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(54) Title: METHODS AND COMPOSITIONS FOR PLANT PEST CONTROL

(57) Abstract: The present invention provides methods and compositions to improve fungal disease resistance and/or nematode resistance in various crop plants. The present invention also provides for combinations of compositions and methods to improve fungal disease resistance and/or nematode resistance in various crop plants.

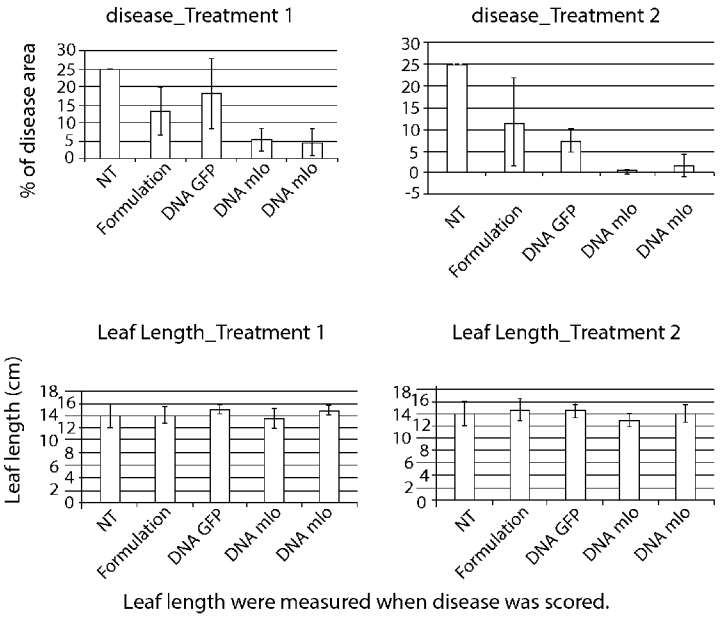

FIGURE 2

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METHODS AND COMPOSITIONS FOR PLANT PEST CONTROL

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 61/715,549, filed October 18, 2012, which is incorporated herein by reference in its entirety.

INCORPORATION OF SEQUENCE LISTING

[0002] A sequence listing containing the file named "MTC58633_PCT_SeqListing.txt", which is 366,930 bytes (measured in MS-Windows®), contains 213 sequences, and was created on October 14, 2013, is provided herewith and is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

[0003] Powdery mildews are fungal diseases that affect a wide range of plants including cereals, grasses, vegetables, ornamentals, weeds, shrubs, fruit trees, broad-leaved shade and forest trees, that is caused by different species of fungi in the order *Erysiphales*. The disease is characterized by spots or patches of white to grayish, talcum-powder-like growth that produce tiny, pinhead-sized, spherical fruiting structures (the cleistothecia or overwintering bodies of the fungus), that are first white, later yellow-brown and finally black. The fungi that cause powdery mildews are host specific and cannot survive without the proper host plant. They produce mycelium (fungal threads) that grow only on the surface of the plant and feed by sending haustoria, or root-like structures, into the epidermal cells of the plant. The fungi overwinter on plant debris as cleistothecia or mycelia. In the spring, the cleistothecia produce spores that are moved to susceptible hosts by rain, wind or insects.

[0004] Powdery mildew disease is particularly prevalent in temperate and humid climates, where they frequently cause significant yield losses and quality reductions in various agricultural settings including greenhouse and field farming. This affects key cereals (e.g. barley and wheat), horticultural crops (e.g. grapevine, pea and tomato) and economically important ornamentals (e.g. roses). Limited access to natural sources of resistance to powdery mildews, rapid changes in pathogen virulence and the time consuming introgression of suitable resistance genes into elite varieties has led to the widespread use of fungicides to control the disease. This has, not surprisingly, led to the evolution and spread of fungicide

resistance, which is especially dramatic amongst the most economically important powdery mildews.

[0005] Downy mildew diseases are caused by oomycete microbes from the family *Peronosporaceae* that are parasites of plants. *Peronosporaceae* are obligate biotrophic plant pathogens and parasitize their host plants as an intercellular mycelium using haustoria to penetrate the host cells. The downy mildews reproduce asexually by forming sporangia on distinctive white sporangiophores usually formed on the lower surface of infected leaves. These constitute the "downy mildew" and the initial symptoms appear on leaves as light green to yellow spots. The sporangia are wind-dispersed to the surface of other leaves. Depending on the genus, the sporangia may germinate by forming zoospores or by germ-tube. In the latter case, the sporangia behave like fungal conidia and are often referred to as such. Sexual reproduction is via oospores.

[0006] Most *Peronosporaceae* are pathogens of herbaceous dicots. Some downy mildew genera have relatively restricted host ranges, e.g. *Basidiophora*, *Paraperonospora*, *Protobremia* and *Bremia* on *Asteraceae*; *Perofascia* and *Hyaloperonospora* almost exclusively on *Brassicaceae*; *Viennotia*, *Graminivora*, *Poakatesthia*, *Sclerospora* and *Peronosclerospora* on *Poaceae*, *Plasmoverna* on *Ranunculaceae*. However, the largest genera, *Peronospora* and *Plasmopara*, have very wide host ranges.

[0007] In commercial agriculture, downy mildews are a particular problem for growers of crucifers, grapes and vegetables that grow on vines. *Peronosporaceae* of economic importance include *Plasmopara viticola* which infect grapevines, *Peronospora tabacina* which causes blue mold on tobacco, *Bremia lactucae,* a parasite on lettuce, and *Plasmopara halstedii* on sunflower.

[0008] Rusts (*Pucciniales*, formerly *Uredinales*) are obligate biotrophic parasites of vascular plants. Rusts affect a variety of plants; leaves, stems, fruits and seeds and is most commonly seen as coloured powder, composed of tiny aeciospores which land on vegetation producing pustules, or uredia, that form on the lower surfaces. During late spring or early summer, yellow orange or brown, hairlike or ligulate structures called telia grow on the leaves or emerge from bark of woody hosts. These telia produce teliospores which will germinate into aerial basidiospores, spreading and causing further infection.

[0009] In the monocot barley (*Hordeum vulgare*, Piffanelli et al. Nature. 2004 430 (7002):887-91) and the dicots *Arabidopsis thaliana* (Consonni et al. Nat Genet. 2006 38(6):716-20), tomato (*Solanum lycopersicum*, Bai et al. Mol Plant Microbe Interact. 2008 21(1):30-9) and pea (*Pisum sativum*, Humphry et al. Mol Plant Pathol. 2011 Apr 21. EPUB),

loss-of-function mutations in MLO (Mildew Resistance Locus O) genes confer highly effective broad-spectrum powdery mildew resistance. MLO resistance appears to act early and typically terminates fungal pathogenesis before invasion of the first host cell. The exceptional efficacy and longevity of MLO resistance, has resulted in elite barley lines carrying introgressed MLO alleles being successfully used in European agriculture for about three decades. However, MLO mutants have several undesirable agronomic qualities including environment-dependent necrotic leaf spotting and reduced yields (Molina-Cano et al. Theor Appl Genet. 2003 107(7):1278-87). In addition, barley MLO mutants also show enhanced susceptibility to the hemibiotroph *Magnaporthe grisea* and the necrotroph *Bipolaris sorokinianaare*. Lab studies with *Arabidopsis* powdery resistant MLO mutants suggest that these agronomic defects, including others such as spontaneous cell wall appositions, cell death, senescence-like chlorosis and enhanced susceptibility to *Alternaria alternata*, *A. brassicicola* and *Phytophthora infestans* (necrotrophic *Alternaria* spp.and hemibiotrophic P. infestans), respectively, are pleiotropic effects not simply linkage drag (Consonni et al. Nat Genet. 2006 38(6):716-20).

[0010] Recently a method to increase resistance to soybean rust via the transgenic knockdown of MLO genes has been disclosed (Markus et al. United States Patent Application 20100192254).

SUMMARY OF THE INVENTION

[0011] The present invention provides for compositions comprising polynucleotide molecules and methods for treating a plant to alter or regulate gene or gene transcript expression in the plant, for example, by providing RNA or DNA for inhibition of expression. Various aspects of the invention provide compositions comprising polynucleotide molecules and related methods for topically applying such compositions to plants to regulate endogenous Mildew Resistance Locus O (MLO) genes in a plant cell. The polynucleotides, compositions, and methods disclosed herein are useful in decreasing levels of MLO transcript and improving fungal disease and/or nematode resistance of a plant.

[0012] In an aspect of the invention, the polynucleotide molecules are provided in compositions that can permeate or be absorbed into living plant tissue to initiate localized, partially systemic, or systemic gene inhibition or regulation. In certain embodiments of the invention, the polynucleotide molecules ultimately provide to a plant, or allow the *in planta* production of, RNA that is capable of hybridizing under physiological conditions in a plant cell to RNA transcribed from a target endogenous gene or target transgene in the plant cell,

thereby effecting regulation of the endogenous MLO target gene. In certain embodiments, regulation of the MLO target gene, such as by silencing or suppression of the target gene, leads to the upregulation of another gene that is itself affected or regulated by decreasing the MLO target gene's expression.

[0013] In certain aspects or embodiments of the invention, the topical application of a composition comprising an exogenous polynucleotide and a transfer agent to a plant or plant part according to the methods described herein does not necessarily result in nor require the exogenous polynucleotide's integration into a chromosome of the plant. In certain aspects or embodiments of the invention, the topical application of a composition comprising an exogenous polynucleotide and a transfer agent to a plant or plant part according to the methods described herein does not necessarily result in nor require transcription of the exogenous polynucleotide from DNA integrated into a chromosome of the plant. In certain embodiments, topical application of a composition comprising an exogenous polynucleotide and a transfer agent to a plant according to the methods described herein also does not necessarily require that the exogenous polynucleotide be physically bound to a particle, such as in biolistic mediated introduction of polynucleotides associated with a gold or tungsten particles into internal portions of a plant, plant part, or plant cell. An exogenous polynucleotide used in certain methods and compositions provided herein can optionally be associated with an operably linked promoter sequence in certain embodiments of the methods provided herein. However, in other embodiments, an exogenous polynucleotide used in certain methods and compositions provided herein is not associated with an operably linked promoter sequence. Also, in certain embodiments, an exogenous polynucleotide used in certain methods and compositions provided herein is not operably linked to a viral vector.

[0014] In certain embodiments, methods for improving fungal disease resistance and/or nematode resistance in a plant comprising topically applying compositions comprising a polynucleotide that suppresses the targeted MLO gene and a transfer agent are provided. In certain embodiments, methods for selectively suppressing the targeted MLO gene by topically applying the polynucleotide composition to a plant surface at one or more selected seed, vegetative, or reproductive stage(s) of plant growth are provided. Such methods can provide for gene suppression in a plant or plant part on an as needed or as desired basis. In certain embodiments, methods for selectively suppressing the target MLO gene by topically applying the polynucleotide composition to a plant surface at one or more pre-determined seed, vegetative, or reproductive stage(s) of plant growth are provided. Such methods can provide for MLO gene suppression in a plant or plant part that obviates any undesired or

unnecessary effects of suppressing gene expression at certain seed, vegetative, or reproductive stage(s) of plant development.

