclerophthora*, and *Sclerospora*. In a further aspect, a corn plant or seed comprising DM resistance QTLs or DM resistant alleles disclosed herein exhibits high resistance to DM infection from oomycetes from the group consisting of *Peronosclerospora*, *Sclerophthora*, and *Sclerospora*. In an aspect, DM infection is caused by an oomycete selected from the group consisting of *Peronosclerospora eriochloae, Peronosclerospora graminicola, Peronosclerospora heteropogoni, Peronosclerospora maydis, Peronosclerospora miscanthi, Peronosclerospora philippinensis, Peronosclerospora sacchari, Peronosclerospora sorghi, Peronosclerospora spontanea, Peronosclerospora zeae, Sclerophthora macrospora, Scleropthora rayssiae var. zeae,* and *Sclerospora graminicola*. In another aspect, a corn plant or seed comprising DM resistance QTLs or DM resistant alleles disclosed herein exhibits high resistance to DM infection from *P. philippinensis*. In another aspect, a corn plant or seed comprising DM resistance QTLs or DM resistant alleles disclosed herein exhibits high resistance to DM infection from *P. maydis*. In another aspect, a corn plant or seed comprising DM resistance QTLs or DM resistant alleles disclosed herein exhibits high resistance to DM infection from *P. sorghi*.

[00140] In an aspect, a DM resistance QTL or DM resistance allele disclosed herein confers no yield penalties under a low DM stress condition. In another aspect, a combination of one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more DM resistance QTLs disclosed herein confer no yield penalties under a low DM stress condition.

[00141] In another aspect, a corn plant or seed disclosed herein comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more DM resistance QTLs or DM resistance alleles disclosed herein exhibits a reduction of DM rating score of about 0.5% or more, 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, or 80% or more compared to a corn plant or seed without the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00142] In another aspect, a corn plant or seed disclosed herein comprising one or more QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_ 2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of about 0.5% or more, 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, or 80% or more compared to a corn plant or seed without the one or more QTLs under a high DM stress condition.

[00143] In another aspect, a corn plant or seed disclosed herein comprising two or more QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of about 0.5% or more, 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, or 80% or more compared to a corn plant or seed without the two or more QTLs under a high DM stress condition.

[00144] In another aspect, a corn plant or seed disclosed herein comprising three or more QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of about 0.5% or more, 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more,

or 80% or more compared to a corn plant or seed without the three or more QTLs under a high DM stress condition.

[00145] In another aspect, a corn plant or seed disclosed herein comprising four or more QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of about 0.5% or more, 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, or 80% or more compared to a corn plant or seed without the four or more QTLs under a high DM stress condition.

[00146] In another aspect, a corn plant or seed disclosed herein comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs or DM resistance alleles disclosed herein exhibits a reduction of DM rating score of between 0.5% and 80%, between 0.5% and 70%, between 0.5% and 60%, between 0.5% and 50%, between 0.5% and 40%, between 0.5% and 30%, between 0.5% and 20%, between 0.5% and 15%, between 1% and 10%, between 0.5% and 5%, between 0.5% and 4%, between 0.5% and 3%, between 0.5% and 2%, between 0.5% and 1%, between 1% and 70%, between 2% and 60%, between 3% and 50%, between 4% and 40%, between 5% and 30%, between 10% and 20%, or between 5% and 15% compared to a corn plant or seed without the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00147] In another aspect, a corn plant or seed disclosed herein comprising one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of between 0.5% and 80%, between 0.5% and 70%, between 0.5% and 60%, between 0.5% and 50%, between 0.5% and 40%, between 0.5% and 30%, between 0.5% and 20%, between 0.5% and 15%, between 1% and 10%, between 0.5% and 5%, between 0.5% and 4%, between 0.5% and 3%, between 0.5% and 2%, between 0.5% and 1%, between 1% and 70%, between 2% and 60%, between 3% and 50%, between 4% and 40%, between 5% and 30%, between 10% and 20%, or between 5% and 15% compared to a corn plant or seed

without the one or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00148] In another aspect, a corn plant or seed disclosed herein comprising two or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of between 0.5% and 80%, between 0.5% and 70%, between 0.5% and 60%, between 0.5% and 50%, between 0.5% and 40%, between 0.5% and 30%, between 0.5% and 20%, between 0.5% and 15%, between 1% and 10%, between 0.5% and 5%, between 0.5% and 4%, between 0.5% and 3%, between 0.5% and 2%, between 0.5% and 1%, between 1% and 70%, between 2% and 60%, between 3% and 50%, between 4% and 40%, between 5% and 30%, between 10% and 20%, or between 5% and 15% compared to a corn plant or seed without the two or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00149] In another aspect, a corn plant or seed disclosed herein comprising three or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of between 0.5% and 80%, between 0.5% and 70%, between 0.5% and 60%, between 0.5% and 50%, between 0.5% and 40%, between 0.5% and 30%, between 0.5% and 20%, between 0.5% and 15%, between 1% and 10%, between 0.5% and 5%, between 0.5% and 4%, between 0.5% and 3%, between 0.5% and 2%, between 0.5% and 1%, between 1% and 70%, between 2% and 60%, between 3% and 50%, between 4% and 40%, between 5% and 30%, between 10% and 20%, or between 5% and 15% compared to a corn plant or seed without the three or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00150] In another aspect, a corn plant or seed disclosed herein comprising four or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a reduction of DM rating score of between 0.5% and 80%, between 0.5% and 70%, between 0.5% and 60%, between 0.5% and 50%, between 0.5% and 40%, between 0.5% and 30%, between 0.5% and 20%, between 0.5% and 15%, between 1% and 10%, between 0.5% and 5%, between 0.5% and

4%, between 0.5% and 3%, between 0.5% and 2%, between 0.5% and 1%, between 1% and 70%, between 2% and 60%, between 3% and 50%, between 4% and 40%, between 5% and 30%, between 10% and 20%, or between 5% and 15% compared to a corn plant or seed without the four or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00151] In an aspect, a corn plant or seed disclosed herein comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs or DM resistance alleles disclosed herein exhibits a seed yield increase of about 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 25% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, 90% or more, or 100% or more than seed yield of a corn plant or seed without the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00152] In an aspect, a corn plant or seed disclosed herein comprising one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of about 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 25% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, 90% or more, or 100% or more than seed yield of a corn plant or seed without the one or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00153] In an aspect, a corn plant or seed disclosed herein comprising two or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of about 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 25% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, 90% or more, or 100% or more than seed yield of a corn plant or seed without the two or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00154] In an aspect, a corn plant or seed disclosed herein comprising three or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of about 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 25% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, 90% or more, or 100% or more than seed yield of a corn plant or seed without the three or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00155] In an aspect, a corn plant or seed disclosed herein comprising four or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of about 1% or more, 2% or more, 3% or more, 4% or more, 5% or more, 10% or more, 15% or more, 20% or more, 25% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, 90% or more, or 100% or more than seed yield of a corn plant or seed without the four or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00156] In another aspect, a corn plant or seed disclosed herein comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs or DM resistance alleles disclosed herein exhibits a seed yield increase of between 1% and 100%, between 1% and 90%, between 1% and 80%, between 1% and 70%, between 1% and 60%, between 1% and 50%, between 1% and 40%, between 1% and 30%, between 1% and 25%, between 1% and 20%, between 1% and 15%, between 1% and 10%, between 1% and 5%, between 1% and 4%, between 1% and 3%, between 1% and 2%, between 2% and 90%, between 3% and 80%, between 4% and 70%, between 5% and 60%, between 10% and 50%, between 15% and 40%, between 20% and 30%, or between 5% and 25% of seed yield of a corn plant or seed without the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00157] In another aspect, a corn plant or seed disclosed herein comprising one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of between 1% and 25%, between 1% and 20%, between 1% and 15%, between 1% and 10%, between 1% and 5%, between 1% and 4%, between 1% and 3%, between 1% and 2%, between 2% and 90%, between 3% and 80%, between 4% and 70%, between 5% and 60%, between 10% and 50%, between 15% and 40%, between 20% and 30%, or between 5% and 25% of seed yield of a corn plant or seed without the one or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00158] In another aspect, a corn plant or seed disclosed herein comprising two or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of between 1% and 25%, between 1% and 20%, between 1% and 15%, between 1% and 10%, between 1% and 5%, between 1% and 4%, between 1% and 3%, between 1% and 2%, between 2% and 90%, between 3% and 80%, between 4% and 70%, between 5% and 60%, between 10% and 50%, between 15% and 40%, between 20% and 30%, or between 5% and 25% of seed yield of a corn plant or seed without the two or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00159] In another aspect, a corn plant or seed disclosed herein comprising three or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of between 1% and 25%, between 1% and 20%, between 1% and 15%, between 1% and 10%, between 1% and 5%, between 1% and 4%, between 1% and 3%, between 1% and 2%, between 2% and 90%, between 3% and 80%, between 4% and 70%, between 5% and 60%, between 10% and 50%, between 15% and 40%, between 20% and 30%, or between 5% and 25% of seed yield of a corn plant or seed without the three or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00160] In another aspect, a corn plant or seed disclosed herein comprising four or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01,

DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield increase of between 1% and 25%, between 1% and 20%, between 1% and 15%, between 1% and 10%, between 1% and 5%, between 1% and 4%, between 1% and 3%, between 1% and 2%, between 2% and 90%, between 3% and 80%, between 4% and 70%, between 5% and 60%, between 10% and 50%, between 15% and 40%, between 20% and 30%, or between 5% and 25% of seed yield of a corn plant or seed without the four or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00161] In an aspect, a corn plant or seed disclosed herein comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs or DM resistance alleles disclosed herein exhibits a seed yield about 0.1 quintal/hectare or more, 0.25 quintal/hectare or more, 0.5 quintal/hectare or more, 0.75 quintal/hectare or more, 1 quintal/hectare or more, 1.5 quintal/hectare or more, 2 quintal/hectare or more, 2.5 quintal/hectare or more, 3 quintal/hectare or more, 3.5 quintal/hectare or more, 4 quintal/hectare or more, 4.5 quintal/hectare or more, 5 quintal/hectare or more, 6 quintal/hectare or more, 7 quintal/hectare or more, 8 quintal/hectare or more, 9 quintal/hectare or more, or 10 quintal/hectare or more higher than seed yield of a corn plant or seed without the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00162] In an aspect, a corn plant or seed disclosed herein comprising one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield about 0.1 quintal/hectare or more, 0.25 quintal/hectare or more, 0.5 quintal/hectare or more, 0.75 quintal/hectare or more, 1 quintal/hectare or more, 1.5 quintal/hectare or more, 2 quintal/hectare or more, 2.5 quintal/hectare or more, 3 quintal/hectare or more, 3.5 quintal/hectare or more, 4 quintal/hectare or more, 4.5 quintal/hectare or more, 5 quintal/hectare or more, 6 quintal/hectare or more, 7 quintal/hectare or more, 8 quintal/hectare or more, 9 quintal/hectare or more, or 10 quintal/hectare or more higher than seed yield of a corn plant or seed without the one or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00163] In an aspect, a corn plant or seed disclosed herein comprising two or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield about 0.1 quintal/hectare or more, 0.25 quintal/hectare or more, 0.5 quintal/hectare or more, 0.75 quintal/hectare or more, 1 quintal/hectare or more, 1.5 quintal/hectare or more, 2 quintal/hectare or more, 2.5 quintal/hectare or more, 3 quintal/hectare or more, 3.5 quintal/hectare or more, 4 quintal/hectare or more, 4.5 quintal/hectare or more, 5 quintal/hectare or more, 6 quintal/hectare or more, 7 quintal/hectare or more, 8 quintal/hectare or more, 9 quintal/hectare or more, or 10 quintal/hectare or more higher than seed yield of a corn plant or seed without the two or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00164] In an aspect, a corn plant or seed disclosed herein comprising three or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield about 0.1 quintal/hectare or more, 0.25 quintal/hectare or more, 0.5 quintal/hectare or more, 0.75 quintal/hectare or more, 1 quintal/hectare or more, 1.5 quintal/hectare or more, 2 quintal/hectare or more, 2.5 quintal/hectare or more, 3 quintal/hectare or more, 3.5 quintal/hectare or more, 4 quintal/hectare or more, 4.5 quintal/hectare or more, 5 quintal/hectare or more, 6 quintal/hectare or more, 7 quintal/hectare or more, 8 quintal/hectare or more, 9 quintal/hectare or more, or 10 quintal/hectare or more higher than seed yield of a corn plant or seed without the three or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00165] In an aspect, a corn plant or seed disclosed herein comprising four or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield about 0.1 quintal/hectare or more, 0.25 quintal/hectare or more, 0.5 quintal/hectare or more, 0.75 quintal/hectare or more, 1 quintal/hectare or more, 1.5 quintal/hectare or more, 2 quintal/hectare or more, 2.5 quintal/hectare or more, 3 quintal/hectare or more, 3.5 quintal/hectare or more, 4 quintal/hectare or more, 4.5 quintal/hectare or more, 5 quintal/hectare or more, 6 quintal/hectare or more, 7 quintal/hectare or more, 8 quintal/hectare or more, 9