[0015] In certain embodiments, methods for selectively improving fungal disease resistance and/or nematode resistance in a plant by topically applying the polynucleotide composition to the plant surface at one or more selected seed, vegetative, or reproductive stage(s) are provided. Such methods can provide for improved fungal disease resistance and/or nematode disease resistance in a plant or plant part on an as needed or as desired basis. In certain embodiments, methods for selectively improving fungal disease and/or nematode resistance in a plant by topically applying the polynucleotide composition to the plant surface at one or more predetermined seed, vegetative, or reproductive stage(s) are provided. Such methods can provide for improving fungal disease and/or nematode resistance in a plant or plant part that obviates any undesired or unnecessary effects of suppressing MLO gene expression at certain seed, vegetative, or reproductive stage(s) of plant development.

[0016] Polynucleotides that can be used to suppress a MLO include, but are not limited to, any of: i) polynucleotides comprising at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a transcript of the gene(s) encoding a protein of Table 2 or 3 (SEQ ID NO:1-27, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, or 78); ii) polynucleotides comprising at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a MLO or MLO-like gene of Table 3 comprising a polynucleotide of SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 42, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79; or, polynucleotides comprising at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a polynucleotide of SEQ ID NO:80-195. In some embodiments, a polynucleotide that comprises a nucleotide sequence that is essentially identical or essentially complementary to at least 18 contiguous nucleotides of SEQ ID NO: 197-213 is provided. In some embodiments, the polynucleotide comprises a nucleotide sequence that is essentially identical or essentially complementary to SEQ ID NO: 197-213. Methods and compositions that provide for the topical application of certain polynucleotides in the presence of transfer agents can be used to suppress Mildew Resistance Locus O (MLO) gene expression in an optimal manner. In certain embodiments, the compositions provided herein can be applied on an "as needed" basis upon scouting for the occurrence of fungal disease or nematodes. In certain embodiments, the compositions provided herein can be applied as a prophylactic measure to prevent the occurrence of fungal disease or nematodes. In certain embodiments, the compositions can be applied in a manner that obviates any deleterious effects on yield or

other characteristics that can be associated with suppression of MLO gene expression in a crop plant. The applied polynucleotides are complementary to the MLO target host gene in plants and their topical application leads to suppression of the MLO gene's activity.

[0017] Provided herein are compositions and methods for controlling plant fungal diseases. Plant fungal diseases that can be controlled with the methods and compositions provided herein include, but are not limited to, obligate biotrophic powdery mildew, downy mildew and rust fungal infestations. Certain embodiments relate to methods and compositions for reducing expression of one or more host plant MLO polynucleotide and/or protein molecules in one or more cells or tissues of the host plant such that the host plant is rendered less susceptible to fungal infections from the order *Erysiphales*, the family *Peronosporaceae,* or the order *Pucciniales*. In certain embodiments, nucleotide and amino acid sequences of plant Mildew Resistance Locus O (MLO) genes and gene products which can be downregulated by methods and compositions provided herein to increase plant resistance to powdery mildew, downy mildew or rust infection are disclosed.

[0018] Also provided herein are methods and compositions that provide for reductions in expression of targeted MLO polynucleotide and protein molecules in at least the cells of a plant root for improved resistance to nematodes. Nematodes that can be controlled by the methods and compositions provided herein include, but are not limited to, root knot nematodes (such as *Meloidogyne sp.*), cyst nematodes (such as *Globodera sp.* and *Heterodera sp.*), lesion nematodes (such as *Pratylenchus sp.*), and the like. In certain embodiments, MLO expression is reduced in plant root cells from which nematodes feed by providing topically to plant leaves, shoots, roots and/or seeds, compositions comprising polynucleotides that comprise at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or to a transcript of a MLO gene; and a transfer agent.

[0019] Also provided are methods and compositions where topically induced reductions in MLO transcript or protein levels are used to achieve powdery mildew, downy mildew or rust control while minimizing deleterious pleotropic effects in the host plant. Such methods and compositions provide for optimized levels of MLO gene inhibition and/or optimized timing of MLO gene inhibition.

[0020] Certain embodiments of the invention are directed to methods for producing a plant exhibiting an improvement in fungal disease resistance and/or nematode resistance comprising topically applying to a plant surface a composition that comprises:

a. at least one polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or to a transcript of the gene; and

b. a transfer agent, wherein the plant exhibits an improvement in fungal disease resistance and/or nematode resistance that results from suppression of the Mildew Resistance Locus O (MLO) gene. In certain embodiments, the polynucleotide molecule comprises sense ssDNA, sense ssRNA, dsRNA, dsDNA, a double stranded DNA/RNA hybrid, anti-sense ssDNA, or anti-sense ssRNA. In certain embodiments, the polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. In some embodiments, a polynucleotide that comprises a nucleotide sequence that is essentially identical or essentially complementary to at least 18 contiguous nucleotides of SEQ ID NO: 197-213 is provided. In some embodiments, the polynucleotide comprises a nucleotide sequence that is essentially identical or essentially complementary to SEQ ID NO: 197-213. In certain embodiments: (a) the plant is a corn plant, the gene or the transcript is a corn Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69; (b) the plant is a soybean plant, the gene or the transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47, (c) the plant is a cotton plant, the gene or the transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4; (d) the plant is a barley plant, the gene or the transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, 194, and SEQ ID NO: 197-213, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29; (e) the plant is a cucumber plant, the gene or the transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and

SEQ ID NO:99, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;(f) the plant is a lettuce plant, the gene or the transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39; (g) the plant is a pea plant, the gene or the transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;(h) the plant is a *Medicago* plant, the gene or the transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43; (i) the plant is a pepper plant, the gene or the transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49; (j) the plant is a tomato plant, the gene or the transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53; (k) the plant is a wheat plant, the gene or the transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59; (l) the plant is a grape plant, the gene or the transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67; (m) the plant is a sorghum plant, the gene or the transcript is a sorghum Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group

consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or, (n) the plant is a rice plant, the gene or the transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:183, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79. In certain embodiments, the composition comprises any combination of two or more polynucleotide molecules. In certain embodiments, the polynucleotide is at least 18 to about 24, about 25 to about 50, about 51 to about 100, about 101 to about 300, about 301 to about 500, or at least about 500 or more residues in length. In certain embodiments, the composition further comprises a non-polynucleotide herbicidal molecule, a polynucleotide herbicidal molecule, a polynucleotide that suppresses an herbicide target gene, an insecticide, a fungicide, a nematocide, or a combination thereof. In certain embodiments, the composition further comprises a non-polynucleotide herbicidal molecule and the plant is resistant to the herbicidal molecule. In certain embodiments, the transfer agent comprises an organosilicone preparation. In certain embodiments, the polynucleotide is not operably linked to a viral vector. In certain embodiments, the polynucleotide is not integrated into the plant chromosome. Further embodiments of the invention are directed to: a plant made according to any of the above-described methods; progeny of plants that exhibit the improvements in fungal disease resistance and/or nematode resistance; seed of the plants, wherein seed from the plants exhibits the improvement in fungal disease resistance and/or nematode resistance; and a processed product of the plants, the progeny plants, or the seeds, wherein the processed products exhibit the improvement in fungal disease resistance and/or nematode resistance. In certain embodiments, the processed product of the plant or plant part exhibits an improved attribute relative to a processed product of an untreated control plant and the improved attribute results from the improved fungal disease resistance and/or nematode resistance. An improved attribute of a processed product can include, but is not limited to, decreased mycotoxin content, improved nutritional content, improved storage characteristics, improved flavor, improved consistency, and the like when compared to a processed product obtained from an untreated plant or plant part.

[0021] An additional embodiment of the invention is directed to a composition comprising a polynucleotide molecule that comprises at least 18 contiguous nucleotides that are essentially

identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of the gene, wherein the polynucleotide is not operably linked to a promoter; and, b) a transfer agent. In certain embodiments, the polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. In some embodiments, a polynucleotide that comprises a nucleotide sequence that is essentially identical or essentially complementary to at least 18 contiguous nucleotides of SEQ ID NO: 197-213 is provided. In some embodiments, the polynucleotide comprises a nucleotide sequence that is essentially identical or essentially complementary to SEQ ID NO: 197-213. In certain embodiments: (a) the gene or the transcript is a corn Mildew Resistance Locus O (MLO) Gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69; (b) the gene or the transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47; (c) the gene or the transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4; (d) the gene or the transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, 194, and SEQ ID NO:197-213, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29; (e) the gene or the transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37; (f) the gene or the transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39; (g) the gene or the

transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41; (h) the gene or the transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43; (i) the gene or the transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49; (j) the gene or the transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53; (k) the gene or the transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59; (l) the gene or the transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67; (m) the gene or the transcript is a sorghum Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or, (n) the gene or the transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:195, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79. In certain embodiments, the polynucleotide is at least 18 to about 24, about 25 to about 50, about 51 to about 100, about 101 to about 300, about 301 to about 500, or at least about 500 or more

residues in length. In certain embodiments, the composition further comprises a non-polynucleotide herbicidal molecule, a polynucleotide herbicidal molecule, a polynucleotide that suppresses an herbicide target gene, an insecticide, a fungicide, a nematocide, or a combination thereof. In certain embodiments, the transfer agent is an organosilicone preparation. In certain embodiments, the polynucleotide is not physically bound to a biolistic particle.

[0022] Another embodiment of the invention is directed to a method of making a composition comprising the step of combining at least:(a) a polynucleotide molecule comprising at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of a plant, wherein the polynucleotide is not operably linked to a promoter or a viral vector; and, (b) a transfer agent. In certain embodiments, the polynucleotide is obtained by *in vivo* biosynthesis, *in vitro* enzymatic synthesis, or chemical synthesis. In certain embodiments, the method further comprises combining with the polynucleotide and the transfer agent at least one of a non-polynucleotide herbicidal molecule, a polynucleotide herbicidal molecule, an insecticide, a fungicide, and/or a nematocide. In certain embodiments, the transfer agent is an organosilicone preparation.