quintal/hectare or more, or 10 quintal/hectare or more higher than seed yield of a corn plant or seed without the four or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00166] In another aspect, a corn plant or seed disclosed herein comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs or DM resistance alleles disclosed herein exhibits a seed yield between 0.1 and 10 quintal/hectare, between 0.1 and 9 quintal/hectare, between 0.1 and 8 quintal/hectare, between 0.1 and 7 quintal/hectare, between 0.1 and 6 quintal/hectare, between 0.1 and 5 quintal/hectare, between 0.1 and 4.5 quintal/hectare, between 0.1 and 4 quintal/hectare, between 0.1 and 3.5 quintal/hectare, between 0.1 and 3 quintal/hectare, between 0.1 and 2.5 quintal/hectare, between 0.1 and 2 quintal/hectare, between 0.1 and 1.5 quintal/hectare, between 0.1 and 1 quintal/hectare, between 0.1 and 0.75 quintal/hectare, between 0.1 and 0.5 quintal/hectare, between 0.1 and 0.25 quintal/hectare, between 0.25 and 9 quintal/hectare, between 0.5 and 8 quintal/hectare, between 0.75 and 7 quintal/hectare, between 1 and 6 quintal/hectare, between 1.5 and 5 quintal/hectare, between 2 and 4.5 quintal/hectare, between 2.5 and 4 quintal/hectare, or between 3 and 3.5 quintal/hectare higher than seed yield of a corn plant or seed without the one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00167] In another aspect, a corn plant or seed disclosed herein comprising one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield between 0.1 and 5 quintal/hectare, between 0.1 and 4.5 quintal/hectare, between 0.1 and 4 quintal/hectare, between 0.1 and 3.5 quintal/hectare, between 0.1 and 3 quintal/hectare, between 0.1 and 2.5 quintal/hectare, between 0.1 and 2 quintal/hectare, between 0.1 and 1.5 quintal/hectare, between 0.1 and 1 quintal/hectare, between 0.1 and 0.75 quintal/hectare, between 0.1 and 0.5 quintal/hectare, between 0.1 and 0.25 quintal/hectare, between 0.25 and 9 quintal/hectare, between 0.5 and 8 quintal/hectare, between 0.75 and 7 quintal/hectare, between 1 and 6 quintal/hectare, between 1.5 and 5 quintal/hectare, between 2 and 4.5 quintal/hectare, between 2.5 and 4 quintal/hectare, or between 3 and 3.5 quintal/hectare higher than seed yield

of a corn plant or seed without the one or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00168] In another aspect, a corn plant or seed disclosed herein comprising two or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield between 0.1 and 5 quintal/hectare, between 0.1 and 4.5 quintal/hectare, between 0.1 and 4 quintal/hectare, between 0.1 and 3.5 quintal/hectare, between 0.1 and 3 quintal/hectare, between 0.1 and 2.5 quintal/hectare, between 0.1 and 2 quintal/hectare, between 0.1 and 1.5 quintal/hectare, between 0.1 and 1 quintal/hectare, between 0.1 and 0.75 quintal/hectare, between 0.1 and 0.5 quintal/hectare, between 0.1 and 0.25 quintal/hectare, between 0.25 and 9 quintal/hectare, between 0.5 and 8 quintal/hectare, between 0.75 and 7 quintal/hectare, between 1 and 6 quintal/hectare, between 1.5 and 5 quintal/hectare, between 2 and 4.5 quintal/hectare, between 2.5 and 4 quintal/hectare, or between 3 and 3.5 quintal/hectare higher than seed yield of a corn plant or seed without the two or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00169] In another aspect, a corn plant or seed disclosed herein comprising three or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield between 0.1 and 5 quintal/hectare, between 0.1 and 4.5 quintal/hectare, between 0.1 and 4 quintal/hectare, between 0.1 and 3.5 quintal/hectare, between 0.1 and 3 quintal/hectare, between 0.1 and 2.5 quintal/hectare, between 0.1 and 2 quintal/hectare, between 0.1 and 1.5 quintal/hectare, between 0.1 and 1 quintal/hectare, between 0.1 and 0.75 quintal/hectare, between 0.1 and 0.5 quintal/hectare, between 0.1 and 0.25 quintal/hectare, between 0.25 and 9 quintal/hectare, between 0.5 and 8 quintal/hectare, between 0.75 and 7 quintal/hectare, between 1 and 6 quintal/hectare, between 1.5 and 5 quintal/hectare, between 2 and 4.5 quintal/hectare, between 2.5 and 4 quintal/hectare, or between 3 and 3.5 quintal/hectare higher than seed yield of a corn plant or seed without the three or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00170] In another aspect, a corn plant or seed disclosed herein comprising four or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01,

DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits a seed yield between 0.1 and 5 quintal/hectare, between 0.1 and 4.5 quintal/hectare, between 0.1 and 4 quintal/hectare, between 0.1 and 3.5 quintal/hectare, between 0.1 and 3 quintal/hectare, between 0.1 and 2.5 quintal/hectare, between 0.1 and 2 quintal/hectare, between 0.1 and 1.5 quintal/hectare, between 0.1 and 1 quintal/hectare, between 0.1 and 0.75 quintal/hectare, between 0.1 and 0.5 quintal/hectare, between 0.1 and 0.25 quintal/hectare, between 0.25 and 9 quintal/hectare, between 0.5 and 8 quintal/hectare, between 0.75 and 7 quintal/hectare, between 1 and 6 quintal/hectare, between 1.5 and 5 quintal/hectare, between 2 and 4.5 quintal/hectare, between 2.5 and 4 quintal/hectare, or between 3 and 3.5 quintal/hectare higher than seed yield of a corn plant or seed without the four or more DM resistance QTLs or DM resistance alleles under a high DM stress condition.

[00171] In an aspect, this disclosure provides a DM resistant corn plant or seed comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen introgressed DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01. In an aspect, a corn plant or seed disclosed herein comprises DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, or DM_9.01 obtainable, obtained, or introgressed from any one of corn lines CV357626 and CV368354.

[00172] In an aspect, a corn plant or seed disclosed herein comprises DM resistance QTLs DM_5.01, DM_6.02, and DM_7.01. In an aspect, a corn plant or seed disclosed herein comprises DM resistance QTLs DM_5.01, DM_6.02, DM_7.01, and DM_8.01. In an aspect, a corn plant or seed disclosed herein comprises DM resistance QTLs DM_5.01, DM_6.02, and DM_8.01. In an aspect, a corn plant or seed disclosed herein comprises DM resistance QTLs DM_6.02, DM_7.01, and DM_8.01. In an aspect, a corn plant or seed disclosed herein comprises DM resistance QTLs DM_1.01, DM_2.03, and DM_6.01. In an aspect, a corn plant or seed disclosed herein comprises DM resistance QTLs DM_1.01, DM_4.01, and DM_6.01. In an aspect, a corn plant or seed disclosed herein comprises one or more QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_4.01, DM_6.01, DM_6.02, DM_8.01, and any combination thereof

[00173] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_1.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00174] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_1.02 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00175] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_2.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00176] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_2.02 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00177] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_2.03 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00178] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_3.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or

twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00179] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_4.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00180] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_5.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00181] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_6.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

[00182] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_6.02 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_7.01, DM_8.01, and DM_9.01.

[00183] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_7.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_8.01, and DM_9.01.

[00184] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_8.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, and DM_9.01.

[00185] In another aspect, a corn plant or seed disclosed herein comprises DM resistance QTL DM_9.01 and at least one or more, two or more, three or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, or twelve DM resistance QTLs from the group consisting of DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, and DM_8.01.

[00186] In an aspect, a corn plant or seed comprising one or more DM resistance QTLs disclosed herein exhibits reduced premature death compared to a corn plant or seed lacking the one or more DM resistance QTLs under a high DM stress condition. In another aspect, a corn plant or seed comprising one or more DM resistance QTLs disclosed herein exhibit reduced stunted growth, reduced leaf chlorosis, reduced number of narrow leaves, reduced number of erect leaves, reduced number of shredded leaves, reduced number of failed cobs, reduced vegetative tissue in tassels, or any combination thereof, compared to a corn plant or seed lacking the one or more DM resistance QTL under a high DM stress condition.

[00187] In an aspect, this disclosure provides a method comprising providing a set of corn seeds comprising one or more DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01, to a person desirous of planting the set of corn seeds in a field plot. In an aspect, a method comprising a field plot that exhibits DM infection in any one of the previous one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, or ten or more planting seasons.

[00188] In an aspect, this disclosure provides a method comprising growing a population of corn plants in a field plot, which method comprising planting a population of corn seeds comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen introgressed DM resistance QTLs selected from the group consisting of

DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 in the field plot. In an aspect, a method disclosed herein comprises staggered planting. In another aspect, a corn plant or seed comprising a combination of one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen introgressed DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01 exhibits increased seed yield under staggered planting conditions and a high DM stress condition compared to a corn plant or seed lacking the combination of DM resistance QTLs.

[00189] In an aspect, a method, a corn plant, or a corn seed disclosed herein is used in combination with one or more pesticides including, but not limited to, herbicides, fungicides (*e.g.* metalaxyl, fosetyl-Al, furalaxyl, Patafol, and benalaxyl), insecticides, microbiocides, nematicides, insect repellents, bactericides, and other substances used to control pests. In another aspect, a method, a corn plant, or a corn seed disclosed herein is used in combination with one or more triazoles, strobilurins, acylamino acids, pyrimidines, pyridines, arylphenyl ketones, amides, benzanilides, imidazoles, dinitrophenols, morpholines, phenylsulfamides and organophosphorus cpds, derivatives thereof and combinations thereof which may be applied as seed, foliar, drench, or drip treatments.

[00190] In an aspect, corn seeds disclosed herein are untreated. In another aspect, corn seeds disclosed herein can be subjected to various treatments. For example, the seeds can be treated to improve germination by priming the seeds or by disinfection to protect against seed borne pathogens. In another aspect, seeds can be coated with any available coating to improve, for example, plantability, seed emergence, and protection against seed borne pathogens. Seed coating can be any form of seed coating including, but not limited to, pelleting, film coating, and encrustments.

[00191] In a further aspect, the instant disclosure provides methods to enhance DM resistance by combining two or more DM resistance QTLs disclosed herein. In an aspect, the combined DM resistance QTLs have additive effects in providing DM resistance. In another aspect, the combined DM resistance QTLs have synergistic effects in providing DM resistance. In a further aspect, the combination of two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or

more, twelve or more, or thirteen DM resistance QTLs disclosed herein has no negative effects over corn physiology, resistance, yield, or performance in general. In a further aspect, the combination of two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, or thirteen DM resistance QTLs disclosed herein has no statistically significant negative effects over corn physiology, resistance, yield, or performance in general.

[00192] In an aspect, this disclosure provides corn plant cells, tissues, and organs that are not reproductive material and do not mediate the natural reproduction of the plant. In another aspect, this disclosure also provides corn plant cells, tissues, and organs that are reproductive material and mediate the natural reproduction of the plant. In another aspect, this disclosure provides corn plant cells, tissues, and organs that cannot maintain themselves via photosynthesis. In another aspect, this disclosure provides somatic corn plant cells. Somatic cells, contrary to germline cells, do not mediate plant reproduction.

[00193] The provided cells, tissues and organs may be from seed, fruit, leaf, cotyledon, hypocotyl, meristem, embryos, endosperm, root, shoot, stem, pod, flower, inflorescence, stalk, pedicel, style, stigma, receptacle, petal, sepal, pollen, anther, filament, ovary, ovule, pericarp, phloem, bud, or vascular tissue. In another aspect, this disclosure provides a corn plant chloroplast. In a further aspect, this disclosure provides epidermal cells, stomata cell, trichomes, root hairs, a storage root, or a tuber. In another aspect, this disclosure provides a corn protoplast.

[00194] Skilled artisans understand that corn plants naturally reproduce via seeds, not via asexual reproduction or vegetative propagation. In an aspect, this disclosure provides corn endosperm. In another aspect, this disclosure provides corn endosperm cells. In a further aspect, this disclosure provides a male or female sterile corn plant, which cannot reproduce without human intervention.

[00195] In a further aspect, this disclosure provides processed products made from a disclosed corn plant or seed. Such products include, but are not limited to, meal, oil, plant extract, starch, or fermentation or digestion products. In another aspect, this disclosure also provides a corn meal, which is substantially oil free and which is produced using the oilseed of any of the plants disclosed herein. In another aspect, this disclosure also provides a method of providing a corn meal by crushing oilseed of any of the plants disclosed herein.

[00196] A corn plants or seed disclosed herein can also be genetically engineered to express various phenotypes of agronomic interest. Exemplary genes implicated in this regard

include, but are not limited to, genes that confer resistance to pests or disease, genes that confer resistance or tolerance to an herbicide, genes that control male sterility, genes that affect abiotic stress resistance, and other genes and transcription factors that affect plant growth and agronomic traits such as yield, flowering, plant growth, or plant architecture.

Corn Transformation

[00197] A corn plant or seed disclosed herein can be genetically transformed. Numerous methods for plant transformation have been developed including biological and physical plant transformation protocols. *See*, for example, Mild, *et al.*, "Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology*, Glick B. R. and Thompson, J. E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 67-88. In addition, expression vectors and in vitro culture methods for plant cell or tissue transformation and regeneration of plants are available. *See*, for example, Gruber, *et al.*, "Vectors for Plant Transformation" in *Methods in Plant Molecular Biology and Biotechnology*, Glick B. R. and Thompson, J. E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 89-119.