[0023] Yet another embodiment of the invention is directed to a method of identifying a polynucleotide for improving fungal disease resistance and/or nematode resistance in a plant comprising; (a) selecting a population of polynucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of a plant; b) topically applying to a surface of at least one of the plants a composition comprising at least one polynucleotide from the population and an transfer agent to obtain a treated plant; and, c) identifying a treated plant that exhibits suppression of the Mildew Resistance Locus O (MLO) gene or exhibits an improvement in fungal disease resistance or exhibits an improvement in nematode resistance, thereby identifying a polynucleotide that improves fungal disease resistance and/or nematode resistance in the plant. In certain embodiments, the polynucleotide is selected from the group consisting of wherein the polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. In some embodiments, a polynucleotide that comprises a nucleotide sequence that is essentially identical or essentially complementary to at least 18 contiguous nucleotides of SEQ ID NO: 197-213 is provided. In some

embodiments, the polynucleotide comprises a nucleotide sequence that is essentially identical or essentially complementary to SEQ ID NO: 197-213. In certain embodiments: (a) the plant is a corn plant, the gene or the transcript is a corn Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69; (b) the plant is a soybean plant, the gene or the transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47, (c) the plant is a cotton plant, the gene or the transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4; (d) the plant is a barley plant, the gene or the transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, 194, and SEQ ID NO: 197-213, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29; (e) the plant is a cucumber plant, the gene or the transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;(f) the plant is a lettuce plant, the gene or the transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39; (g) the plant is a pea plant, the gene or the transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;(h) the plant is a *Medicago* plant, the gene or the transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and

SEQ ID NO:111, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43; (i) the plant is a pepper plant, the gene or the transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49; (j) the plant is a tomato plant, the gene or the transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53; (k) the plant is a wheat plant, the gene or the transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59; (l) the plant is a grape plant, the gene or the transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67; (m) the plant is a sorghum plant, the gene or the transcript is a sorghum Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or, (n) the plant is a rice plant, the gene or the transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:183, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79.

[0024] A further embodiment of the invention is directed to a plant comprising an exogenous polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of the gene, wherein the exogenous polynucleotide is not operably linked to a promoter or to a viral vector, is not integrated into the chromosomal DNA of the plant, and is not found in a non-transgenic plant; and, wherein the plant exhibits an improvement in fungal disease

resistance and/or nematode resistance that results from suppression of the Mildew Resistance Locus O (MLO) gene. In certain embodiments, plant further comprises an organosilicone compound or a component thereof. In certain embodiments, the polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37,39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. In some embodiments, a polynucleotide that comprises a nucleotide sequence that is essentially identical or essentially complementary to at least 18 contiguous nucleotides of SEQ ID NO: 197-213 is provided. In some embodiments, the polynucleotide comprises a nucleotide sequence that is essentially identical or essentially complementary to SEQ ID NO: 197-213. In certain embodiments: (a) the plant is a corn plant, the gene or the transcript is a corn Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69; (b) the plant is a soybean plant, the gene or the transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47, (c) the plant is a cotton plant, the gene or the transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4; (d) the plant is a barley plant, the gene or the transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, , and SEQ ID NO: 197-213, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29; (e) the plant is a cucumber plant, the gene or the transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;(f) the plant is a lettuce plant, the gene or the transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or the polynucleotide comprises at

least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39; (g) the plant is a pea plant, the gene or the transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41; (h) the plant is a *Medicago* plant, the gene or the transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43; (i) the plant is a pepper plant, the gene or the transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49; (j) the plant is a tomato plant, the gene or the transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53; (k) the plant is a wheat plant, the gene or the transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59; (l) the plant is a grape plant, the gene or the transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67; (m) the plant is a sorghum plant, the gene or the transcript is a sorghum Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or, (n) the plant is a rice plant, the gene or the transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:183, or the

polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79.

[0025] An additional embodiment of the invention is directed to a plant part comprising an exogenous polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of the gene, wherein the exogenous polynucleotide is not operably linked to a promoter or to a viral vector and is not found in a non-transgenic plant; and, wherein the plant part exhibits an improvement in fungal disease resistance and/or nematode resistance that results from suppression of the Mildew Resistance Locus O (MLO) gene. In certain embodiments, the polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. In some embodiments, a polynucleotide that comprises a nucleotide sequence that is essentially identical or essentially complementary to at least 18 contiguous nucleotides of SEQ ID NO: 197-213 is provided. In some embodiments, the polynucleotide comprises a nucleotide sequence that is essentially identical or essentially complementary to SEQ ID NO: 197-213. In certain embodiments: (a) the plant part is a corn plant part, the gene or the transcript is a corn Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69; (b) the plant part is a soybean plant part, the gene or the transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47, (c) the plant part is a cotton plant part, the gene or the transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4; (d) the plant part is a barley plant part, the gene or the transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, 194, and SEQ ID NO: 197-213, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29; (e)

the plant part is a cucumber plant part, the gene or the transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;(f) the plant part is a lettuce plant part, the gene or the transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39; (g) the plant part is a pea plant part, the gene or the transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;(h) the plant part is a *Medicago* plant part, the gene or the transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43; (i) the plant part is a pepper plant part, the gene or the transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49; (j) the plant part is a tomato plant part, the gene or the transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53; (k) the plant part is a wheat plant part, the gene or the transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59; (l) the plant part is a grape plant part, the gene or the transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or the polynucleotide comprises at least 18 contiguous nucleotides

that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67; (m) the plant part is a sorghum plant part, the gene or the transcript is a sorghum Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or, (n) the plant part is a rice plant part, the gene or the transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and the polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:, or the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79. In certain embodiments, the plant part is a flower, meristem, ovule, stem, tuber, fruit, anther, pollen, leaf, root, or seed. In certain embodiments, the plant part is a seed. Also provided are processed plant products obtained from any of the aforementioned plant parts, wherein the processed plant products exhibit an improved attribute relative to a processed plant product of an untreated control plant and wherein the improved attribute results from the improved fungal disease resistance and/or nematode resistance. In certain embodiments, the processed product is a meal, a pulp, a feed, or a food product. Another embodiment of the invention is directed to a plant that exhibits an improvement in fungal disease resistance and/or nematode resistance, wherein the plant was topically treated with a composition that comprises: (a) at least one polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or to a transcript of the gene; and (b) a transfer agent; and, wherein the plant exhibits an improvement in fungal disease resistance and/or nematode resistance that results from suppression of the Mildew Resistance Locus O (MLO) gene.

BRIEF DESCRIPTION OF THE DRAWINGS

[0026] Figure 1 presents a bootstrapped phylogenetic tree of MLO proteins

[0027] Figure 2 presents graphs showing % disease area and leaf length measurements in untreated barley plants (NT) and barley plants treated with various liquid formulations as described in Table 6.

[0028] Figure 3 presents a graph showing disease control measurements (percentage leaf area infected) in untreated barley plants (NT) and barley plants treated with various liquid formulations as described in Table 12.

[0029] Figure 4 presents a graph showing disease control measurements (percentage leaf area infected) in barley plants treated with short dsRNA polynucleotides at 6 day post-infection.

[0030] Figure 5 presents a graph showing disease control measurements (percentage leaf area infected) in barley plants treated with short dsRNA polynucleotides at 13 day post-infection.

[0031] Figure 6 presents a graph showing disease control measurements (percentage leaf area infected) in barley plants treated with long dsRNA polynucleotides at 6 day post-infection.

DETAILED DESCRIPTION

I. Definitions

[0032] The following definitions and methods are provided to better define the present invention and to guide those of ordinary skill in the art in the practice of the present invention. Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art.

[0033] Where a term is provided in the singular, the inventors also contemplate aspects of the invention described by the plural of that term.

[0034] As used herein, the terms "DNA," "DNA molecule," and "DNA polynucleotide molecule" refer to a single-stranded DNA or double-stranded DNA molecule of genomic or synthetic origin, such as, a polymer of deoxyribonucleotide bases or a DNA polynucleotide molecule.

[0035] As used herein, the terms "DNA sequence," "DNA nucleotide sequence," and "DNA polynucleotide sequence" refer to the nucleotide sequence of a DNA molecule.

[0036] As used herein, the term "gene" refers to any portion of a nucleic acid that provides for expression of a transcript or encodes a transcript. A "gene" thus includes, but is not limited to, a promoter region, 5' untranslated regions, transcript encoding regions that can include intronic regions, and 3' untranslated regions.

[0037] As used herein, the terms "RNA," "RNA molecule," and "RNA polynucleotide molecule" refer to a single-stranded RNA or double-stranded RNA molecule of genomic or synthetic origin, such as, a polymer of ribonucleotide bases that comprise single or double stranded regions.

[0038] Unless otherwise stated, nucleotide sequences in the text of this specification are given, when read from left to right, in the 5' to 3' direction. The nomenclature used herein is that required by Title 37 of the United States Code of Federal Regulations § 1.822 and set forth in the tables in WIPO Standard ST.25 (1998), Appendix 2, Tables 1 and 3.

[0039] As used herein, a "plant surface" refers to any exterior portion of a plant. Plant surfaces thus include, but are not limited to, the surfaces of flowers, stems, tubers, fruit, anthers, pollen, leaves, roots, or seeds. A plant surface can be on a portion of a plant that is attached to other portions of a plant or on a portion of a plant that is detached from the plant.

[0040] As used herein, the phrase "polynucleotide is not operably linked to a promoter" refers to a polynucleotide that is not covalently linked to a polynucleotide promoter sequence that is specifically recognized by either a DNA dependent RNA polymerase II protein or by a viral RNA dependent RNA polymerase in such a manner that the polynucleotide will be transcribed by the DNA dependent RNA polymerase II protein or viral RNA dependent RNA polymerase. A polynucleotide that is not operably linked to a promoter can be transcribed by a plant RNA dependent RNA polymerase.

[0041] As used herein, any polynucleotide sequences of SEQ ID NO: 80-195, though displayed in the sequence listing in the form of ssDNA, encompass all other polynucleotide forms such as dsDNA equivalents, ssDNA equivalents, ssRNA equivalents, ssRNA complements, dsRNA, and ssDNA complements.

[0042] As used herein, any polynucleotide sequences of SEQ ID NO: 197-213, though displayed in the sequence listing in the form of one strand of a dsRNA molecule, encompass all other polynucleotide forms such as dsDNA equivalents, ssDNA equivalents, ssRNA equivalents, ssRNA complements, dsRNA, and ssDNA complements.

[0043] As used herein, a first nucleic-acid sequence is "operably" connected or "linked" with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to an RNA and/or protein-coding sequence if the promoter provides for transcription or expression of the RNA or coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein-coding regions, are in the same reading frame.

[0044] As used herein, the phrase "organosilicone preparation" refers to a liquid comprising one or more organosilicone compounds, wherein the liquid or components contained therein, when combined with a polynucleotide in a composition that is topically applied to a target plant surface, enable the polynucleotide to enter a plant cell. Examples of organosilicone preparations include, but are not limited to, preparations marketed under the trade names "Silwet®" or "BREAK-THRU®" and preparations provided in Table 1. In certain embodiments, an organosilicone preparation can enable a polynucleotide to enter a plant cell

in a manner permitting a polynucleotide suppression of target gene expression in the plant cell.

[0045] As used herein, the phrase "provides for an improvement in fungal disease resistance and/or nematode resistance" refers to any measurable increase in a plant's resistance to fungal- and/or nematode- induced damage. In certain embodiments, an improvement in fungal disease resistance and/or nematode resistance in a plant or plant part can be determined in a comparison to a control plant or plant part that has not been treated with a composition comprising a polynucleotide and a transfer agent. When used in this context, a control plant is a plant that has not undergone treatment with polynucleotide and a transfer agent. Such control plants would include, but are not limited to, untreated plants or mock treated plants.

[0046] As used herein, the phrase "provides for a reduction", when used in the context of a transcript or a protein in a plant or plant part, refers to any measurable decrease in the level of transcript or protein in a plant or plant part. In certain embodiments, a reduction of the level of a transcript or protein in a plant or plant part can be determined in comparison to a control plant or plant part that has not been treated with a composition comprising a polynucleotide and a transfer agent. When used in this context, a control plant or plant part is a plant or plant part that has not undergone treatment with polynucleotide and a transfer agent. Such control plants or plant parts would include, but are not limited to, untreated or mock treated plants and plant parts.

[0047] As used herein, the phrase "wherein said plant does not comprise a transgene" refers to a plant that lacks either a DNA molecule comprising a promoter that is operably linked to an exogenous polynucleotide or a recombinant viral vector.

[0048] As used herein, the phrase "suppressing expression" or "suppression", when used in the context of a gene, refers any measurable decrease in the amount and/or activity of a product encoded by the gene. Thus, expression of a gene can be suppressed when there is a reduction in levels of a transcript from the gene, a reduction in levels of a protein encoded by the gene, a reduction in the activity of the transcript from the gene, a reduction in the activity of a protein encoded by the gene, any one of the preceding conditions, or any combination of the preceding conditions. In this context, the activity of a transcript includes, but is not limited to, its ability to be translated into a protein and/or to exert any RNA-mediated biologic or biochemical effect. In this context, the activity of a protein includes, but is not limited to, its ability to exert any protein-mediated biologic or biochemical effect. In certain embodiments, a suppression of gene expression in a plant or plant part can be determined in a

comparison of gene product levels or activities in a treated plant to a control plant or plant part. When used in this context, a control plant or plant part is a plant or plant part that has not undergone treatment with a composition comprising a polynucleotide and a transfer agent. Such control plants or plant parts would include, but are not limited to, untreated or mock treated plants and plant parts.

[0049] As used herein, the term "transcript" corresponds to any RNA that is produced from a gene by the process of transcription. A transcript of a gene can thus comprise a primary transcription product which can contain introns or can comprise a mature RNA that lacks introns.

[0050] As used herein, the term "liquid" refers to both homogeneous mixtures such as solutions and non-homogeneous mixtures such as suspensions, colloids, micelles, and emulsions.

II. Overview

[0051] Provided herein are certain methods and polynucleotide compositions that can be applied to living plant cells/tissues to suppress expression of target genes and that provide improved fungal disease resistance and/or nematode resistance to a crop plant. Also provided herein are plants and plant parts exhibiting fungal disease resistance and/or nematode resistance as well as processed products of such plants or plant parts. The compositions may be topically applied to the surface of a plant, such as to the surface of a leaf, and include a transfer agent. Aspects of the method can be applied to various crops, for example, including but not limited to: i) row crop plants including, but are not limited to, corn, barley, sorghum, soybean, cotton, canola, sugar beet, alfalfa, sugarcane, rice, and wheat; ii) vegetable plants including, but not limited to, tomato, potato, sweet pepper, hot pepper, melon, watermelon, cucumber, eggplant, cauliflower, broccoli, lettuce, spinach, onion, peas, carrots, sweet corn, Chinese cabbage, leek, fennel, pumpkin, squash or gourd, radish, Brussels sprouts, tomatillo, garden beans, dry beans, or okra; iii) culinary plants including, but not limited to, basil, parsley, coffee, or tea; iv) fruit plants including but not limited to apple, pear, cherry, peach, plum, apricot, banana, plantain, table grape, wine grape, citrus, avocado, mango, or berry; v) a tree grown for ornamental or commercial use, including, but not limited to, a fruit or nut tree; or, vi) an ornamental plant (e. g., an ornamental flowering plant or shrub or turf grass). The methods and compositions provided herein can also be applied to plants produced by a cutting, cloning, or grafting process (i. e., a plant not grown from a seed) that include fruit trees and plants. Fruit trees produced by such processes include, but are not limited to, citrus

and apple trees. Plants produced by such processes include, but are not limited to, avocados, tomatoes, eggplant, cucumber, melons, watermelons, and grapes as well as various ornamental plants.

[0052] Without being bound by a particular theory, the compositions and methods of the present invention are believed to operate through one or more of the several natural cellular pathways involved in RNA-mediated gene suppression as generally described in Brodersen and Voinnet (2006), *Trends Genetics*, 22:268-280; Tomari and Zamore (2005) *Genes & Dev.*, 19:517-529; Vaucheret (2006) *Genes Dev.*, 20:759-771; Meins et al. (2005) *Annu. Rev. Cell Dev. Biol.*, 21:297-318; and Jones-Rhoades et al. (2006) *Annu. Rev. Plant Biol.*, 57:19-53. RNA-mediated gene suppression generally involves a double-stranded RNA (dsRNA) intermediate that is formed intra-molecularly within a single RNA molecule or inter-molecularly between two RNA molecules. This longer dsRNA intermediate is processed by a ribonuclease of the RNAase III family (Dicer or Dicer-like ribonuclease) to one or more shorter double-stranded RNAs, one strand of which is incorporated into the RNA-induced silencing complex ("RISC"). For example, the siRNA pathway involves the cleavage of a longer double-stranded RNA intermediate to small interfering RNAs ("siRNAs"). The size of siRNAs is believed to range from about 19 to about 25 base pairs, but the most common classes of siRNAs in plants include those containing 21 to 24 base pairs (See, Hamilton et al. (2002) *EMBO J.*, 21:4671-4679).

Polynucleotides

[0053] As used herein, "polynucleotide" refers to a DNA or RNA molecule containing multiple nucleotides and generally refers both to "oligonucleotides" (a polynucleotide molecule of 18-25 nucleotides in length) and longer polynucleotides of 26 or more nucleotides. Embodiments of this invention include compositions including polynucleotides having a length of 18-25 nucleotides (18-mers, 19-mers, 20-mers, 21-mers, 22-mers, 23-mers, 24-mers, or 25-mers), or medium-length polynucleotides having a length of 26 or more nucleotides (polynucleotides of 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, about 65, about 70, about 75, about 80, about 85, about 90, about 95, about 100, about 110, about 120, about 130, about 140, about 150, about 160, about 170, about 180, about 190, about 200, about 210, about 220, about 230, about 240, about 250, about 260, about 270, about 280, about 290, or about 300 nucleotides), or long polynucleotides having a length greater than about 300 nucleotides (*e. g.*, polynucleotides of between about 300 to about 400 nucleotides, between

about 400 to about 500 nucleotides, between about 500 to about 600 nucleotides, between about 600 to about 700 nucleotides, between about 700 to about 800 nucleotides, between about 800 to about 900 nucleotides, between about 900 to about 1000 nucleotides, between about 300 to about 500 nucleotides, between about 300 to about 600 nucleotides, between about 300 to about 700 nucleotides, between about 300 to about 800 nucleotides, between about 300 to about 900 nucleotides, or about 1000 nucleotides in length, or even greater than about 1000 nucleotides in length, for example up to the entire length of a target gene including coding or non-coding or both coding and non-coding portions of the target gene). Where a polynucleotide is double-stranded, its length can be similarly described in terms of base pairs.

[0054] Polynucleotide compositions used in the various embodiments of this invention include compositions including including: RNA or DNA or RNA/DNA hybrids or chemically modified polynucleotides or a mixture thereof. In certain embodiments, the polynucleotide may be a combination of ribonucleotides and deoxyribonucleotides, for example, synthetic polynucleotides consisting mainly of ribonucleotides but with one or more terminal deoxyribonucleotides or synthetic polynucleotides consisting mainly of deoxyribonucleotides but with one or more terminal dideoxyribonucleotides. In certain embodiments, the polynucleotide includes non-canonical nucleotides such as inosine, thiouridine, or pseudouridine. In certain embodiments, the polynucleotide includes chemically modified nucleotides. Examples of chemically modified polynucleotides are well known in the art; see, for example, U.S. Patent Publication 2011/0171287, U.S. Patent Publication 2011/0171176, U.S. Patent Publication 2011/0152353, U.S. Patent Publication 2011/0152346, and U.S. Patent Publication 2011/0160082, which are herein incorporated by reference. Illustrative examples include, but are not limited to, the naturally occurring phosphodiester backbone of a polynucleotide which can be partially or completely modified with phosphorothioate, phosphorodithioate, or methylphosphonate internucleotide linkage modifications, modified nucleoside bases or modified sugars can be used in polynucleotide synthesis, and polynucleotides can be labeled with a fluorescent moiety (*e. g.*, fluorescein or rhodamine) or other label (*e. g.*, biotin).

[0055] Polynucleotides can be single- or double-stranded RNA, single- or double-stranded DNA, double-stranded DNA/RNA hybrids, and modified analogues thereof. In certain embodiments of the invention, the polynucleotides that provide single-stranded RNA in the plant cell may be: (a) a single-stranded RNA molecule (ssRNA), (b) a single-stranded RNA molecule that self-hybridizes to form a double-stranded RNA molecule, (c) a double-stranded

RNA molecule (dsRNA), (d) a single-stranded DNA molecule (ssDNA), (e) a single-stranded DNA molecule that self-hybridizes to form a double-stranded DNA molecule, (f) a single-stranded DNA molecule including a modified Pol III gene that is transcribed to an RNA molecule, (g) a double-stranded DNA molecule (dsDNA), (h) a double-stranded DNA molecule including a modified Pol III gene that is transcribed to an RNA molecule, and (i) a double-stranded, hybridized RNA/DNA molecule, or combinations thereof. In certain embodiments, these polynucleotides can comprise both ribonucleic acid residues and deoxyribonucleic acid residues. In certain embodiments, these polynucleotides include chemically modified nucleotides or non-canonical nucleotides. In certain embodiments of the methods, the polynucleotides include double-stranded DNA formed by intramolecular hybridization, double-stranded DNA formed by intermolecular hybridization, double-stranded RNA formed by intramolecular hybridization, or double-stranded RNA formed by intermolecular hybridization. In certain embodiments where the polynucleotide is a dsRNA, the anti-sense strand will comprise at least 18 nucleotides that are essentially complementary to the target gene. In certain embodiments the polynucleotides include single-stranded DNA or single-stranded RNA that self-hybridizes to form a hairpin structure having an at least partially double-stranded structure including at least one segment that will hybridize to RNA transcribed from the gene targeted for suppression. Not intending to be bound by any mechanism, it is believed that such polynucleotides are or will produce single-stranded RNA with at least one segment that will hybridize to RNA transcribed from the gene targeted for suppression. In certain embodiments, the polynucleotides can be operably linked to a promoter – generally a promoter functional in a plant, for example, a pol II promoter, a pol III promoter, a pol IV promoter, or a pol V promoter.