[00198] A. *Agrobacterium*-Mediated Transformation—One method for introducing an expression vector into plants is based on the natural transformation system of *Agrobacterium*. *See, e.g.*, Horsch, *et al.*, A Simple and General Method for Transferring Genes into Plants. *Science*, 227:1229-1231 (1985). *A. tumefaciens* and *A. rhizogenes* are plant pathogenic soil bacteria which genetically transform plant cells. Descriptions of *Agrobacterium* vector systems and methods for *Agrobacterium*-mediated gene transfer are provided by, for example, U.S. Pat. No. 5,563,055, incorporated herein by reference in its entirety.

[00199] B. Direct Gene Transfer—Several methods of plant transformation, collectively referred to as direct gene transfer, have been developed as an alternative to *Agrobacterium*-mediated transformation. A generally applicable method of plant transformation is microprojectile-mediated transformation wherein DNA is carried on the surface of microprojectiles. The expression vector is introduced into plant tissues with a biolistic device that accelerates the microprojectiles to speeds of 300 to 600 m/s which is sufficient to penetrate plant cell walls and membranes.

[00200] Another method for physical delivery of DNA to plants is sonication of target cells. Alternatively, liposome and spheroplast fusion have been used to introduce expression vectors into plants. Electroporation of protoplasts and whole cells and tissues can also be used.

[00201] Following transformation of corn target tissues, expression of the above-described selectable marker genes allows for preferential selection of transformed cells, tissues, and/or plants, using regeneration and selection methods well-known in the art.

[00202] The foregoing methods for transformation would typically be used for producing a transgenic variety. The transgenic variety could then be crossed with another (non-transformed or transformed) variety, in order to produce a new transgenic variety. Alternatively, a genetic trait which has been engineered into a particular corn line using the foregoing transformation techniques could be moved into another line using traditional backcrossing techniques that are well-known in the plant breeding arts. For example, a backcrossing approach could be used to move an engineered trait from a public, non-elite variety into an elite variety, or from a variety containing a foreign gene in its genome into a variety or varieties which do not contain that gene.

[00203] A corn plant or seed disclosed herein can also be produced by one or more genome engineering techniques or subject to further genomic editing. For example, one or more DM resistance alleles can be introduced into a DM susceptible background. Exemplary genome engineering techniques include meganucleases, zinc-finger nucleases, TALENs, and CRISPR/Cas9 systems. *See, e.g.,* Gaj *et al.,* ZFN, TALEN, and CRISPR/Cas-based methods for genome engineering. *Trends in Biotechnology*, 31:397-405 (2013).

Additional Breeding

[00204] A corn plant or seed disclosed herein can also be subject to additional breeding using one or more known methods in the art, *e.g.*, pedigree breeding, recurrent selection, mass selection, and mutation breeding. Pedigree breeding starts with the crossing of two genotypes, such as a corn variety comprising a DM resistance QTL or DM resistance allele disclosed herein and another corn variety lacking such a locus. If the two original parents do not provide all the desired characteristics, other sources can be included in the breeding population. In the pedigree method, superior plants are selfed and selected in successive filial generations. In the succeeding filial generations the heterozygous condition gives way to homogeneous varieties as a result of self-fertilization and selection. Typically in the pedigree method of breeding, five or more successive filial generations of selfing and selection is practiced: F_1 to F_2; F_2 to F_3; F_3 to F_4; F_4 to F_5, etc. After a sufficient amount of inbreeding, successive filial generations will serve to increase seed of the developed variety. The developed variety may comprise homozygous alleles at about 95% or more of its loci.

[00205] In addition to being used to create a backcross conversion, backcrossing can also be used in combination with pedigree breeding. As discussed previously, backcrossing can be used to transfer one or more specifically desirable traits from one variety, the donor parent, to a developed variety called the recurrent parent, which has overall good agronomic characteristics yet lacks that desirable trait or traits. However, the same procedure can be used to move the progeny toward the genotype of the recurrent parent but at the same time retain many components of the non-recurrent parent by stopping the backcrossing at an early stage and proceeding with selfing and selection. For example, a corn variety may be crossed with another variety to produce a first generation progeny plant. The first generation progeny plant may then be backcrossed to one of its parent varieties to create a BC1 or BC2. Progenies are selfed and selected so that the newly developed variety has many of the attributes of the recurrent parent and yet several of the desired attributes of the non-recurrent parent. This approach leverages the value and strengths of the recurrent parent for use in new corn varieties.

[00206] Recurrent selection is a method used in a plant breeding program to improve a population of plants. The method entails individual plants cross pollinating with each other to form progeny. The progeny are grown and the superior progeny selected by any number of selection methods, which include individual plant, half-sib progeny, full-sib progeny and selfed progeny. The selected progeny are cross pollinated with each other to form progeny for another population. This population is planted and again superior plants are selected to cross pollinate with each other. Recurrent selection is a cyclical process and therefore can be repeated as many times as desired. The objective of recurrent selection is to improve the traits of a population. The improved population can then be used as a source of breeding material to obtain new varieties for commercial or breeding use, including the production of a synthetic line. A synthetic line is the resultant progeny formed by the intercrossing of several selected varieties.

[00207] Mass selection is another useful technique when used in conjunction with molecular marker enhanced selection. In mass selection, seeds from individuals are selected based on phenotype or genotype. These selected seeds are then bulked and used to grow the next generation. Bulk selection requires growing a population of plants in a bulk plot, allowing the plants to self-pollinate, harvesting the seed in bulk and then using a sample of the seed harvested in bulk to plant the next generation. Also, instead of self-pollination, directed pollination could be used as part of the breeding program.

[00208] Mutation breeding can also be used to introduce new traits into a corn plant or seed disclosed herein. Mutations that occur spontaneously or are artificially induced can be useful sources of variability for a plant breeder. The goal of artificial mutagenesis is to increase the rate of mutation for a desired characteristic. Mutation rates can be increased by many different means including temperature, long-term seed storage, tissue culture conditions, radiation (such as X-rays, gamma rays (*e.g.* cobalt-60 or cesium-137), neutrons (product of nuclear fission by uranium-235 in an atomic reactor), beta radiation (emitted from radioisotopes such as phosphorus-32 or carbon-14), or ultraviolet radiation (from 2500 to 2900 nm)), or chemical mutagens (such as base analogues (5-bromo-uracil), related compounds (8-ethoxy caffeine), antibiotics (streptonigrin), alkylating agents (sulfur mustards, nitrogen mustards, epoxides, ethylenamines, sulfates, sulfonates, sulfones, lactones), azide, hydroxylamine, nitrous acid, or acridines). Transposon- or T-DNA-based mutagenesis is also encompassed by the present disclosure. Once a desired trait is observed through mutagenesis the trait may then be incorporated into existing germplasm by traditional breeding techniques.

[00209] In an aspect, the instant disclosure provides a doubled haploid corn plant and seed that comprise a DM resistance QTL or DM resistance marker alleles disclosed herein. The doubled haploid (DH) approach achieves isogenic plants in a shorter time frame, and is particularly useful for generating inbred lines and quantitative genetics studies. DH plants can be produced according to methods known in the art. For example, the initial step involves the haploidization of the plant which results in the production of a population comprising haploid seed. Non-homozygous lines are crossed with an inducer parent, resulting in the production of haploid seeds. Seeds that have haploid embryos, but normal triploid endosperm, advance to the second stage. After selecting haploid seeds from the population, the selected seeds undergo chromosome doubling to produce doubled haploid seeds. A spontaneous chromosome doubling in a cell lineage will lead to normal gamete production or the production of unreduced gametes from haploid cell lineages. Application of a chemical compound, such as colchicine, can be used to increase the rate of diploidization. Colchicine binds to tubulin and prevents its polymerization into microtubules, thus arresting mitosis at metaphase, can be used to increase the rate of diploidization, *i.e.* doubling of the chromosome number. These chimeric plants are self-pollinated to produce diploid (doubled haploid) seed. This DH seed is cultivated and subsequently evaluated and used in hybrid testcross production.

[00210] In an aspect, this disclosure also provides methods for making a substantially homozygous corn plant by producing or obtaining a seed from a cross of a corn plant comprising a DM resistance allele and another corn plant and applying doubled haploid methods to the F_1 seed or F_1 plant or to any successive filial generation.

Hybrid production

[00211] In an aspect, this disclosure provides a hybrid corn plant or seed, and their production. The development of a corn hybrid in a corn plant breeding program generally involves three steps: (1) the selection of plants from various germplasm pools for initial breeding crosses; (2) the selfing of the selected plants from the breeding crosses for several generations to produce a series of inbred lines, which, although different from each other, breed true and are highly uniform; and (3) crossing the selected inbred lines with different inbred lines to produce the hybrids. During the inbreeding process in corn, the vigor of the lines decreases. Vigor is restored when two different inbred lines are crossed to produce the hybrid. An important consequence of the homozygosity and homogeneity of the inbred lines is that the hybrid between a defined pair of inbreds will always be the same. Once the inbreds that give a superior hybrid have been identified, the hybrid seed can be reproduced indefinitely as long as the homogeneity of the inbred parents is maintained.

[00212] Combining ability of a line, as well as the performance of the line, is a factor in the selection of improved corn lines that may be used as inbreds. Combining ability refers to a line's contribution as a parent when crossed with other lines to form hybrids. The hybrids formed for the purpose of selecting superior lines are designated test crosses. One way of measuring combining ability is by using breeding values. Breeding values are based on the overall mean of a number of test crosses. This mean is then adjusted to remove environmental effects and it is adjusted for known genetic relationships among the lines.

[00213] Hybrid seed production requires inactivation of pollen produced by the female parent. A pollination control system and effective transfer of pollen from one parent to the other offers improved plant breeding and an effective method for producing hybrid corn seed and plants. For example, a male sterility system can be used to produce corn hybrids.

[00214] Male sterility genes can increase the efficiency with which hybrids are made, in that they eliminate the need to physically emasculate the plant used as a female in a given cross. Where one desires to employ male-sterility systems, it may be beneficial to also utilize one or more male-fertility restorer genes. For example, where cytoplasmic male sterility (CMS) is used, hybrid crossing requires three inbred lines: (1) a cytoplasmically male-sterile

line having a CMS cytoplasm; (2) a fertile inbred with normal cytoplasm, which is isogenic with the CMS line for nuclear genes ("maintainer line"); and (3) a distinct, fertile inbred with normal cytoplasm, carrying a fertility restoring gene ("restorer" line). The CMS line is propagated by pollination with the maintainer line, with all of the progeny being male sterile, as the CMS cytoplasm is derived from the female parent. These male sterile plants can then be efficiently employed as the female parent in hybrid crosses with the restorer line, without the need for physical emasculation of the male reproductive parts of the female parent.

Marker Detection

[00215] In an aspect, the present disclosure provides markers that are in linkage disequilibrium with at least one DM resistance QTL or DM resistance allele and can be used to select for DM resistance. Exemplary markers comprise SEQ ID NOs: 1-114 with their DM resistance alleles shown in Table 7. Markers within approximately 20 cM, 15 cM, 10 cM, 5 cM, 4 cM, 3 cM, 2 cM, 1 cM, 0.5 cM or less than 0.5 cM of these exemplary markers can also be identified from the known art.

[00216] Genetic markers are distinguishable from each other (as well as from the plurality of alleles of any one particular marker) on the basis of polynucleotide length and/or sequence. In general, any differentially inherited polymorphic trait (including a nucleic acid polymorphism) that segregates among progeny is a potential genetic marker.

[00217] As a set, polymorphic markers serve as a useful tool for fingerprinting plants to inform the degree of identity of lines or varieties. These markers can form a basis for determining associations with phenotype and can be used to drive genetic gain. The implementation of marker-assisted selection is dependent on the ability to detect and analyze underlying genetic differences between individuals.

[00218] Herein, nucleic acid analysis methods include, but are not limited to, PCR-based detection methods, microarray methods, mass spectrometry-based methods, and/or nucleic acid sequencing methods. In an aspect, the detection of polymorphic sites in a sample of DNA, RNA, or cDNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis, fluorescence detection methods, or other means.

[00219] A method of achieving such amplification employs the polymerase chain reaction (PCR) using primer pairs that are capable of hybridizing to the proximal sequences

that define a polymorphism in its double-stranded form. Methods for typing DNA based on mass spectrometry have been disclosed in U.S. Patent Nos. 6,613,509 and 6,503,710, and references found therein.

[00220] Polymorphisms in DNA sequences can be detected or typed by a variety of effective methods well known in the art including, but not limited to, those disclosed in U.S. Patent Nos. 5,468,613, 5,217,863; 5,210,015; 5,876,930; 6,030,787; 6,004,744; 6,013,431; 5,595,890; 5,762,876; 5,945,283; 5,468,613; 6,090,558; 5,800,944; 5,616,464; 7,312,039; 7,238,476; 7,297,485; 7,282,355; 7,270,981; and 7,250,252 all of which are incorporated herein by reference in their entireties. However, the compositions and methods of the present disclosure can be used in conjunction with any polymorphism typing method to type polymorphisms in genomic DNA samples. These genomic DNA samples used include but are not limited to genomic DNA isolated directly from a plant, cloned genomic DNA, or amplified genomic DNA.

[00221] For instance, polymorphisms in DNA sequences can be detected by hybridization to allele-specific oligonucleotide (ASO) probes as disclosed in U.S. Patent Nos. 5,468,613 and 5,217,863. U.S. Patent No. 5,468,613 discloses allele specific oligonucleotide hybridizations where single or multiple nucleotide variations in nucleic acid sequence can be detected in nucleic acids by a process in which the sequence containing the nucleotide variation is amplified, spotted on a membrane and treated with a labeled sequence-specific oligonucleotide probe.