[0056] The polynucleotide molecules of the present invention are designed to modulate expression by inducing regulation or suppression of an endogenous gene in a plant and are designed to have a nucleotide sequence essentially identical or essentially complementary to the nucleotide sequence of an endogenous gene of a plant or to the sequence of RNA transcribed from an endogenous gene of a plant, which can be coding sequence or non-coding sequence. These effective polynucleotide molecules that modulate expression are referred to herein as "a trigger, or triggers". By "essentially identical" or "essentially complementary" it is meant that the trigger polynucleotides (or at least one strand of a double-stranded polynucleotide) have sufficient identity or complementarity to the endogenous gene or to the RNA transcribed from the endogenous gene (e.g. the transcript) to suppress expression of the endogenous gene (e.g., to effect a reduction in levels or activity of the gene transcript and/or

encoded protein). Polynucleotides of the methods and compositions provided herein need not have 100 percent identity or complementarity to the endogenous gene or to the RNA transcribed from the endogenous gene (i.e. the transcript) to suppress expression of the endogenous gene (i.e. to effect a reduction in levels or activity of the gene transcript or encoded protein). Thus, in certain embodiments, the polynucleotide or a portion thereof is designed to be essentially identical to, or essentially complementary to, a sequence of at least 18 or 19 contiguous nucleotides in either the target gene or messenger RNA transcribed from the target gene (e.g. the transcript). In certain embodiments, an "essentially identical" polynucleotide has 100 percent sequence identity or at least about 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent sequence identity when compared to the sequence of 18 or more contiguous nucleotides in either the endogenous target gene or to an RNA transcribed from the target gene (e.g. the transcript). In certain embodiments, an "essentially complementary" polynucleotide has 100 percent sequence complementarity or at least about 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent sequence complementarity when compared to the sequence of 18 or more contiguous nucleotides in either the target gene or RNA transcribed from the target gene.

[0057] In certain embodiments, polynucleotides used in the methods and compositions provided herein can be essentially identical or essentially complementary to any of: i) conserved regions of Mildew Resistance Locus O (MLO) genes of both monocot and dicot plants; ii) conserved regions of Mildew Resistance Locus O (MLO) genes of monocot plants; or iii) conserved regions of Mildew Resistance Locus O (MLO) genes of dicot plants. Such polynucleotides that are essentially identical or essentially complementary to such conserved regions can be used to improve fungal disease resistance and/or nematode disease resistance by suppressing expression of Mildew Resistance Locus O (MLO) genes in any of: i) both dicot and monocot plants, including, but not limited to, corn, barley, wheat, sorghum, rice, cucumber, pea, *Medicago sp.*, soybean, pepper, tomato, and grape; ii) monocot plants, including, but not limited to, corn, barley, wheat, sorghum, and rice, and; or iii) dicot plants, including, but not limited to, cucumber, pea, *Medicago sp.*, soybean, pepper, tomato, and grape.

[0058] Polynucleotides containing mismatches to the target gene or transcript can thus be used in certain embodiments of the compositions and methods provided herein. In certain embodiments, a polynucleotide can comprise at least 19 contiguous nucleotides that are essentially identical or essentially complementary to said gene or said transcript or comprises at least 19 contiguous nucleotides that are essentially identical or essentially complementary

to the target gene or target gene transcript. In certain embodiments, a polynucleotide of 19 continuous nucleotides that is essentially identical or essentially complementary to the endogenous target gene or to RNA transcribed from the target gene (e.g. the transcript) can have 1 or 2 mismatches to the target gene or transcript. In certain embodiments, a polynucleotide of 20 or more nucleotides that contains a contiguous 19 nucleotide span of identity or complementarity to the endogenous target gene or to an RNA transcribed from the target gene can have 1 or 2 mismatches to the target gene or transcript. In certain embodiments, a polynucleotide of 21 continuous nucleotides that is essentially identical or essentially complementary to the endogenous target gene or to RNA transcribed from the target gene (e.g. the transcript) can have 1, 2, or 3 mismatches to the target gene or transcript. In certain embodiments, a polynucleotide of 22 or more nucleotides that contains a contiguous 21 nucleotide span of identity or complementarity to the endogenous target gene or to an RNA transcribed from the target gene can have 1, 2, or 3 mismatches to the target gene or transcript. In designing polynucleotides with mismatches to an endogenous target gene or to an RNA transcribed from the target gene, mismatches of certain types and at certain positions that are more likely to be tolerated can be used. In certain embodiments, mismatches formed between adenine and cytosine or guanosine and uracil residues are used as described by Du et al. Nucleic Acids Research, 2005, Vol. 33, No. 5 1671–1677. In certain embodiments, mismatches in 19 base pair overlap regions can be at the low tolerance positions 5, 7, 8 or 11 (from the 5' end of a 19 nucleotide target) with well tolerated nucleotide mismatch residues, at medium tolerance positions 3, 4, and 12-17, and/or at the high tolerance nucleotide positions at either end of the region of complementarity (i.e. positions 1, 2, 18, and 19) as described by Du et al. Nucleic Acids Research, 2005, Vol. 33, No. 5 1671–1677. It is further anticipated that tolerated mismatches can be empirically determined in assays where the polynucleotide is applied to the plants via the methods provided herein and the treated plants assayed for suppression of Mildew Resistance Locus O (MLO) expression or appearance of fungal disease resistance and/or nematode resistance.

[0059] In certain embodiments, polynucleotide molecules are designed to have 100 percent sequence identity with or complementarity to one allele or one family member of a given target gene coding or non-coding sequence of a MLO target gene. In other embodiments, the polynucleotide molecules are designed to have 100 percent sequence identity with or complementarity to multiple alleles or family members of a given Mildew Resistance Locus O (MLO) target gene. In certain embodiments, the polynucleotide can thus comprises at least 18 contiguous nucleotides that are identical or complementary to SEQ ID NO: 4, 29, 31,

33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. In certain embodiments, the polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79.

[0060] In certain embodiments, polynucleotide compositions and methods provided herein typically effect regulation or modulation (e. g., suppression) of gene expression during a period during the life of the treated plant of at least 1 week or longer and typically in systemic fashion. For instance, within days of treating a plant leaf with a polynucleotide composition of this invention, primary and transitive siRNAs can be detected in other leaves lateral to and above the treated leaf and in apical tissue. In certain embodiments, methods of systemically suppressing expression of a gene in a plant, the methods comprising treating said plant with a composition comprising at least one polynucleotide and a transfer agent, wherein said polynucleotide comprises at least 18 or at least 19 contiguous nucleotides that are essentially identical or essentially complementary to a gene or a transcript encoding a Mildew Resistance Locus O (MLO) gene of the plant are provided, whereby expression of the gene in said plant or progeny thereof is systemically suppressed in comparison to a control plant that has not been treated with the composition.

[0061] Compositions used to suppress a target gene can comprise one or more polynucleotides that are essentially identical or essentially complementary to multiple genes, or to multiple segments of one or more genes. In certain embodiments, compositions used to suppress a target gene can comprise one or more polynucleotides that are essentially identical or essentially complementary to multiple consecutive segments of a target gene, multiple non-consecutive segments of a target gene, multiple alleles of a target gene, or multiple target genes from one or more species.

[0062] In certain embodiments, the polynucleotide includes two or more copies of a nucleotide sequence (of 18 or more nucleotides) where the copies are arranged in tandem fashion. In another embodiment, the polynucleotide includes two or more copies of a nucleotide sequence (of 18 or more nucleotides) where the copies are arranged in inverted repeat fashion (forming an at least partially self-complementary strand). The polynucleotide can include both tandem and inverted-repeat copies. Whether arranged in tandem or inverted repeat fashion, each copy can be directly contiguous to the next, or pairs of copies can be separated by an optional spacer of one or more nucleotides. The optional spacer can be unrelated sequence (*i. e.*, not essentially identical to or essentially complementary to the copies, nor essentially identical to, or essentially complementary to, a sequence of 18 or more

contiguous nucleotides of the endogenous target gene or RNA transcribed from the endogenous target gene). Alternatively the optional spacer can include sequence that is complementary to a segment of the endogenous target gene adjacent to the segment that is targeted by the copies. In certain embodiments, the polynucleotide includes two copies of a nucleotide sequence of between about 20 to about 30 nucleotides, where the two copies are separated by a spacer no longer than the length of the nucleotide sequence.

Tiling

[0063] Polynucleotide trigger molecules can be identified by "tiling" gene targets in random length fragments, e.g., 200-300 polynucleotides in length, with partially overlapping regions, e.g., 25 or so nucleotide overlapping regions along the length of the target gene. Multiple gene target sequences can be aligned and polynucleotide sequence regions with homology in common are identified as potential trigger molecules for multiple targets. Multiple target sequences can be aligned and sequence regions with poor homology are identified as potential trigger molecules for selectively distinguishing targets. To selectively suppress a single gene, trigger sequences may be chosen from regions that are unique to the target gene either from the transcribed region or the non-coding regions, e.g., promoter regions, 3' untranslated regions, introns and the like.

[0064] Polynucleotides fragments are designed along the length of the full length coding and untranslated regions of a MLO gene or family member as contiguous overlapping fragments of 200-300 polynucleotides in length or fragment lengths representing a percentage of the target gene. These fragments are applied topically (as sense or anti-sense ssDNA or ssRNA, dsRNA, or dsDNA) to determine the relative effectiveness in providing the yield/quality phenotype. Fragments providing the desired activity may be further subdivided into 50-60 polynucleotide fragments which are evaluated for providing the yield/quality phenotype. The 50-60 base fragments with the desired activity may then be further subdivided into 19-30 base fragments which are evaluated for providing the yield/quality phenotype. Once relative effectiveness is determined, the fragments are utilized singly, or in combination in one or more pools to determine effective trigger composition or mixture of trigger polynucleotides for providing the yield/quality phenotype.

[0065] Coding and/or non-coding sequences of gene families in the crop of interest are aligned and 200-300 polynucleotide fragments from the least homologous regions amongst the aligned sequences are evaluated using topically applied polynucleotides (as sense or anti-sense ssDNA or ssRNA, dsRNA, or dsDNA) to determine their relative effectiveness in

providing the yield/quality phenotype. The effective segments are further subdivided into 50-60 polynucleotide fragments, prioritized by least homology, and reevaluated using topically applied polynucleotides. The effective 50-60 polynucleotide fragments are subdivided into 19-30 polynucleotide fragments, prioritized by least homology, and again evaluated for induction of the yield/quality phenotype. Once relative effectiveness is determined, the fragments are utilized singly, or again evaluated in combination with one or more other fragments to determine the trigger composition or mixture of trigger polynucleotides for providing the yield/quality phenotype.

[0066] Coding and/or non-coding sequences of gene families in the crop of interest are aligned and 200-300 polynucleotide fragments from the most homologous regions amongst the aligned sequences are evaluated using topically applied polynucleotides (as sense or anti-sense ssDNA or ssRNA, dsRNA, or dsDNA) to determine their relative effectiveness in inducing the yield/quality phenotype. The effective segments are subdivided into 50-60 polynucleotide fragments, prioritized by most homology, and reevaluated using topically applied polynucleotides. The effective 50-60 polynucleotide fragments are subdivided into 19-30 polynucleotide fragments, prioritized by most homology, and again evaluated for induction of the yield/quality phenotype. Once relative effectiveness is determined, the fragments may be utilized singly, or in combination with one or more other fragments to determine the trigger composition or mixture of trigger polynucleotides for providing the yield/quality phenotype.

[0067] Also, provided herein are methods for identifying a preferred polynucleotide for improving fungal disease and/or nematode resistance in a plant. Populations of candidate polynucleotides that are essentially identical or essentially complementary to a MLO gene or transcript of the gene can be generated by a variety of approaches, including but not limited to, any of the tiling, least homology, or most homology approaches provided herein. Such populations of polynucleotides can also be generated or obtained from any of the polynucleotides or genes provided herewith in SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 42, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. Such populations of polynucleotides can also be generated or obtained from any genes that are orthologous to the genes provided herewith in SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 42, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. Such populations of polynucleotides can also be generated or obtained from any genes that encode proteins that are orthologous to a protein of Table 2 or 3 (SEQ ID NO:1-27, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, or 78). Such polynucleotides can be topically

applied to a surface of plants in a composition comprising at least one polynucleotide from said population and a transfer agent to obtain treated plants. Treated plants that exhibit suppression of the MLO gene and/or exhibit an improvement fungal disease and/or nematode resistance are identified, thus identifying a preferred polynucleotide that improves improving fungal disease and/or nematode resistance in a plant. Suppression of the gene can be determined by any assay for the levels and /or activity of a gene product (i.e., transcript or protein). Suitable assays for transcripts include, but are not limited to, semi-quantitative or quantitative reverse transcriptase PCR® (qRT-PCR) assays. Suitable assays for proteins include, but are not limited to, semi-quantitative or quantitaive immunoassays, biochemical activity assays, or biological activity assays. In certain embodiments, the polynucleotides can be applied alone. In other embodiments, the polynucleotides can be applied in pools of multiple polynucleotides. When a pool of polynucleotides provides for suppression of the MLO gene and/or an improvement in fungal disease resistance and/or nematode disease resistance are identified, the pool can be de-replicated and retested as necessary or desired to identify one or more preferred polynucleotide(s) that improves fungal disease resistance and/or nematode disease resistance in a plant.

[0068] Methods of making polynucleotides are well known in the art. Such methods of making polynucleotides can include *in vivo* biosynthesis, *in vitro* enzymatic synthesis, or chemical synthesis. In certain embodiments, RNA molecules can be made by either *in vivo* or *in vitro* synthesis from DNA templates where a suitable promoter is operably linked to the polynucleotide and a suitable DNA–dependent RNA polymerase is provided. DNA–dependent RNA polymerases include, but are not limited to, E. coli or other bacterial RNA polymerases as well as the bacteriophage RNA polymerases such as the T7, T3, and SP6 RNA polymerases. Commercial preparation of polynucleotides often provides two deoxyribonucleotides on the 3' end of the sense strand. Long polynucleotide molecules can be synthesized from commercially available kits, for example, kits from Applied Biosystems/Ambion (Austin, TX) have DNA ligated on the 5' end that encodes a bacteriophage T7 polymerase promoter that makes RNA strands that can be assembled into a dsRNA. Alternatively, dsRNA molecules can be produced from expression cassettes in bacterial cells that have regulated or deficient RNase III enzyme activity. Long polynucleotide molecules can also be assembled from multiple RNA or DNA fragments. In some embodiments design parameters such as Reynolds score (Reynolds et al. *Nature Biotechnology* 22, 326 - 330 (2004) and Tuschl rules (Pei and Tuschl, Nature Methods 3(9): 670-676, 2006) are known in the art and are used in selecting polynucleotide sequences

effective in gene silencing. In some embodiments random design or empirical selection of polynucleotide sequences is used in selecting polynucleotide sequences effective in gene silencing. In some embodiments, the sequence of a polynucleotide is screened against the genomic DNA of the intended plant to minimize unintentional silencing of other genes.

[0069] While there is no upper limit on the concentrations and dosages of polynucleotide molecules that can be useful in the methods and compositions provided herein, lower effective concentrations and dosages will generally be sought for efficiency. The concentrations can be adjusted in consideration of the volume of spray or treatment applied to plant leaves or other plant part surfaces, such as flower petals, stems, tubers, fruit, anthers, pollen, leaves, roots, or seeds. In one embodiment, a useful treatment for herbaceous plants using 25-mer polynucleotide molecules is about 1 nanomole (nmol) of polynucleotide molecules per plant, for example, from about 0.05 to 1 nmol polynucleotides per plant. Other embodiments for herbaceous plants include useful ranges of about 0.05 to about 100 nmol, or about 0.1 to about 20 nmol, or about 1 nmol to about 10 nmol of polynucleotides per plant. In certain embodiments, about 40 to about 50 nmol of a ssDNA polynucleotide are applied. In certain embodiments, about 0.5 nmol to about 2 nmol of a dsRNA is applied. In certain embodiments, a composition containing about 0.5 to about 2.0 mg/mL, or about 0.14 mg/mL of dsRNA or ssDNA (21-mer) is applied. In certain embodiments, a composition of about 0.5 to about 1.5 mg/mL of a long dsRNA polynucleotide (i.e., about 50 to about 200 or more nucleotides) is applied. In certain embodiments, about 1 nmol to about 5 nmol of a dsRNA is applied to a plant. In certain embodiments, the polynucleotide composition as topically applied to the plant contains the at least one polynucleotide at a concentration of about 0.01 to about 10 milligrams per milliliter, or about 0.05 to about 2 milligrams per milliliter, or about 0.1 to about 2 milligrams per milliliter. In certain embodiments, a composition of about 0.5 to about 1.5 mg/mL of a long dsRNA polynucleotide (i.e. about 50 to about 200 or more nucleotides) is applied. Very large plants, trees, or vines may require correspondingly larger amounts of polynucleotides. When using long dsRNA molecules that can be processed into multiple polynucleotides, lower concentrations can be used. To illustrate embodiments of the invention, the factor 1X, when applied to polynucleotide molecules is arbitrarily used to denote a treatment of 0.8 nmol of polynucleotide molecule per plant; 10X, 8 nmol of polynucleotide molecule per plant; and 100X, 80 nmol of polynucleotide molecule per plant.

[0070] The polynucleotide compositions of this invention are useful in compositions, such as liquids that comprise polynucleotide molecules, alone or in combination with other components either in the same liquid or in separately applied liquids that provide a transfer

agent. As used herein, a transfer agent is an agent that, when combined with a polynucleotide in a composition that is topically applied to a target plant surface, enables the polynucleotide to enter a plant cell. In certain embodiments, a transfer agent is an agent that conditions the surface of plant tissue, e. g., seeds, leaves, stems, roots, flowers, or fruits, to permeation by the polynucleotide molecules into plant cells. The transfer of polynucleotides into plant cells can be facilitated by the prior or contemporaneous application of a polynucleotide-transferring agent to the plant tissue. In some embodiments the transferring agent is applied subsequent to the application of the polynucleotide composition. The polynucleotide transfer agent enables a pathway for polynucleotides through cuticle wax barriers, stomata and/or cell wall or membrane barriers into plant cells. Suitable transfer agents to facilitate transfer of the polynucleotide into a plant cell include agents that increase permeability of the exterior of the plant or that increase permeability of plant cells to polynucleotides. Such agents to facilitate transfer of the composition into a plant cell include a chemical agent, or a physical agent, or combinations thereof. Chemical agents for conditioning or transfer include (a) surfactants, (b) an organic solvent or an aqueous solution or aqueous mixtures of organic solvents, (c) oxidizing agents, (d) acids, (e) bases, (f) oils, (g) enzymes, or combinations thereof. Embodiments of the method can optionally include an incubation step, a neutralization step (e.g., to neutralize an acid, base, or oxidizing agent, or to inactivate an enzyme), a rinsing step, or combinations thereof. Embodiments of agents or treatments for conditioning of a plant to permeation by polynucleotides include emulsions, reverse emulsions, liposomes, and other micellar-like compositions. Embodiments of agents or treatments for conditioning of a plant to permeation by polynucleotides include counter-ions or other molecules that are known to associate with nucleic acid molecules, *e. g.*, inorganic ammonium ions, alkyl ammonium ions, lithium ions, polyamines such as spermine, spermidine, or putrescine, and other cations. Organic solvents useful in conditioning a plant to permeation by polynucleotides include DMSO, DMF, pyridine, *N*-pyrrolidine, hexamethylphosphoramide, acetonitrile, dioxane, polypropylene glycol, other solvents miscible with water or that will dissolve phosphonucleotides in non-aqueous systems (such as is used in synthetic reactions). Naturally derived or synthetic oils with or without surfactants or emulsifiers can be used, *e. g.*, plant-sourced oils, crop oils (such as those listed in the 9th Compendium of Herbicide Adjuvants, publicly available on the worldwide web (internet) at herbicide.adjuvants.com can be used, *e. g.*, paraffinic oils, polyol fatty acid esters, or oils with short-chain molecules modified with amides or polyamines such as polyethyleneimine or *N*-pyrrolidine. Transfer agents include, but are not limited to, organosilicone preparations.