[00222] Target nucleic acid sequence can also be detected by probe ligation methods as disclosed in U.S. Patent No. 5,800,944 where sequence of interest is amplified and hybridized to probes followed by ligation to detect a labeled part of the probe.

[00223] Microarrays can also be used for polymorphism detection, wherein oligonucleotide probe sets are assembled in an overlapping fashion to represent a single sequence such that a difference in the target sequence at one point would result in partial probe hybridization (Borevitz *et al.*, Large-scale identification of single-feature polymorphisms in complex genomes. *Genome Research*, 13:513-523 (2003); Cui *et al.*, Detecting single-feature polymorphisms using oligonucleotide array and robustified projection pursuit. *Bioinformatics*, 21:3852-3858 (2005)). On any one microarray, it is expected there will be a plurality of target sequences, which may represent genes and/or noncoding regions wherein each target sequence is represented by a series of overlapping oligonucleotides, rather than by a single probe. This platform provides for high throughput

screening a plurality of polymorphisms. A single-feature polymorphism (SFP) is a polymorphism detected by a single probe in an oligonucleotide array, wherein a feature is a probe in the array. Typing of target sequences by microarray-based methods is disclosed in U.S. Patent Nos. 6,799,122; 6,913,879; and 6,996,476.

[00224] Target nucleic acid sequence can also be detected by probe linking methods as disclosed in U.S. Patent No. 5,616,464, employing at least one pair of probes having sequences homologous to adjacent portions of the target nucleic acid sequence and having side chains which non-covalently bind to form a stem upon base pairing of the probes to the target nucleic acid sequence. At least one of the side chains has a photoactivatable group which can form a covalent cross-link with the other side chain member of the stem.

[00225] Other methods for detecting SNPs and Indels include single base extension (SBE) methods. Examples of SBE methods include, but are not limited, to those disclosed in U.S. Patent Nos. 6,004,744; 6,013,431; 5,595,890; 5,762,876; and 5,945,283. SBE methods are based on extension of a nucleotide primer that is adjacent to a polymorphism to incorporate a detectable nucleotide residue upon extension of the primer. In an aspect, the SBE method uses four synthetic oligonucleotides. Two of the oligonucleotides serve as PCR primers and are complementary to sequence of the locus of genomic DNA which flanks a region containing the polymorphism to be assayed. Following amplification of the region of the genome containing the polymorphism, the PCR product is mixed with the third and fourth oligonucleotides (called extension primers) which are designed to hybridize to the amplified DNA adjacent to the polymorphism in the presence of DNA polymerase and two differentially labeled dideoxynucleosidetriphosphates. If the polymorphism is present on the template, one of the labeled dideoxynucleosidetriphosphates can be added to the primer in a single base chain extension. The allele present is then inferred by determining which of the two differential labels was added to the extension primer. Homozygous samples will result in only one of the two labeled bases being incorporated and thus only one of the two labels will be detected. Heterozygous samples have both alleles present, and will thus direct incorporation of both labels (into different molecules of the extension primer) and thus both labels will be detected.

[00226] In another method for detecting polymorphisms, SNPs and Indels can be detected by methods disclosed in U.S. Patent Nos. 5,210,015; 5,876,930; and 6,030,787 in which an oligonucleotide probe having a 5' fluorescent reporter dye and a 3' quencher dye covalently linked to the 5' and 3' ends of the probe. When the probe is intact, the proximity

of the reporter dye to the quencher dye results in the suppression of the reporter dye fluorescence, *e.g.* by Forster-type energy transfer. During PCR, forward and reverse primers hybridize to a specific sequence of the target DNA flanking a polymorphism while the hybridization probe hybridizes to polymorphism-containing sequence within the amplified PCR product. In the subsequent PCR cycle DNA polymerase with 5' → 3' exonuclease activity cleaves the probe and separates the reporter dye from the quencher dye resulting in increased fluorescence of the reporter.

[00227] In another aspect, the locus or loci of interest can be directly sequenced using nucleic acid sequencing technologies. Methods for nucleic acid sequencing are known in the art and include technologies provided by 454 Life Sciences (Branford, CT), Agencourt Bioscience (Beverly, MA), Applied Biosystems (Foster City, CA), LI-COR Biosciences (Lincoln, NE), NimbleGen Systems (Madison, WI), Illumina (San Diego, CA), Pac-Bio (Menlo Park, CA) and VisiGen Biotechnologies (Houston, TX). Such nucleic acid sequencing technologies comprise formats such as parallel bead arrays, sequencing by ligation, capillary electrophoresis, electronic microchips, "biochips," microarrays, parallel microchips, and single-molecule arrays, as reviewed by Service, Gene sequencing: the race for the $1000 genome. *Science*, 311:1544-46 (2006).

[00228] In an alternative aspect, *in silico* methods can be used to detect the marker loci of interest. For example, the sequence of a nucleic acid comprising the marker locus of interest can be stored in a computer. The desired marker locus sequence or its homolog can be identified using an appropriate nucleic acid search algorithm as provided by, for example, in such readily available programs as BLAST, or even simple word processors.

[00229] Any of the aforementioned marker types can be employed in the context of this disclosure to identify chromosome intervals encompassing genetic element that contribute to superior agronomic performance (*e.g.*, corn DM resistance).

[00230] The markers to be used in the methods of the present disclosure should preferably be diagnostic of origin in order for inferences to be made about subsequent populations. Experience to date suggests that SNP markers may be ideal for mapping because the likelihood that a particular SNP allele is derived from independent origins in the extant populations of a particular species is very low. As such, SNP markers appear to be useful for tracking and assisting introgression of QTL, particularly in the case of genotypes.

Association Mapping

[00231] In an aspect, the present disclosure also provides chromosome intervals, marker loci, germplasm for conducting genome-wide association mapping for DM resistance. Exemplary chromosome intervals and marker loci are provided in Tables 6 and 7. Genome-wide association mapping is conducted to find signals of association for various complex traits by surveying genetic variation in the whole genome.

[00232] Association mapping relies on chromosomal recombination opportunities over a large number of generations, in the history of a species, which allows the removal of association between a QTL and any marker not tightly linked to it, thus improving the rate of discovery of true association (Jannink and Walsh, *Quantitative Genetics, Genomics and Plant Breeding,* Kang, Ed. CAB International, pp. 59-68 (2002)).

[00233] An approach used to link phenotypic variation with genetic loci is marker-trait association (MTA) mapping, also known as linkage disequilibrium (LD) mapping. LD mapping emerged as an important gene mapping tool in the early 1990's with the advent of high-throughput genotyping technology, and has been widely used in human genetics to identify genes affecting human diseases. This approach was introduced and began to be adopted in plant gene mapping studies in early 2000's (Flint-Garcia *et al.,* Structure of linkage disequilibrium in plants. *Annual Review of Plant Biology*, 54:357-374 (2003)).

[00234] LD mapping assumes that the main cause for LD is linkage that binds loci on the same chromosome together in transmission to next generation. However, due to recombination events accumulated over many generations in a natural population, each chromosome has been shuffled deeply, so that the chromosome has been broken into many tiny regions where loci remain transmitted together, but loci from different regions tend to transmit independently as if they were from different chromosomes. Chromosomal regions where loci are bound together in transmission are commonly known as LD blocks (Reich *et al.,* Linkage disequilibrium in the human genome. *Nature*, 411:199-204 (2001)). LD mapping identifies genes of interest through genetic markers on the LD blocks where the genes are located. This is done by detecting significant associations between the markers and the traits that the genes affect with a sample of unrelated individuals or a sample of unrelated pedigrees that are genotyped on a selected set of markers covering candidate gene regions or the whole genome, and phenotyped on a set of traits of interest.

[00235] Compared with traditional linkage mapping methods that are typically based on artificial biparental segregating populations (*e.g.*, F_2, BC, DH, RIL, etc.), LD mapping

generally produces better mapping resolution, because of the smaller sizes of LD blocks. In addition, LD mapping is useful in identifying more than two functional alleles at associated markers in a germplasm. Further, LD mapping is efficient for evaluating natural populations.

Identification of QTL

[00236] In an aspect, markers, alleles, and haplotypes provided herein can be used for identifying QTLs associated with DM resistance. The statistical principles of QTL identification include penalized regression analysis, ridge regression, single marker analysis, complex pedigree analysis, Bayesian MCMC, identity-by-descent analysis, interval mapping, composite interval mapping (CIM), joint linkage mapping, and Haseman-Elston regression.

[00237] A QTL can act through a single gene mechanism or by a polygenic mechanism. In an aspect, the present disclosure provides a DM resistance QTL interval, where a DM resistance QTL (or multiple DM resistance QTLs) that segregates with an DM resistance trait is contained in the chromosomal interval. As used herein, when a QTL (or multiple QTLs) segregates with the DM resistance trait, it is referred to herein as a "DM resistance locus" (or "DM resistance loci").

[00238] In an aspect of this disclosure, the boundaries of a DM resistance QTL interval are drawn to encompass markers that will be linked to or associated with one or more DM resistance QTLs. In other words, a DM resistance QTL interval is drawn such that any marker that lies within that interval (including the terminal markers that define the boundaries of the interval) is genetically linked to or associated with the DM resistance QTL. Each interval comprises at least one DM resistance QTL, and furthermore, may indeed comprise more than one DM resistance QTL. Close proximity of multiple QTLs in the same interval may obfuscate the correlation of a particular marker with a particular QTL, as one marker may demonstrate linkage to more than one QTL. Conversely, *e.g.*, if two markers in close proximity show co-segregation with the desired phenotypic trait, it is sometimes unclear if each of those markers identifying the same QTL or two different QTLs. Regardless, knowledge of how many QTLs are in a particular interval is not necessary to make or practice the claimed subject matter.

[00239] In an aspect, the present disclosure also provides the mapping of additional SNP markers associated with or linked to one or more DM resistance QTLs disclosed herein. SNP markers are ideal for mapping because the likelihood that a particular SNP allele is derived from independent origins in the extant populations of a particular species is very low. As such, SNP markers are useful for tracking and assisting introgression of DM resistance

QTLs, particularly in the case of haplotypes. In an aspect, a SNP marker is selected for mapping a DM resistance QTL based on the marker's genetic map position. In another aspect, a SNP marker is selected for mapping a DM resistance QTL based on the marker's physical map position.

[00240] The genetic linkage of additional marker molecules can be established by a gene mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, (Lander and Botstein, Mapping Mendelian Factors Underlying Quantitative Traits Using RFLP Linkage Maps. *Genetics,* 121:185-199 (1989)), and the interval mapping, based on maximum likelihood methods described by Lander and Botstein (*supra*), and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL,* Whitehead Institute for Biomedical Research, Massachusetts, (1990). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY, the manual of which is herein incorporated by reference in its entirety).

[00241] A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an odds ratio (LOD) is then calculated as: LOD = $\log_{10}$ (MLE for the presence of a QTL/MLE given no linked QTL). The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL versus in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein, (Lander and Botstein, Mapping Mendelian Factors Underlying Quantitative Traits Using RFLP Linkage Maps. *Genetics,* 121:185-199 (1989), and further described by Arús and Moreno-González , *Plant Breeding*, Hayward, Bosemark, Romagosa (eds.) Chapman & Hall, London, pp. 314-331 (1993).

[00242] Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use of non-parametric methods (Kruglyak and Lander, A Nonparametric Approach for Mapping Quantitative Trait Loci. *Genetics,* 139:1421-1428 (1995), the entirety of which is herein incorporated by reference). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breed*, van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant

Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding,* Blackwell, Berlin, 16 (1994)). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval, and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, High Resolution of Quantitative Traits Into Multiple Loci via Interval Mapping. *Genetics,* 136:1447-1455 (1994) and Zeng, Precision Mapping of Quantitative Trait Loci. *Genetics,* 136:1457-1468 (1994). Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding,* van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994)), thereby improving the precision and efficiency of QTL mapping (Zeng, Precision Mapping of Quantitative Trait Loci. *Genetics,* 136:1457-1468 (1994)). These models can be extended to multi-environment experiments to analyze genotype-environment interactions (Jansen *et al.,* Genotype-by-environment interaction in genetic mapping of multiple quantitative trait loci. *Theoretical and Applied Genetics*, 91:33-37 (1995)).

[00243] In an aspect, this disclosure provides chromosomal intervals comprising QTL associated with DM resistance. In an aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 5 to 8. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by marker loci SEQ ID NOs: 7 and 8. In another aspect, the chromosome intervals of this disclosure are characterized by genome regions including and flanked by any two of marker loci SEQ ID NOs: 12 to 14. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 18 to 20. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 25 to 27. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 29 to 31. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 34 to 36. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 39 to 45. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID

NOs: 49 to 51. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by marker loci SEQ ID NOs: 58 and 59. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by marker loci SEQ ID NOs: 63 and 64. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 77 to 80. In another aspect, the chromosome intervals of this disclosure are characterized by genomic regions including and flanked by any two of marker loci SEQ ID NOs: 99 to 106.

[00244] This disclosure also provides multiple markers linked to or associated with a DM resistance QTL, for example, the markers having the sequence selected from SEQ ID NOs: 1-114. This disclosure therefore provides plants comprising a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1-114, fragments thereof, or complements thereof. The present disclosure further provides a plant comprising alleles of the chromosome interval linked to or associated with DM resistance or fragments and complements thereof as well as any plant comprising any combination of one or more DM resistance alleles of marker loci selected from the group consisting of SEQ ID NOs: 1-114. Plants provided by this disclosure may be homozygous or heterozygous for such alleles.

[00245] The compositions and methods of the present disclosure can be utilized to guide MAS or breeding corn varieties with a desired complement (set) of allelic forms of chromosome intervals associated with superior agronomic performance (*e.g.* DM resistance). Any of the disclosed marker alleles can be introduced into a corn line via introgression, by traditional breeding (or introduced via transformation, or both) to yield a corn plant with superior agronomic performance. The number of alleles associated with DM resistance that can be introduced or be present in a corn plant of the present disclosure ranges from 1 to the number of alleles disclosed herein, each integer of which is incorporated herein as if explicitly recited.

[00246] MAS using additional markers flanking either side of the DNA locus provide further efficiency because an unlikely double recombination event would be needed to simultaneously break linkage between the locus and both markers. Moreover, using markers tightly flanking a locus, one skilled in the art of MAS can reduce linkage drag by more accurately selecting individuals that have less of the potentially deleterious donor parent DNA. Any marker linked to or among the chromosome intervals described herein can thus find use within the scope of this disclosure.

[00247] These marker loci can be introgressed into any desired genomic background, germplasm, plant, line, variety, etc., as part of an overall MAS breeding program designed to enhance DM resistance. This disclosure also provides QTL intervals that can be used in MAS to select plants that demonstrate DM resistance. Similarly, QTL intervals can also be used to counter-select plants that are lacking DM resistance. By identifying plants lacking a desired marker locus, plants lacking DM resistance can be identified and selected or eliminated from subsequent crosses.

[00248] The present disclosure also extends to a method of making a progeny corn plant and the resulting progeny corn plants. In an aspect, the method comprises crossing a first parent corn plant with a second corn plant and growing the corn plant parent under plant growth conditions to yield corn plant progeny. Methods of crossing and growing a corn plant are well within the ability of those of ordinary skill in the art. Such corn plant progeny can be assayed for alleles associated with DM resistance as disclosed herein and, thereby, the desired progeny selected. Such progeny plants or seed thereof can be sold commercially for corn production, used for food, processed to obtain a desired constituent of the corn, or further utilized in subsequent rounds of breeding. At least one of the first or second corn plants may be a corn plant of the present disclosure in that it comprises at least one of the allelic forms of the markers of the present disclosure, such that the progeny are capable of inheriting the allele.

[00249] By providing the positions in the corn genome of QTL intervals and the associated markers within those intervals, this disclosure also allows one skilled in the art to identify and use other markers within the intervals disclosed herein or linked to or associated with the intervals disclosed herein. Having identified such markers, these intervals can be readily identified from public linkage maps.

[00250] Closely linked markers flanking the locus of interest that have alleles in linkage disequilibrium (LD) with a DM resistance allele at that locus may be effectively used to select for progeny plants with DM resistance. Thus, the markers described herein, such as those listed in Table 7, as well as other markers genetically linked to or associated with the same chromosome interval, may be used to select for a corn plant or seed with DM resistance. Often, a set of these markers will be used, (*e.g.*, 2 or more, 3 or more, 4 or more, 5 or more) in the flanking regions of the locus. Optionally, as described above, a marker flanking or within the actual locus may also be used. The parents and their progeny may be screened for these sets of markers, and the markers that are polymorphic between the two

parents used for selection. In an introgression program, this allows for selection of the gene or locus genotype at the more proximal polymorphic markers and selection for the recurrent parent genotype at the more distal polymorphic markers.

[00251] The choice of markers actually used to practice this disclosure is not limited and can be any marker that is genetically linked to or associated with the QTL intervals as described in Table 6, including markers within approximately 20 cM, 15 cM, 10 cM, 5 cM, 4 cM, 3 cM, 2 cM, 1 cM, 0.5 cM or less than 0.5 cM of the intervals provided herein. Examples include, but are not limited to, any marker selected from SEQ ID NOs: 1-114. Furthermore, since there are many different types of marker detection assays known in the art, it is not intended that the type of marker detection assay used to practice this disclosure be limited in any way.

Marker Assisted Selection (MAS) Breeding

[00252] Marker loci and their DM resistance alleles provided herein can be used in MAS breeding of DM resistance. The more tightly linked a marker is with a DNA locus influencing a phenotype (*e.g.*, DM resistance), the more reliable the marker is in MAS, as the likelihood of a recombination event unlinking the marker and the locus decreases. Markers containing the causal mutation for a trait, or that are within the coding sequence of a causative gene, are ideal as no recombination is expected between them and the sequence of DNA responsible for the phenotype. However, markers do not need to contain or correspond to causal mutations in order to be effective in MAS. In fact, most MAS breeding only uses markers linked to or associated with a causal mutation.

[00253] Developing molecular markers in crop species can increase efficiency in plant breeding through MAS. Genetic markers are used to identify plants that contain a desired genotype at one or more loci, and that are expected to transfer the desired genotype, along with a desired phenotype to their progeny. Genetic markers can be used to identify plants containing a desired genotype at one locus, or at several unlinked or linked loci (*e.g.*, a haplotype), and that would be expected to transfer the desired genotype, along with a desired phenotype to their progeny. The present disclosure provides the means to identify plants that exhibit DM resistance by identifying chromosomal intervals and genetic markers associated with drought tolerance.

[00254] In general, MAS uses polymorphic markers that have been identified as having a significant likelihood of co-segregation with a desired trait. Such markers are

presumed to map near a gene or genes that give the plant its desired phenotype, and are considered indicators for the desired trait.

[00255] Identification of plants or germplasm that include a marker locus or marker loci linked to a desired trait or traits provides a basis for performing MAS. Plants that comprise favorable markers or favorable alleles are selected for, while plants that comprise markers or alleles that are negatively correlated with the desired trait can be selected against. Desired markers and/or alleles can be introgressed into plants having a desired (*e.g.*, elite or exotic) genetic background to produce an introgressed plant or germplasm having the desired trait. In an aspect, it is contemplated that a plurality of markers for desired traits are sequentially or simultaneous selected and/or introgressed. The combinations of markers that are selected for in a single plant is not limited, and can include any combination of markers disclosed herein or any marker linked to the markers disclosed herein, or any markers located within the QTL intervals defined herein.

[00256] In an aspect, a first corn plant or germplasm exhibiting a desired trait (the donor, *e.g.*, a DM resistant corn) can be crossed with a second corn plant or germplasm (the recipient, *e.g.*, an elite or exotic corn, depending on characteristics that are desired in the progeny) to create an introgressed corn plant or germplasm as part of a breeding program. In an aspect, the recipient plant can also contain one or more loci associated with one or more desired traits, which can be qualitative or quantitative trait loci. In another aspect, the recipient plant can contain a transgene.

[00257] In an aspect, the recipient corn plant or germplasm will typically lack desired traits as compared to the first corn plant or germplasm, while the introgressed corn plant or germplasm will display improved traits as compared to the second plant or germplasm. An introgressed corn plant or germplasm produced by these methods are also a feature of this disclosure.

[00258] MAS is a powerful shortcut to select for desired phenotypes and for introgressing desired traits into cultivars (*e.g.*, introgressing desired traits into elite lines). MAS is easily adapted to high throughput molecular analysis methods that can quickly screen large numbers of plant or germplasm genetic material for the markers of interest and is much more cost effective than cultivating and observing plants for visible traits.

Introgression of DM resistance QTLs Using MAS

[00259] The instant disclosure provides methods and markers for introgressing a DM resistance QTL disclosed herein into a new corn variety using MAS.

[00260] Multiple methods are available to achieve the introgression. For example, introgression of a desired allele at a specified locus can be transmitted to at least one progeny via a cross between two parents of the same species, where at least one of the parents has the desired allele in its genome. Alternatively, for example, transmission of an allele 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 can be, *e.g.*, a selected allele of a marker, a QTL, a transgene, or the like. In any case, offspring comprising the desired allele can be repeatedly backcrossed to a line having a desired genetic background and selected for the desired allele, to result in the allele becoming fixed in a selected genetic background.

[00261] The introgression of one or more desired loci from a donor line into another line is achieved via repeated backcrossing to a recurrent parent accompanied by selection to retain one or more loci from the donor parent. Markers associated with drought tolerance are assayed in progeny and those progeny with one or more desired markers are selected for advancement. In another aspect, one or more markers can be assayed in the progeny to select for plants with the genotype of the agronomically elite parent.

[00262] It is generally anticipated that trait introgression activities will require more than one generation, wherein progeny are crossed to the recurrent (agronomically elite) parent or selfed. Selections are made based on the presence of one or more markers linked to drought tolerance and can also be made based on the recurrent parent genotype, wherein screening is performed on a genetic marker and/or phenotype basis. In another aspect, markers of this disclosure can be used in conjunction with other markers, ideally at least one on each chromosome of the corn genome, to track the introgression of drought tolerance into elite germplasm. In another aspect, QTL intervals associated with drought tolerance will be useful in conjunction with SNP molecular markers of the present disclosure to combine quantitative and qualitative drought tolerance in the same plant. It is within the scope of this disclosure to utilize the methods and compositions for trait integration of drought tolerance. It is contemplated by the inventors that the present disclosure will be useful for developing commercial varieties with drought tolerance and other agronomically elite phenotypes.

EXAMPLES

Example 1. Identification of QTLs associated with downy mildew resistance in biparental mapping populations.

[00263] Biparental mapping populations are constructed to investigate the genetic basis of downy mildew (DM) resistance in corn. Plant phenotyping is performed in field plots. Plants infected with *Peronosclerospora philippinensis, Peronosclerospora maydis,* or *Peronosclerospora sorghi* are planted as a point source of inoculums in the field 20 days prior to planting experimental plants. Downy mildew (DM) disease resistance is measured by counting the percentage of infected experimental plants per plot at 40 days after planting (Table 1).

Table 1. Description of DM rating scale.

<5%	Highly Resistant
5 - 15%	Moderately Resistant
15 – 35%	Intermediate
35 – 45%	Moderately Susceptible
>45%	Highly Susceptible

[00264] Six mapping populations are shown in Table 2. These populations include two DM resistant parent lines, CV357626 and CV368354, which are used as male and female parents, respectively. Each mapping population is measured for DM resistance in two field replicates and the basic statistics are shown in Table 3. A standard statistical model is used to estimate the variance components and to compute the heritability (H^2) for DM phenotype. The heritability (H^2) is 0.68-0.84 for all mapping populations (Table 4) indicating that the observed DM phenotype is attributed to genetic variation.

[00265] Plants from all mapping populations are genotyped using SNP markers that collectively span each chromosome in the maize genome. Marker-trait association studies are performed to identify DM resistance QTLs and their associated markers using both single-marker analysis (SMA) and composite interval mapping (CIM).

Table 2. Mapping populations.

Mapping Population	Cross	DM Resistant Parent	DM Susceptible Parent	Population Type	Population Size
A	CV374702/CV357626	CV357626	CV374702	F_3	182
B	CV374480/CV357626	CV357626	CV374480	F_3	420
C	CV371812/CV357626	CV357626	CV371812	F_3	350
D	CV368354/CV371792	CV368354	CV371792	F_3	530
E	CV368354/CV364290	CV368354	CV364290	F_3	721
F	CV368354/CV364209	CV368354	CV364209	F_3	455

Table 3. Basic statistics for each mapping population

Mapping Population	Replicate ID	Mean DM score (%)	Number of Lines	Standard Deviation
A	combined	78.7	422	25.9
	1	77.5	212	26.4
	2	79.9	210	25.3
B	combined	17.1	868	14.1
	1	15.3	434	13.5
	2	18.9	434	14.5
C	combined	29.6	728	18.5
	1	30.3	364	18.4
	2	29	364	18.7
D	Combined	46.3	1173	22.7
	1	46.5	592	22.7
	2	46.1	581	22.7
E	Combined	33	1614	22.4
	1	33.3	809	22.5
	2	32.6	805	22.3
F	Combined	43.7	1054	23.3
	1	44	536	22.8
	2	43.3	518	23.9

Table 4. Variance component estimation and heritability analysis.

Mapping Population	Genetic variance	Residue variance	Total phenotypic variance	H^2
A	269.9	56.3	326.2	0.83
B	87.8	41.6	129.3	0.68
C	205.9	64.3	270.2	0.76
D	311.38	77.44	388.82	0.8
E	272.84	65.23	338.07	0.81
F	339.56	62.96	402.52	0.84

Example 2. Identification of DM resistance QTLs via composite interval mapping.

[00266] A composite interval mapping (CIM) approach is taken to identify DM resistance QTL intervals based on the phenotyping and genotyping data collected in Example 1. For each marker, the thresholds of likelihood ratio between full and null models for CIM are based on 1000 random permutation tests (Churchill and Doerg, *Genetics*, 138(3):963-71 (1994)). The composite interval mapping (CIM) analysis revealed several strong QTLs associated with DM resistance. The QTLs are confirmed in multiple genetic backgrounds and summarized in Table 5.

[00267] In Table 5, genetic positions are represented in cM with position zero being the first (most distal) marker known at the beginning of the chromosome on Monsanto's internal consensus genetic map. Each row of Table 5 provides mapping population ID, number of SNP markers genotyped (#Mk), resistant parent, chromosome position, the peak of the likelihood ratio corresponding to DM resistance, left and right flanking positions, p-value, additive effect, and the phenotypic variance (R^2) of individual QTL or Total QTLs.