[0071] In certain embodiments, an organosilicone preparation that is commercially available as Silwet® L-77 surfactant having CAS Number 27306-78-1 and EPA Number: CAL.REG.NO. 5905-50073-AA, and currently available from Momentive Performance Materials, Albany, New York can be used to prepare a polynucleotide composition. In certain embodiments where a Silwet L-77 organosilicone preparation is used as a pre-spray treatment of plant leaves or other plant surfaces, freshly made concentrations in the range of about 0.015 to about 2 percent by weight (wt percent) (*e. g.*, about 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04, 0.045, 0.05, 0.055, 0.06, 0.065, 0.07, 0.075, 0.08, 0.085, 0.09, 0.095, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) are efficacious in preparing a leaf or other plant surface for transfer of polynucleotide molecules into plant cells from a topical application on the surface. In certain embodiments of the methods and compositions provided herein, a composition that comprises a polynucleotide molecule and an organosilicone preparation comprising Silwet L-77 in the range of about 0.015 to about 2 percent by weight (wt percent) (*e. g.*, about 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04, 0.045, 0.05, 0.055, 0.06, 0.065, 0.07, 0.075, 0.08, 0.085, 0.09, 0.095, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) is used or provided. In certain embodiments of the methods and compositions provided herein, a composition that comprises a polynucleotide molecule and an organosilicone preparation comprising Silwet L-77 in the range of about 0.3 to about 1 percent by weight (wt percent) or about 0.5 to about 1%. by weight (wt percent) is used or provided.

[0072] In certain embodiments, any of the commercially available organosilicone preparations provided in the following Table 1 can be used as transfer agents in a polynucleotide composition. In certain embodiments where an organosilicone preparation of Table 1 is used as a pre-spray treatment of plant leaves or other surfaces, freshly made concentrations in the range of about 0.015 to about 2 percent by weight (wt percent) (*e. g.*, about 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04, 0.045, 0.05, 0.055, 0.06, 0.065, 0.07, 0.075, 0.08, 0.085, 0.09, 0.095, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) are efficacious in preparing a leaf or other plant surface for transfer of polynucleotide molecules into plant cells from a topical application on the surface. In certain embodiments of the methods and compositions provided herein, a composition that comprises a polynucleotide molecule and an organosilicone preparation of Table 1 in the range of about 0.015 to about 2 percent by weight (wt percent) (*e. g.*, about 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04, 0.045, 0.05,

0.055, 0.06, 0.065, 0.07, 0.075, 0.08, 0.085, 0.09, 0.095, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) is used or provided.

[0073] Table 1. Examples of organosilicone preparations

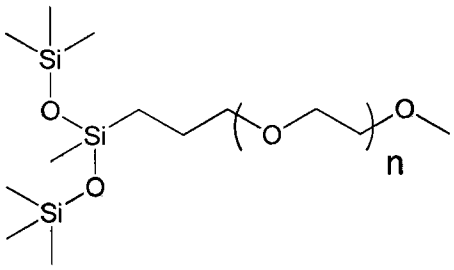
Name	**CAS number**	**Manufacturer** [1,2]
BREAK-THRU® S 321	na	Evonik Industries AG
BREAK-THRU ® S 200	67674-67-3	Evonik Industries AG
BREAK-THRU ® OE 441	68937-55-3	Evonik Industries AG
BREAK-THRU ® S 278	27306-78-1	Evonik Goldschmidt
BREAK-THRU ® S 243	na	Evonik Industries AG
Silwet® L-77	27306-78-1	Momentive Performance Materials
Silwet® HS 429	na	Momentive Performance Materials
Silwet® HS 312	na	Momentive Performance Materials
BREAK-THRU ® S 233	134180-76-0	Evonik Industries AG
Silwet® HS 508		Momentive Performance Materials
Silwet® HS 604		Momentive Performance Materials

[1] Evonik Industries AG, Essen, Germany

[2] Momentive Performance Materials, Albany, New York

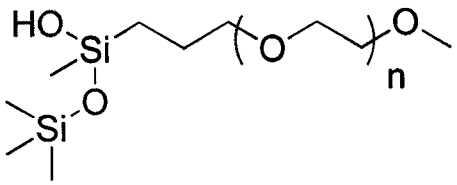
[0074] Organosilicone preparations used in the methods and compositions provided herein can comprise one or more effective organosilicone compounds. As used herein, the phrase "effective organosilicone compound" is used to describe any organosilicone compound that is found in an organosilicone preparation that enables a polynucleotide to enter a plant cell. In certain embodiments, an effective organosilicone compound can enable a polynucleotide to enter a plant cell in a manner permitting a polynucleotide mediated suppression of a target gene expression in the plant cell. In general, effective organosilicone compounds include, but are not limited to, compounds that can comprise: i) a trisiloxane head group that is covalently linked to, ii) an alkyl linker including, but not limited to, an n-propyl linker, that is covalently linked to, iii) a poly glycol chain, that is covalently linked to, iv) a terminal group. Trisiloxane head groups of such effective organosilicone compounds include, but are not limited to, heptamethyltrisiloxane. Alkyl linkers can include, but are not limited to, an n-propyl linker. Poly glycol chains include, but are not limited to, polyethylene glycol or polypropylene glycol. Poly glycol chains can comprise a mixture that provides an average chain length "n" of about "7.5". In certain embodiments, the average chain length "n" can

vary from about 5 to about 14. Terminal groups can include, but are not limited to, alkyl groups such as a methyl group. Effective organosilicone compounds are believed to include, but are not limited to, trisiloxane ethoxylate surfactants or polyalkylene oxide modified heptamethyl trisiloxane.



(Compound I: polyalkyleneoxide heptamethyltrisiloxane, average n=7.5).

One organosilicone compound believed to be ineffective comprises the formula:



[0075] In certain embodiments, an organosilicone preparation that comprises an organosilicone compound comprising a trisiloxane head group is used in the methods and compositions provided herein. In certain embodiments, an organosilicone preparation that comprises an organosilicone compound comprising a heptamethyltrisiloxane head group is used in the methods and compositions provided herein. In certain embodiments, an organosilicone composition that comprises Compound I is used in the methods and compositions provided herein. In certain embodiments, an organosilicone composition that comprises Compound I is used in the methods and compositions provided herein. In certain embodiments of the methods and compositions provided herein, a composition that comprises a polynucleotide molecule and one or more effective organosilicone compound in the range of about 0.015 to about 2 percent by weight (wt percent) (*e. g.*, about 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04, 0.045, 0.05, 0.055, 0.06, 0.065, 0.07, 0.075, 0.08, 0.085, 0.09, 0.095, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.5 wt percent) is used or provided.

[0076] In certain embodiments, the polynucleotide compositions that comprise an organosilicone preparation can comprise a salt such as ammonium chloride, tetrabutylphosphonium bromide, and/or ammonium sulfate. Ammonium chloride, tetrabutylphosphonium bromide, and/or ammonium sulfate can be provided in the polynucleotide composition at a concentration of about 0.5% to about 5% (w/v). An ammonium chloride, tetrabutylphosphonium bromide, and/or ammonium sulfate concentration of about 1% to about 3%, or about 2% (w/v) can also be used in the polynucleotide compositions that comprise an organosilicone preparation. In certain embodiments, the polynucleotide compositions can comprise an ammonium salt at a concentration greater or equal to 300 millimolar. In certain embodiments, the polynucleotide compositions that comprise an organosilicone preparation can comprise ammonium sulfate at concentrations from about 80 to about 1200 mM or about 150 mM to about 600 mM.

[0077] In certain embodiments, the polynucleotide compositions can also comprise a phosphate salt. Phosphate salts used in the compositions include, but are not limited to, calcium, magnesium, potassium, or sodium phosphate salts. In certain embodiments, the polynucleotide compositions can comprise a phosphate salt at a concentration of at least about 5 millimolar, at least about 10 millimolar, or at least about 20 millimolar. In certain embodiments, the polynucleotide compositions will comprise a phosphate salt in a range of about 1mM to about 25mM or in a range of about 5mM to about 25mM. In certain embodiments, the polynucleotide compositions can comprise sodium phosphate at a concentration of at least about 5 millimolar, at least about 10 millimolar, or at least about 20 millimolar. In certain embodiments, the polynucleotide compositions can comprise sodium phosphate at a concentration of about 5 millimolar, about 10 millimolar, or about 20 millimolar. In certain embodiments, the polynucleotide compositions will comprise a sodium phosphate salt in a range of about 10mM to about 160mM or in a range of about 20mM to about 40mM. In certain embodiments, the polynucleotide compositions can comprise a sodium phosphate buffer at a pH of about 6.8.

[0078] In certain embodiments, other useful transfer agents or adjuvants to transfer agents that can be used in polynucleotide compositions provided herein include surfactants and/or effective molecules contained therein. Surfactants and/or effective molecules contained therein include, but are not limited to, sodium or lithium salts of fatty acids (such as tallow or tallowamines or phospholipids) and organosilicone surfactants. In certain embodiments, the polynucleotide compositions that comprise a transfer agent are formulated with counter-ions or other molecules that are known to associate with nucleic acid molecules. Illustrative

examples include, but are not limited to, tetraalkyl ammonium ions, trialkyl ammonium ions, sulfonium ions, lithium ions, and polyamines such as spermine, spermidine, or putrescine. In certain embodiments, the polynucleotide compositions are formulated with a non-polynucleotide herbicide. Non-polynucleotide herbicidal molecules include, but are not limited to, glyphosate, auxin-like benzoic acid herbicides including dicamba, chloramben and TBA, glufosinate, auxin-like herbicides including phenoxy carboxylic acid herbicide, pyridine carboxylic acid herbicide, quinoline carboxylic acid herbicide, pyrimidine carboxylic acid herbicide, and benazolin-ethyl herbicide, sulfonylureas, imidazolinones, bromoxynil, delapon, cyclohezanedione, protoporphyrionogen oxidase inhibitors, and 4-hydroxyphenyl-pyruvate-dioxygenase inhibiting herbicides.

[0079] In certain embodiments, the polynucleotides used in the compositions that are essentially identical or essentially complementary to the MLO target gene or transcript will comprise the predominant nucleic acid in the composition. Thus in certain embodiments, the polynucleotides that are essentially identical or essentially complementary to the target gene or transcript will comprise at least about 50%, 75%, 95%, 98%, or 100% of the nucleic acids provided in the composition by either mass or molar concentration. However, in certain embodiments, the polynucleotides that are essentially identical or essentially complementary to the target gene or transcript can comprise at least about 1% to about 50%, about 10% to about 50%, about 20% to about 50%, or about 30% to about 50% of the nucleic acids provided in the composition by either mass or molar concentration. Also provided are compositions where the polynucleotides that are essentially identical or essentially complementary to the target gene or transcript can comprise at least about 1% to 100%, about 10% to 100%, about 20% to about 100%, about 30% to about 50%, or about 50% to a 100% of the nucleic acids provided in the composition by either mass or molar concentration.