Table 5. CIM results from all mapping populations. *p-value is based on 1,000 permutation tests

Mapping population	#Mk	Resistant Parent	Chr	QTL Positions (cM)			p-value	Additive	QTL R^2	Total R^2
				Peak	Left Flank	Right Flank				
A	132	CV357626	6	96.5	87.2	102.5	0.05	7.6	0.1	0.55
A	132	CV357626	3	90.5	81.2	100.5	0.01	12.8	0.27	0.58
B	156	CV357626	1	74	63	79.1	0.01	3.4	0.061	0.33
B	156	CV357626	2	43.6	38.6	52.2	0.01	3	0.048	0.363
C	143	CV357626	1	60.1	51.1	68.1	0.01	7.1	0.114	0.625
C	143	CV357626	2	36.6	24.4	39.6	0.01	4.7	0.052	0.602
C	143	CV357626	4	160.1	152.3	170.8	0.01	9.7	0.17	0.6
C	143	CV357626	6	91.2	81.3	103.2	0.01	6.4	0.095	0.613
D	186	CV368354	2	48.8	35.2	57.3	0.01	9.9	0.15	0.24
D	186	CV368354	2	209.3	195.7	212	0.01	6.7	0.07	0.21
D	186	CV368354	5	138.5	125.4	142.2	0.05	4.3	0.05	0.21
D	186	CV368354	8	98.4	68.1	108.4	0.01	8.7	0.12	0.31
D	186	CV368354	9	75.7	65.7	80.2	0.01	6.8	0.06	0.25
E	186	CV368354	2	207.7	195.7	211.7	0.01	8.3	0.12	0.55
E	186	CV368354	2	50.8	39.2	57.3	0.01	5.9	0.05	0.53
E	186	CV368354	8	84.1	75.3	102.4	0.01	8.1	0.11	0.52
E	186	CV368354	9	87.7	77.2	97.5	0.01	8.2	0.11	0.53
F	149	CV368354	2	63.3	53.3	72.3	0.05	7.5	0.08	0.56
F	149	CV368354	6	58.1	39.3	59.1	0.01	11.1	0.14	0.5
F	149	CV368354	8	102.6	92.6	112.6	0.01	8.8	0.11	0.53
F	149	CV368354	9	75.9	70.9	80.9	0.1	5	0.07	0.57

Example 3. Fine-mapping downy mildew resistance QTLs via joint linkage mapping.

[00268] As shown in Examples 1 and 2, QTLs associated with DM resistance are identified from three bi-parental mapping populations (A, B, and C) by crossing one resistant line (CV357626) with three different susceptible lines. These three mapping populations are merged for joint linkage mapping. Additional QTLs associated with DM resistance are identified from three bi-parental mapping populations (D, E, and F) by crossing one resistant line (CV368354) with three different susceptible lines. These three mapping populations are also merged for joint linkage mapping. The most informative markers are selected with bootstrapping probabilities from 3000 bootstrapping samples. Thirteen QTLs are identified through the joint linkage fine mapping. These thirteen QTLs are designated as DM_1.01, DM_1.02, DM_2.03, DM_3.01, DM_4.01, DM_6.01, DM_2.01, DM_2.02, DM_5.01, DM_6.02, DM_7.01, DM_8.01 and DM_9.01 (Table 7).

Table 6. Fine-mapping of DM resistance QTL by JLM.

Chr	JLM interval CV357626 (cM)	Left Flank Marker	Right Flank Marker	IBM2008 Map (IcM)	QTL Designation
1	54-69	SEQ ID NO: 5	SEQ ID NO: 8	158.5-196	DM_1.01
1	68.4-73.2	SEQ ID NO: 7	SEQ ID NO: 8	194.6-206.8	DM_1.02
2	21.4-33.6	SEQ ID NO: 12	SEQ ID NO: 14	49.7-88.2	DM_2.03
3	80.2-92.6	SEQ ID NO: 29	SEQ ID NO: 31	208.6-318.2	DM_3.01
4	152.7-162.3	SEQ ID NO: 34	SEQ ID NO: 36	525.8-572.3	DM_4.01
6	85.1-90.7	SEQ ID NO: 58	SEQ ID NO: 59	374.1-389.9	DM_6.01
Chr	**JLM interval CV368354 (cM)**	**Left Flank Marker**	**Right Flank Marker**	**IBM2008 Map (IcM)**	**QTL Designation**
2	46.8-57	SEQ ID NO: 18	SEQ ID NO: 20	138.6-169.1	DM_2.01
2	200.8-212	SEQ ID NO: 25	SEQ ID NO: 27	655.6-709.5	DM_2.02
5	125.4-142.2	SEQ ID NO: 39	SEQ ID NO: 45	432.3-491.7	DM_5.01
6	39.7-52.7	SEQ ID NO: 49	SEQ ID NO: 51	204.2-239.6	DM_6.02
7	66.4-78.5	SEQ ID NO: 63	SEQ ID NO: 64	209.6-284.6	DM_7.01
8	82.6-89.4	SEQ ID NO: 77	SEQ ID NO: 80	288.3-313.8	DM_8.01
9	67.9-80.7	SEQ ID NO: 99	SEQ ID NO: 106	226.5-308.9	DM_9.01

Example 4. Identification of molecular markers associated with DM resistance via single-marker analysis (SMA)

[00269] Single-marker analysis (SMA) is performed to identify markers associated with DM resistance using the genotypic data from Example 1. For each marker, the thresholds (p-value) for SMA are based on 10,000 random permutation tests (Churchill and Doerg, *Genetics*, 138(3):963-71 (1994)).

[00270] In total, 114 SNP markers are identified to be linked to DM resistance (Table 7). Table 7 also provides the effect estimates on DM rating score for each marker linked to DM resistance. Further provided are the SEQ ID NO of the marker, chromosome position, marker position on Monsanto's internal consensus genetic map, corresponding marker position on the Neighbors 2008 maize genetic map (publicly available at Maize GDB website), genetic source of favorable allele, resistant allele SNP, susceptible allele SNP, the estimated effect that the marker polymorphism had on the DM rating score, and p-value based on 10,000 random permutation tests. For example, SEQ ID NO: 1 is associated with a 4.28% reduction in DM rating score by one copy of the resistant allele. However, one of skill in the art recognizes that a "resistant" allele at one locus may be a "susceptible" allele in a different genetic background. Thus, this disclosure is not limited to the "resistant" and "susceptible" alleles exemplified herein.

[00271] The primer sequences for amplifying exemplary SNP marker loci linked to the DM and the probes used to genotype the corresponding SNP sequences are provided in Table 8. In an illustrative example, SNP marker SEQ ID NO: 1 can be amplified using the primers described in Table 5 as SEQ ID NO: 115 (forward primer) and SEQ ID NO: 229 (reverse primer), and detected with probes indicated as SEQ ID NO: 343 (Probe 1) and SEQ ID NO: 457 (Probe 2).

[00272] One of skill in the art recognizes that sequences to either side of the given primers can be used in place of the given primers, so long as the primers can amplify a region that includes the allele to be detected. The precise probe used for detection can vary, *e.g.*, any probe that can identify the region of a marker amplicon to be detected can be substituted for those probes exemplified herein. Configuration of the amplification primers and detection probes can also be varied. Thus, this disclosure is not limited to the primers, probes, or marker sequences specifically listed in the tables.

Table 7. Estimate effects of markers linked to DM resistance from all mapping populations by SMA.

SEQ ID NO.	Chromosome	MON Map (cM)	IBM2008 Map (IcM)	Genetic Source of Favorable Allele	Exemplary Resistant Allele	Exemplary Susceptible Allele	Single Allele Effect	Permutation Testing Probability
1	1	42.8	124.7	CV357626	A	G	4.28	0.001
2	1	46.7	137	CV357626	G	A	3.04	0.001
3	1	47.5	139.8	CV357626	C	T	4.95	0.001
4	1	50.1	146.9	CV357626	C	G	5.58	0.001
5	1	54	158.5	CV357626	G	A	3.29	0.001
6	1	64.1	184.3	CV357626	G	A	3.74	0.001
7	1	68.4	194.6	CV357626	A	G	7.63	0.001
8	1	69	196	CV357626	T	C	3.41	0.001
9	1	79.3	223.2	CV357626	T	C	2.76	0.001
10	1	82.7	242.2	CV357626	A	G	7.98	0.001
11	1	88.2	270.6	CV357626	C	T	2.80	0.001
12	2	21.4	49.7	CV357626	T	A	3.38	0.001
13	2	32.2	82.8	CV368354	G	A	5.70	0.001
14	2	33.6	88	CV357626	G	A	4.21	0.001
15	2	40.6	111.8	CV368354	A	G	5.18	0.001
16	2	43	122.1	CV368354	A	G	5.95	0.001
17	2	44.2	127.2	CV368354	A	T	4.21	0.001
18	2	46.8	138.6	CV368354	G	A	7.15	0.001
19	2	52.3	156.9	CV368354	A	C	6.26	0.001
20	2	57	169.1	CV368354	A	G	6.23	0.001
21	2	58.3	172.6	CV368354	G	T	6.23	0.001
22	2	60.6	179.5	CV368354	T	A	8.43	0.001
23	2	184.4	598.4	CV368354	C	A	5.58	0.001
24	2	195.7	639	CV368354	C	A	6.24	0.001
25	2	200.8	655.6	CV368354	T	G	5.11	0.001
26	2	202.3	659.5	CV368354	T	C	5.11	0.001
27	2	212	709.5	CV368354	A	G	5.51	0.001
28	2	212.1	709.6	CV368354	G	A	6.80	0.001
29	3	80.2	208.6	CV357626	A	G	13.13	0.001

SEQ ID NO.	Chromosome	MON Map (cM)	IBM2008 Map (IcM)	Genetic Source of Favorable Allele	Exemplary Resistant Allele	Exemplary Susceptible Allele	Single Allele Effect	Permutation Testing Probability
30	3	86.5	276.6	CV357626	G	C	12.67	0.001
31	3	92.6	318.2	CV357626	A	G	12.94	0.001
32	3	110.9	382.6	CV357626	G	A	12.33	0.001
33	4	145.3	467.1	CV357626	C	A	6.30	0.001
34	4	153.2	527	CV357626	C	T	6.61	0.001
35	4	157.1	550.2	CV357626	A	G	7.86	0.001
36	4	162.3	572.3	CV357626	G	T	8.19	0.001
37	4	165.8	579.6	CV357626	T	A	8.50	0.001
38	4	176.7	615.8	CV357626	G	A	5.05	0.001
39	5	125.4	432.3	CV368354	C	T	2.10	0.049
40	5	126.5	437.9	CV368354	T	A	2.17	0.044
41	5	131.3	460.4	CV368354	T	A	3.36	0.007
42	5	131.9	462.5	CV368354	T	C	3.62	0.003
43	5	132.1	463.2	CV368354	C	T	4.11	0.001
44	5	132.8	465.5	CV368354	C	T	3.97	0.002
45	5	133.1	466.6	CV368354	A	G	4.05	0.001
46	6	25.2	147.9	CV368354	T	C	5.71	0.001
47	6	34	187.7	CV368354	A	G	8.03	0.001
48	6	38.6	201.1	CV368354	G	A	8.95	0.001
49	6	39.7	204.2	CV368354	G	A	10.40	0.001
50	6	39.8	204.5	CV368354	A	G	10.12	0.001
51	6	52.7	239.7	CV368354	T	C	9.27	0.001
52	6	53.9	242.7	CV368354	G	A	9.25	0.001
53	6	54.1	243.2	CV368354	C	A	9.32	0.001
54	6	59.4	267.1	CV368354	A	G	10.04	0.001
55	6	70	324.7	CV368354	G	A	8.82	0.001
56	6	74.3	341.9	CV357626	G	A	5.02	0.001
57	6	74.7	343.2	CV368354	G	A	6.83	0.001
58	6	85.1	374.2	CV357626	C	A	7.45	0.001
59	6	87.2	380.8	CV357626	C	G	5.21	0.001
60	6	97.8	417.4	CV357626	C	T	8.06	0.001
61	6	103.8	434.3	CV357626	T	A	7.03	0.001
62	6	108.2	444.8	CV357626	C	T	7.73	0.001

SEQ ID NO.	Chromosome	MON Map (cM)	IBM2008 Map (IcM)	Genetic Source of Favorable Allele	Exemplary Resistant Allele	Exemplary Susceptible Allele	Single Allele Effect	Permutation Testing Probability
63	7	67.5	231.7	CV368354	C	T	7.14	0.001
64	7	75.4	264.8	CV368354	A	G	7.14	0.001
65	8	64.8	193.7	CV368354	G	A	6.37	0.001
66	8	67.1	204	CV368354	C	A	7.41	0.001
67	8	67.7	205.2	CV368354	G	A	6.13	0.001
68	8	71.7	216.2	CV368354	C	T	6.78	0.001
69	8	71.7	216.2	CV368354	A	T	7.11	0.001
70	8	71.9	216.7	CV368354	T	A	7.01	0.001
71	8	71.9	216.7	CV368354	A	G	7.25	0.001
72	8	74.2	231.1	CV368354	G	A	7.43	0.001
73	8	74.8	236.2	CV368354	G	A	7.62	0.001
74	8	75.3	240.4	CV368354	A	T	7.81	0.001
75	8	75.3	240.4	CV368354	T	G	7.30	0.001
76	8	75.9	251.6	CV368354	C	G	7.30	0.001
77	8	82.6	288.3	CV368354	A	G	8.07	0.001
78	8	84.1	291.7	CV368354	C	G	8.34	0.001
79	8	84.5	293.6	CV368354	C	G	7.67	0.001
80	8	89.4	313.8	CV368354	A	G	8.16	0.001
81	8	101.1	354.7	CV368354	G	T	9.20	0.001
82	8	102.6	362.2	CV368354	G	A	10.00	0.001
83	8	103.1	363.9	CV368354	G	A	8.02	0.001
84	8	103.1	363.9	CV368354	A	G	8.55	0.001
85	8	103.1	363.9	CV368354	G	A	8.12	0.001
86	8	104	374.5	CV368354	G	T	7.65	0.001
87	8	104.8	374.5	CV368354	A	G	9.80	0.001
88	8	106.4	380.7	CV368354	T	G	8.54	0.001
89	8	112.1	394.3	CV368354	G	A	8.07	0.001
90	8	113.1	396.8	CV368354	T	C	6.84	0.001
91	9	56.8	158.5	CV368354	C	T	6.11	0.001
92	9	61.4	188.5	CV368354	G	A	5.06	0.001
93	9	61.5	189.3	CV368354	G	C	5.13	0.001
94	9	66.2	212.3	CV368354	G	A	5.78	0.001
95	9	67.2	245.5	CV368354	G	C	6.73	0.001

SEQ ID NO.	Chromosome	MON Map (cM)	IBM2008 Map (IcM)	Genetic Source of Favorable Allele	Exemplary Resistant Allele	Exemplary Susceptible Allele	Single Allele Effect	Permutation Testing Probability
96	9	67.8	226.4	CV368354	G	A	7.15	0.001
97	9	67.8	226.4	CV368354	G	A	7.00	0.001
98	9	67.8	226.4	CV368354	C	A	7.00	0.001
99	9	67.9	226.5	CV368354	G	A	6.98	0.001
100	9	67.9	245.5	CV368354	A	C	6.58	0.001
101	9	67.9	226.5	CV368354	A	G	6.87	0.001
102	9	68.2	245.5	CV368354	A	G	7.16	0.001
103	9	68.4	227	CV368354	G	A	7.16	0.001
104	9	74.7	263.6	CV368354	C	T	7.40	0.001
105	9	77.2	283.6	CV368354	A	T	7.54	0.001
106	9	80.7	304.9	CV368354	T	G	6.35	0.001
107	9	82.6	314.5	CV368354	G	T	8.69	0.001
108	9	87.4	321.6	CV368354	C	A	7.66	0.001
109	9	87.7	321.8	CV368354	A	C	9.25	0.001
110	9	88.5	338.7	CV368354	C	T	8.83	0.001
111	9	88.6	339.2	CV368354	A	G	8.69	0.001
112	9	88.6	339.2	CV368354	G	A	8.79	0.001
113	9	89.3	349.3	CV368354	C	T	8.36	0.001
114	9	96.5	392.9	CV368354	A	G	6.60	0.001

Table 8. Exemplary primers and probes used for genotyping representative SNP markers associated with DM resistance

		SEQ ID NO.			
SEQ ID NO.	**SNP Position**	**Forward Primer**	**Reverse Primer**	**Probe 1**	**Probe 2**
1	483	115	229	343	457
2	146	116	230	344	458
3	137	117	231	345	459
4	73	118	232	346	460
5	82	119	233	347	461
6	174	120	234	348	462
7	328	121	235	349	463
8	29	122	236	350	464
9	177	123	237	351	465
10	39	124	238	352	466
11	160	125	239	353	467
12	34	126	240	354	468
13	674	127	241	355	469
14	44	128	242	356	470
15	254	129	243	357	471
16	267	130	244	358	472
17	365	131	245	359	473
18	195	132	246	360	474
19	321	133	247	361	475
20	227	134	248	362	476
21	428	135	249	363	477
22	197	136	250	364	478
23	406	137	251	365	479
24	404	138	252	366	480
25	342	139	253	367	481
26	630	140	254	368	482
27	102	141	255	369	483
28	92	142	256	370	484
29	49	143	257	371	485
30	118	144	258	372	486
31	291	145	259	373	487

		SEQ ID NO.			
SEQ ID NO.	SNP Position	Forward Primer	Reverse Primer	Probe 1	Probe 2
32	46	146	260	374	488
33	353	147	261	375	489
34	379	148	262	376	490
35	362	149	263	377	491
36	999	150	264	378	492
37	115	151	265	379	493
38	207	152	266	380	494
39	280	153	267	381	495
40	281	154	268	382	496
41	81	155	269	383	497
42	241	156	270	384	498
43	299	157	271	385	499
44	336	158	272	386	500
45	468	159	273	387	501
46	284	160	274	388	502
47	250	161	275	389	503
48	262	162	276	390	504
49	496	163	277	391	505
50	44	164	278	392	506
51	82	165	279	393	507
52	52	166	280	394	508
53	409	167	281	395	509
54	115	168	282	396	510
55	256	169	283	397	511
56	91	170	284	398	512
57	47	171	285	399	513
58	525	172	286	400	514
59	253	173	287	401	515
60	174	174	288	402	516
61	250	175	289	403	517
62	148	176	290	404	518
63	130	177	291	405	519
64	258	178	292	406	520
65	324	179	293	407	521
66	66	180	294	408	522

		SEQ ID NO.			
SEQ ID NO.	SNP Position	Forward Primer	Reverse Primer	Probe 1	Probe 2
67	621	181	295	409	523
68	39	182	296	410	524
69	149	183	297	411	525
70	158	184	298	412	526
71	263	185	299	413	527
72	538	186	300	414	528
73	49	187	301	415	529
74	499	188	302	416	530
75	139	189	303	417	531
76	159	190	304	418	532
77	342	191	305	419	533
78	422	192	306	420	534
79	54	193	307	421	535
80	832	194	308	422	536
81	100	195	309	423	537
82	232	196	310	424	538
83	434	197	311	425	539
84	473	198	312	426	540
85	435	199	313	427	541
86	140	200	314	428	542
87	366	201	315	429	543
88	249	202	316	430	544
89	574	203	317	431	545
90	218	204	318	432	546
91	701	205	319	433	547
92	182	206	320	434	548
93	444	207	321	435	549
94	288	208	322	436	550
95	295	209	323	437	551
96	327	210	324	438	552
97	100	211	325	439	553
98	1052	212	326	440	554
99	204	213	327	441	555
100	128	214	328	442	556
101	242	215	329	443	557

		SEQ ID NO.			
SEQ ID NO.	**SNP Position**	**Forward Primer**	**Reverse Primer**	**Probe 1**	**Probe 2**
102	448	216	330	444	558
103	560	217	331	445	559
104	309	218	332	446	560
105	58	219	333	447	561
106	466	220	334	448	562
107	363	221	335	449	563
108	155	222	336	450	564
109	436	223	337	451	565
110	600	224	338	452	566
111	418	225	339	453	567
112	539	226	340	454	568
113	382	227	341	455	569
114	83	228	342	456	570

Example 5. Validation of DM QTLs

[00273] Multiple corn populations are used to validate effects of the DM QTLs identified herein. First, effects of individual DM resistance QTLs are tested using BC_3F_3 inbred plants derived from CV357626/CV523685 (Table 9). Plants carrying a resistant allele of DM-4.01 show a reduction of 15.9% in DM rating score (89.6%-73.7%=15.9%) when compared to plants carrying a susceptible allele. Plants carrying a resistant allele of DM-6.01 show a reduction of 26.6% in DM rating score (83.2%-56.6%=26.6%) when compared to plants carrying a susceptible allele. BC_3F_3 inbred plants are also derived from or CV368354/CV358560. Plants carrying a resistant allele of DM-8.01 show a reduction of 7.5% in DM rating score (85.6%-78.1%=7.5%) when compared to plants carrying a susceptible allele (Table 9).

Table 9. Efficacy test of individual QTLs on BC_3F_3 inbred plants.

Cross	QTL	QTL Profile	Mean (%)	p-value
CV357626/CV523685	DM_4.01	4-	89.6	<0.001
		4+	73.7	
CV357626/CV523685	DM_6.01	6-	83.2	<0.001
		6+	56.6	
CV368354/CV358560	DM_8.01	8-	85.6	<0.001
		8+	78.1	

[00274] Effects of various DM resistance QTL combinations are also tested using F_2 lines derived from CV375547/CV357626, CV523685/CV357626, CV356987/CV357626, CV358560/CV368354, CV368354/CV356389, CV368354/CV356054, CV353840/CV368354, and CV353184/CV368354. Inbred plants carrying multiple DM resistant QTLs from CV357626 show a reduction of 16-34% in DM rating scores when compared to plants carrying susceptible alleles. Inbred plants carrying multiple DM resistant QTLs from CV368354 show a reduction of 17.2-57.5% in DM rating scores when compared to plants carrying susceptible alleles (Table 10).

Table 10. Test of multiple QTL model in F_2 plants.

Cross	QTL model	DM rating score (%)		Efficacy (%)	p-value
		All negative	All positive		
CV375547/CV357626	DM_1.01 - DM_4.01 - DM_6.01	38	9.8	28.2	<0.001
CV523685/CV357626	DM_1.01 - DM_3.01- DM_4.01	43.8	9.8	34	<0.001
CV356987/CV357626	DM_1.01 - DM_3.01 - DM_4.01	23.8	7.8	16	<0.001
CV358560/CV368354	DM_2.01 - DM_4.01	57.47	34.27	23.2	<0.001
CV368354/CV356389	DM_6.02 - DM_8.01	57.04	17.39	39.65	<0.001
CV368354/CV356054	DM_6.02 - DM_8.01 - DM_9.01	78.79	21.26	57.53	<0.001
CV353840/CV368354	DM_8.01 - DM_9.01	37.29	17.92	19.37	<0.001
CV353184/CV368354	DM_2.01 - DM_6.02 -DM_8.01	26.44	9.23	17.21	<0.001

[00275] Effects of DM resistance QTL combinations in hybrid plants are also tested by crossing BC_6F_4 inbred lines derived from CV368354/CV371792 with two highly susceptible testers to generate hybrid plants. The efficacy, equivalency, and yield protection of various combinations of DM resistance QTLs are evaluated. Several combinations of DM resistant QTLs provide a reduction of 2.1-5.8% in DM rating score across testers (shown in bold text in Table 11). DM_6.02 appear shared among these QTL combinations.

Table 11. Efficacy trials of multiple QTL models. DM rating score differences by least-squares means (LSM_DIFF) are provided (LSM_DIFF = % of infected plants without DM resistant QTLs - % of infected plants with DM resistant QTLs).

QTL model	LSM_DIFF (%)	p-value
Under high disease pressure		
DM_5.01 - DM_6.02 - DM_7.01	0.9	0.330215
DM_5.01 - DM_6.02 - DM_7.01 - DM_8.01	**4.7**	**1.13E-06**
DM_5.01 - DM_6.02 - DM_8.01	**2.9**	**0.002377**
DM_5.01 - DM_7.01	-5.4	2.66E-08
DM_5.01 - DM_7.01 - DM_8.01	-2.4	0.014362
DM_6.02 - DM_7.01 - DM_8.01	**2.1**	**0.031126**
Under low disease pressure		
DM_5.01 - DM_6.02 - DM_7.01	**2.9**	**0.002548**
DM_5.01 - DM_6.02 - DM_7.01 - DM_8.01	**5.8**	**1.36E-09**
DM_5.01 - DM_6.02 - DM_8.01	**4.4**	**4.03E-06**
DM_5.01 - DM_7.01	-5.4	2.83E-08
DM_5.01 - DM_7.01 - DM_8.01	-2.7	0.00471
DM_6.02 - DM_7.01 - DM_8.01	**3.4**	**0.00045**

[00276] Under high disease pressure as exemplified in Example 1 (*e.g.*, a field with a DM infected corn plant as a source inoculum), hybrid plants carrying multiple DM resistant QTLs provide a yield advantage of 3.7-4.3 quintal per hectare when compared to hybrid plants carrying the susceptible QTLs (highlighted in bold text in Table 12). Under low disease pressure (*e.g.*, a field without a DM infected corn plant as a source inoculum), there is no statistical difference in yield between hybrid plants with or without DM resistant QTLs (Table 12) indicating no yield

penalty from these QTLs. It is noted in Table 12 that negative values correspond to yield increases, while positive values correspond to yield decreases.

Table 12. Yield protection and equivalency trials of multiple QTL model. Yield differences by least-squares means (LSM_DIFF) are provided (LSM_DIFF = yield from plants without DM resistant QTLs - yield from plants with DM resistant QTLs).

QTL model	LSM_DIFF (quintal/hectare)	p-value
Under high disease pressure		
DM_5.01 - DM_6.02 - DM_7.01	-1.4	0.348081
DM_5.01 - DM_6.02 - DM_7.01 - DM_8.01	**-3.9**	**0.009734**
DM_5.01 - DM_6.02 - DM_8.01	**-4.3**	**0.004883**
DM_5.01 - DM_7.01	3.1	0.039359
DM_5.01 - DM_7.01 - DM_8.01	2.6	0.093428
DM_6.02 - DM_7.01 - DM_8.01	**-3.7**	**0.013656**
Under low disease pressure		
DM_5.01 - DM_6.02 - DM_7.01	0.9	0.495734
DM_5.01 - DM_6.02 - DM_7.01 - DM_8.01	1.1	0.382852
DM_5.01 - DM_6.02 - DM_8.01	1	0.4349
DM_5.01 - DM_7.01	1.3	0.321979
DM_5.01 - DM_7.01 - DM_8.01	0.9	0.480224
DM_6.02 - DM_7.01 - DM_8.01	-1.3	0.318478

Example 6. Further Validation of DM QTLs

[00277] Efficacy of individual and multiple DM resistance QTLs are further tested using BC_3F_3 inbred plants derived from the crosses listed in Tables 13 and 14. Non-resistant plants are used as recurrent parent plants in the backcrosses to generate these BC_3F_3 plants. Inbred plants carrying resistant alleles of DM_4.01 show a reduction of 37.25% in DM rating score (67.75%-30.5%=37.25%) when compared to plants carrying susceptible alleles (Table 13). Inbred plants carrying multiple DM resistant QTLs (*e.g.*, DM_1.01-DM_4.01-DM_6.01) show a reduction in DM rating scores when compared to plants carrying susceptible alleles (Table 14).

[00278] Efficacy of individual and multiple DM resistance QTLs are also tested by crossing BC_3F_3 inbred plants with two highly susceptible tester lines to generate hybrid plants. Hybrid plants carrying multiple DM resistant QTLs (*e.g.*, DM_1.01-DM_4.01-DM_6.01) show a reduction in DM rating scores when compared to plants carrying susceptible alleles (Table 14).

[00279] These hybrid plants are also evaluated using equivalency tests (Tables 15 and 16). Hybrid plants carrying the resistant allele of DM_2.03 provide a yield advantage of 26.16 (87.77-61.61=26.16) quintal per hectare when compared to hybrid plants carrying the susceptible QTL (highlighted in bold text in Table 15). No significant yield drag was detected in equivalency tests for multiple QTLs in hybrid plants.

Table 13. Efficacy test of individual QTLs (* the presence and absence of a selected resistance QTL is shown by plus (+) and minus (-), respectively).

			INBRED TEST		HYBRID TEST	
Cross	**QTL**	**QTL Profile***	**Mean(%)**	**p-value**	**Mean (%)**	**p-value**
CV357626/CV375547	DM_1.01	1+	51.30	0.102	37.67	0.805
		1-	77.00		44.20	
	DM_4.01	4+	30.50	0.007	38.34	0.140
		4-	67.75		56.86	
	DM_6.01	6+	NA	NA	47.21	0.299
		6-	NA		19.08	
CV523685/CV357626	DM_6.01	6+	87.67	0.637	NA	NA
		6-	100.00		NA	
CV343114/CV357626	DM_1.01	1+	NA	NA	53.23	0.244
		1-	NA		37.21	
	DM_2.03	2+	89.00	0.723	50.41	0.711
		2-	82.83		45.74	

Table 14. Efficacy test of multiple QTLs. Differences in disease resistance by least-squares means (LSM_DIFF) are provided (LSM_DIFF =% of infected plants without DM resistance QTLs - % of infected plants with DM resistance QTLs). "All Negative" refers to plants lacking each of the three resistance QTLs, while "All Positive" refers to plants having all three resistance QTLs.

		INBRED TEST				HYBRID TEST			
		DM rating score (%)				DM rating score (%)			
Cross	**QTLs**	**All Negative**	**All Positive**	**LSM_DIFF (%)**	**p-value**	**All Negative**	**All Positive**	**LSM_DIFF (%)**	**p-value**
CV339885/CV357626	DM_1.01-DM_2.03_DM_6.01	90.20	85.00	5.20	0.3031	4.33	4.87	-0.54	0.7066
CV523685/CV357626	DM_1.01-DM_4.01_DM_6.01	79.42	62.23	17.19	0.0001	67.33	50.16	17.17	0.0060
CV338784/CV357626		74.08	61.00	13.08	<0.0001	57.45	41.99	15.46	0.0062
CV337135/CV357626		73.50	93.68	-20.18	0.3996	43.58	43.53	0.06	0.9968
CV335787/CV357626		86.67	76.00	10.67	0.2029	64.88	54.84	10.03	0.3744
CV356987/CV357626		65.58	35.72	29.86	<0.0001	50.54	28.94	21.59	<0.0001
CV357626/CV375547		97.71	60.64	37.08	0.0005	NA	NA	NA	NA

Table 15. Equivalency test of individual QTLs (* the presence and absence of a selected resistance QTL is shown by plus (+) and minus (-), respectively).

Cross	QTL	QTL Profile*	Yield (quintal/hectare)	p-value
CV357626/CV375547	DM_1.01	1+	70.30	0.129
		1-	56.30	
	DM_4.01	4+	80.78	0.761
		4-	84.53	
	DM_6.01	6+	62.18	0.557
		6-	59.01	
CV523685/CV357626	DM_4.01	4+	97.99	0.883
		4-	96.49	
CV343114/CV357626	DM_1.01	1+	72.89	0.879
		1-	70.81	
	DM_2.03	**2+**	**87.77**	**0.011**
		2-	**61.61**	

Table 16. Equivalency test of multiple QTLs. Yield differences by least-squares means (LSM_DIFF) are provided (LSM_DIFF = yield from plants without DM resistance QTLs - yield from plants with DM resistance QTLs; measured in quintals/hectare). "All Negative" refers to plants lacking each of the three resistance QTLs, while "All Positive" refers to plants having all three resistance QTLs.

		HYBRID TEST			
Cross	**QTL model**	**All Negative**	**All Positive**	**LSM_ DIFF**	**p-value**
CV339885/CV357626	DM_1.01-DM_2.03_DM_6.01	68.4383769	60.84911512	7.59	0.1391
CV523685/CV357626	DM_1.01-DM_4.01_DM_6.01	67.06	54.49	12.57	0.0965
CV338784/CV357626		63.89661472	60.56268131	3.33	<0.0001
CV337135/CV357626		65.38536565	55.94532966	9.44	0.6530
CV335787/CV357626		64.48961024	62.26780695	2.22	0.0001
CV356987/CV357626		71.46531304	73.94449948	-2.48	<0.0001

Example 7: Introgression of downy mildew resistance QTLs into additional maize lines.

[00280] A maize plant comprising one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, or ten or more DM resistance QTLs is crossed with an elite maize line comprising a desirable trait (*e.g.*, improved yield under water, temperature, or pest stress conditions), but susceptible to DM. F_1 progeny plants from this cross are assayed for one or more SNP markers exemplified in Tables 7 and 8 to select for DM resistance QTLs. A selected F_1 progeny plant is then backcrossed with the parent elite maize line comprising the desirable trait (recurrent parent). Plants from the BC_1 generation are also genotyped using SNP markers exemplified in Table 8 to select for DM resistance QTLs. After multiple rounds of backcrossing (*e.g.,* 5-7 generations) with the recurrent parent line, a new elite maize line is obtained comprising both DM resistance and the desirable trait in the recurrent parent line. Using the above introgression and marker-assisted selection strategy, the pyramiding or stacking of multiple DM resistance QTLs can be achieved.

[00281] As various modifications could be made in the constructions and methods herein described and illustrated without departing from the scope of this disclosure, it is intended that all matter contained in the foregoing description or shown in the accompanying drawings shall be interpreted as illustrative rather than limiting. The breadth and scope of the present disclosure should not be limited by any of the above-described exemplary embodiments, but should be defined only in accordance with the following claims appended hereto and their equivalents. All patent and non-patent documents cited in this specification are incorporated herein by reference in their entireties.

CLAIMS

What is claimed is:

1. A method of creating a population of corn plants or seeds resistant to Downy Mildew (DM), said method comprising:
    a. genotyping a first population of corn plants or seeds at one or more marker loci associated with and within about 20 cM of one or more DM resistance quantitative trait loci (QTLs) selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02, DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01;
    b. selecting from said first population one or more corn plants or seeds comprising one or more DM resistance alleles of said one or more marker loci; and
    c. producing from said selected one or more corn plants or seeds a second population of corn plants or seeds comprising said one or more DM resistance QTLs.
2. The method of claim 1, wherein said one or more marker loci are located in a chromosomal interval flanked by:
    any two of marker loci SEQ ID NOs: 1 to 11;
    any two of marker loci SEQ ID NOs: 12 to 22;
    any two of marker loci SEQ ID NOs: 23 to 28;
    any two of marker loci SEQ ID NOs: 29 to 32;
    any two of marker loci SEQ ID NOs: 33 to 38;
    any two of marker loci SEQ ID NOs: 39 to 45;
    any two of marker loci SEQ ID NOs: 46 to 55, and 57;
    any two of marker loci SEQ ID NOs: 56, and 58 to 62;
    marker loci SEQ ID NOs: 63 and 64;
    any two of marker loci SEQ ID NOs: 65 to 90; or
    any two of marker loci SEQ ID NOs: 91 to 114.
3. The method of claim 1, wherein said one or more marker loci are located in a chromosomal interval flanked by:
    any two marker loci selected from the group consisting of SEQ ID NOs: 5 to 8;
    SEQ ID NOs: 7 and 8;

any two marker loci selected from the group consisting of SEQ ID NOs: 12 to 14;
any two marker loci selected from the group consisting of SEQ ID NOs: 18 to 20;
any two marker loci selected from the group consisting of SEQ ID NOs: 25 to 27;
any two marker loci selected from the group consisting of SEQ ID NOs: 29 to 31;
any two marker loci selected from the group consisting of SEQ ID NOs: 34 to 36;
any two marker loci selected from the group consisting of SEQ ID NOs: 39 to 45;
any two marker loci selected from the group consisting of SEQ ID NOs: 49 to 51;
marker loci SEQ ID NOs: 58 and 59;
marker loci SEQ ID NOs: 63 and 64;
any two marker loci selected from the group consisting of SEQ ID NOs: 77 to 80;
or
any two marker loci selected from the group consisting of SEQ ID NOs: 99 to 106.

4. The method of claim 1, wherein said one or more marker loci are within about 15 cM, 10 cM, 5 cM, 1 cM, 0.5 cM, or less than 0.5 cM of any one of marker loci selected from the group consisting of SEQ ID NOs: 1-114.
5. The method of claim 1, wherein said one or more DM resistance QTLs provide moderate resistance or intermediate resistance to infection by an oomycete selected from the group consisting of *Peronosclerospora philippinensis. Peronosclerospora maydis, Peronosclerospora sorghi,* and a combination thereof.
6. The method of claim 1, wherein said second population of corn plants or seeds exhibit reduced premature death, reduced stunted growth, reduced leaf chlorosis, reduced number of narrow leaves, reduced number of erect leaves, reduced number of shredded leaves, reduced number of failed cobs, reduced vegetative tissue in tassels, or any combination thereof compared to corn plants or seeds lacking said DM resistance QTL under a high DM stress condition.
7. The method of claim 1, wherein said one or more DM resistance QTLs confer no yield penalty under a low DM stress condition.
8. The method of claim 1, wherein said step (a) comprises assaying a single nucleotide polymorphism marker.
9. The method of claim 1, wherein said step (a) comprises the use of an oligonucleotide probe.

10. The method of claim 9, wherein said oligonucleotide probe is adjacent to a polymorphic nucleotide position in said marker locus.

11. The method of claim 1, wherein said step (a) comprises detecting a haplotype.

12. A method of introgressing a DM resistance QTL, said method comprising:

a. crossing a first corn plant comprising a DM resistance QTL with a second corn plant of a different genotype to produce one or more progeny plants or seeds; and

b. selecting a progeny plant or seed comprising a DM resistance allele of a polymorphic locus linked to said DM resistance QTL, wherein said polymorphic locus is in a chromosomal segment flanked by:

any two of marker loci SEQ ID NOs: 1 to 11;
any two of marker loci SEQ ID NOs: 12 to 22;
any two of marker loci SEQ ID NOs: 23 to 28;
any two of marker loci SEQ ID NOs: 29 to 32;
any two of marker loci SEQ ID NOs: 33 to 38;
any two of marker loci SEQ ID NOs: 39 to 45;
any two of marker loci SEQ ID NOs: 46 to 55, and 57;
any two of marker loci SEQ ID NOs: 56, and 58 to 62;
marker loci SEQ ID NOs: 63 and 64;
any two of marker loci SEQ ID NOs: 65 to 90; or
any two of marker loci SEQ ID NOs: 91 to 114.

13. The method of claim 12, wherein said polymorphic locus is within about 20 cM, 10 cM, 5 cM, 1 cM, 0.5 cM, or less than 0.5 cM of any one of marker loci selected from the group consisting of SEQ ID NOs: 1-114.

14. The method of claim 12, further comprising:

c. crossing said progeny plant with itself or said second plant to produce one or more further progeny plants or seeds; and

d. selecting a further progeny plant or seed comprising said DM resistance allele.

15. A DM resistant corn plant or seed comprising a combination of one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more, twelve or more, or thirteen introgressed DM resistance QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_1.02,

DM_2.01, DM_2.02, DM_2.03, DM_3.01, DM_4.01, DM_5.01, DM_6.01, DM_6.02, DM_7.01, DM_8.01, and DM_9.01.

16. The corn plant or seed of claim 15, wherein said combination of introgressed DM resistance QTLs comprises one or more QTLs selected from the group consisting of DM resistance QTLs DM_1.01, DM_4.01, DM_6.01, DM_6.02, DM_8.01, and any combination thereof.
17. The corn plant or seed of claim 15, wherein seed yield of said corn plant is about 1% or more, 3% or more, 5% or more, 10% or more, 20% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, 90% or more, or 100% or more higher than seed yield of a corn plant without said combination of introgressed DM resistance QTLs under a high DM stress condition.
18. The corn plant or seed of claim 15, wherein said corn plant or seed is in an agronomically elite background.
19. The corn plant or seed of claim 15, wherein said corn plant or seed is a transgenic hybrid plant or seed.