[0080] Polynucleotides comprising ssDNA, dsDNA, ssRNA, dsRNA, or RNA/DNA hybrids that are essentially identical or complementary to certain plant target genes or transcripts and that can be used in compositions containing transfer agents that include, but are not limited to, organosilicone preparations, to suppress those target genes when topically applied to plants are disclosed in co-assigned U.S. Patent Application No. 13/042856. Various polynucleotide herbicidal molecules, compositions comprising those polynucleotide herbicidal molecules and transfer agents that include, but are not limited to, organosilicone preparations, and methods whereby herbicidal effects are obtained by the topical application of such compositions to plants are also disclosed in co-assigned U.S. Patent Application No. 13/042,856, and those polynucleotide herbicidal molecules, compositions, and methods are

incorporated herein by reference in their entireties. Genes encoding proteins that can provide tolerance to an herbicide and/or that are targets of a herbicide are collectively referred to herein as "herbicide target genes". Herbicide target genes include, but are not limited to, a 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), a glyphosate oxidoreductase (GOX), a glyphosate decarboxylase, a glyphosate-N-acetyl transferase (GAT), a dicamba monooxygenase, a phosphinothricin acetyltransferase, a 2,2- dichloropropionic acid dehalogenase, an acetohydroxyacid synthase, an acetolactate synthase, a haloarylnitrilase, an acetyl-coenzyme A carboxylase (ACCase), a dihydropteroate synthase, a phytoene desaturase (PDS), a protoporphyrin IX oxygenase (PPO), a hydroxyphenylpyruvate dioxygenase (HPPD), a para-aminobenzoate synthase, a glutamine synthase, a cellulose synthase, a beta tubulin, and a serine hydroxymethyltransferase gene. The effects of applying certain compositions comprising polynucleotides that are essentially identical or complementary to certain herbicide target genes and transfer agents on plants containing the herbicide target genes was shown to be potentiated or enhanced by subsequent application of an herbicide that targets the same gene as the polynucleotide in co-assigned U.S. Patent Application No. 13/042,856. For example, compositions comprising polynucleotides targeting the EPSPS herbicide target gene were potentiated by glyphosate in experiments disclosed in co-assigned U.S. Patent Application No. 13/042,856.

[0081] In certain embodiments of the compositions and methods disclosed herein, the composition comprising a polynucleotide and a transfer agent can thus further comprise a second polynucleotide comprising at least 19 contiguous nucleotides that are essentially identical or essentially complementary to a transcript to a protein that confers resistance to a herbicide. In certain embodiments, the second polynucleotide does not comprise a polynucleotide that is essentially identical or essentially complementary to a transcript encoding a protein of a target plant that confers resistance to said herbicidal molecule. Thus, in an exemplary and non-limiting embodiment, the second polynucleotide could be essentially identical or essentially complementary to a transcript encoding a protein that confers resistance to a herbicide in a weed (such as an EPSPS encoding transcript) but would not be essentially identical or essentially complementary to a transcript encoding a protein that confers resistance to that same herbicide in a crop plant.

[0082] In certain embodiments, the polynucleotide compositions that comprise a transfer agent can comprise glycerin. Glycerin can be provided in the composition at a concentration of about 0.1% to about 1% (w/v or v/v). A glycerin concentration of about 0.4% to about

0.6%, or about 0.5% (w/v or v/v) can also be used in the polynucleotide compositions that comprise a transfer agent.

[0083] In certain embodiments, the polynucleotide compositions that comprise a transfer agent can further comprise organic solvents. Such organic solvents include, but are not limited to, DMSO, DMF, pyridine, N-pyrrolidine, hexamethylphosphoramide, acetonitrile, dioxane, polypropylene glycol, other solvents miscible with water or that will dissolve phosphonucleotides in non-aqueous systems (such as is used in synthetic reactions).

[0084] In certain embodiments, the polynucleotide compositions that comprise a transfer agent can further comprise naturally derived or synthetic oils with or without surfactants or emulsifiers. Such oils include, but are not limited to, plant-sourced oils, crop oils (such as those listed in the 9th Compendium of Herbicide Adjuvants, publicly available on line at www.herbicide.adjuvants.com), paraffinic oils, polyol fatty acid esters, or oils with short-chain molecules modified with amides or polyamines such as polyethyleneimine or N-pyrrolidine.

[0085] In aspects of the invention, methods include one or more applications of the composition comprising a polynucleotide and a transfer agent or one or more effective components contained therein. In certain embodiments of the methods, one or more applications of a transfer agent or one or more effective components contained therein can precede one or more applications of the composition comprising a polynucleotide and a transfer agent. In embodiments where a transfer agent and/or one or more effective molecules contained therein is used either by itself as a pre-treatment or as part of a composition that includes a polynucleotide, embodiments of the polynucleotide molecules are double-stranded RNA polynucleotides, single-stranded RNA polynucleotides, double-stranded DNA polynucleotides, single-stranded DNA polynucleotides, chemically modified RNA or DNA polynucleotides or mixtures thereof.

[0086] Compositions and methods of the invention are useful for modulating or suppressing the expression of an endogenous Mildew Resistance Locus O (MLO) target gene or transgenic Mildew Resistance Locus O (MLO) target gene in a plant cell or plant. In certain embodiments of the methods and compositions provided herein, expression of MLO target genes can be suppressed completely, partially and/or transiently to result in an improvement in in fungal disease resistance and/or nematode resistance. In various embodiments, a Mildew Resistance Locus O (MLO) target gene includes coding (protein-coding or translatable) sequence, non-coding (non-translatable) sequence, or both coding and non-coding sequence. Compositions of the invention can include polynucleotides designed to

target multiple Mildew Resistance Locus O (MLO) genes, or multiple segments of one or more Mildew Resistance Locus O (MLO) genes. The target gene can include multiple consecutive segments of a target Mildew Resistance Locus O (MLO) gene, multiple non-consecutive segments of a Mildew Resistance Locus O (MLO) target gene, multiple alleles of a target gene, or multiple Mildew Resistance Locus O (MLO) target genes from one or more species. Mildew Resistance Locus O (MLO) target genes include, but are not limited to, the endogenous Mildew Resistance Locus O (MLO) plant genes of SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79. Mildew Resistance Locus O (MLO) target genes include, but are not limited to, Mildew Resistance Locus O (MLO) plant genes that encode proteins that are orthologous to the proteins of SEQ ID NO: 1-28. Mildew Resistance Locus O (MLO) target genes include, but are not limited to, Mildew Resistance Locus O (MLO) plant genes that encode the proteins of SEQ ID NO: 1-28.

[0087] Target genes and plants containing those target genes can be obtained from: i) row crop plants including, but are not limited to, corn, soybean, cotton, canola, sugar beet, alfalfa, sugarcane, rice, and wheat; ii) vegetable plants including, but not limited to, tomato, potato, sweet pepper, hot pepper, melon, watermelon, cucumber, eggplant, cauliflower, broccoli, lettuce, spinach, onion, peas, carrots, sweet corn, Chinese cabbage, leek, fennel, pumpkin, squash or gourd, radish, Brussels sprouts, tomatillo, garden beans, dry beans, or okra; iii) culinary plants including, but not limited to, basil, parsley, coffee, or tea; iv) fruit plants including but not limited to apple, pear, cherry, peach, plum, apricot, banana, plantain, table grape, wine grape, citrus, avocado, mango, or berry; v) a tree grown for ornamental or commercial use, including, but not limited to, a fruit or nut tree; or, vi) an ornamental plant (e. g., an ornamental flowering plant or shrub or turf grass). The methods and compositions provided herein can also be applied to plants produced by a cutting, cloning, or grafting process (i. e., a plant not grown from a seed) include fruit trees and plants that include, but are not limited to, citrus, apples, avocados, tomatoes, eggplant, cucumber, melons, watermelons, and grapes as well as various ornamental plants. Such row crop, vegetable, culinary, fruit, tree, or ornamental plants exhibiting improvements in fungal disease resistance and/or nematode resistance that result from suppressing Mildew Resistance Locus O (MLO) gene expression are provided herein. Such row crop, vegetable, culinary, fruit, tree, or ornamental plant parts or processed plant products exhibiting improvements in fungal disease resistance and/or nematode resistance that result from suppressing Mildew Resistance Locus O (MLO) gene expression are also provided herein. Such plant parts can include, but

are not limited to, flowers, stems, tubers, fruit, anthers, meristems, ovules, pollen, leaves, or seeds. Such processed plant products obtained from the plant parts can include, but are not limited to, a meal, a pulp, a feed, or a food product.

[0088] An aspect of the invention provides a method for modulating or suppressing expression of an Mildew Resistance Locus O (MLO) gene in a plant including (a) conditioning of a plant to permeation by polynucleotides and (b) treatment of the plant with the polynucleotide molecules, wherein the polynucleotide molecules include at least one segment of 18 or more contiguous nucleotides cloned from or otherwise identified from the Mildew Resistance Locus O (MLO) target gene in either anti-sense or sense orientation, whereby the polynucleotide molecules permeate the interior of the plant and induce modulation of the target gene. The conditioning and polynucleotide application can be performed separately or in a single step. When the conditioning and polynucleotide application are performed in separate steps, the conditioning can precede or can follow the polynucleotide application within minutes, hours, or days. In some embodiments more than one conditioning step or more than one polynucleotide molecule application can be performed on the same plant. In embodiments of the method, the segment can be cloned or identified from (a) coding (protein-encoding), (b) non-coding (promoter and other gene related molecules), or (c) both coding and non-coding parts of the Mildew Resistance Locus O (MLO) target gene. Non-coding parts include DNA, such as promoter regions or the RNA transcribed by the DNA that provide RNA regulatory molecules, including but not limited to: introns, 5' or 3' untranslated regions, and microRNAs (miRNA), *trans*-acting siRNAs, natural anti-sense siRNAs, and other small RNAs with regulatory function or RNAs having structural or enzymatic function including but not limited to: ribozymes, ribosomal RNAs, t-RNAs, aptamers, and riboswitches. In certain embodiments where the polynucleotide used in the composition comprises a promoter sequence essentially identical to, or essentially complementary to, at least 18 contiguous nucleotides of the promoter of the endogenous target gene, the promoter sequence of the polynucleotide is not operably linked to another sequence that is transcribed from the promoter sequence.

[0089] Compositions comprising a polynucleotide and a transfer agent provided herein can be topically applied to a plant or plant part by any convenient method, e.g., spraying or coating with a powder, or with a liquid composition comprising any of an emulsion, suspension, or solution. Such topically applied sprays or coatings can be of either all or of any a portion of the surface of the plant or plant part. Similarly, compositions that comprise a transfer agent or other pre-treatment can in certain embodiments be applied to the plant or

plant part by any convenient method, e. g., spraying or wiping a solution, emulsion, or suspension. Compositions comprising a polynucleotide and a transfer agent provided herein can be topically applied to plant parts that include, but are not limited to, flowers, stems, tubers, meristems, ovules, fruit, anthers, pollen, leaves, or seeds.

[0090] Application of compositions comprising a polynucleotide and a transfer agent to seeds is specifically provided herein. Seeds can be contacted with such compositions by spraying, misting, immersion, and the like.

[0091] In certain embodiments, application of compositions comprising a polynucleotide and a transfer agent to plants, plant parts, or seeds in particular can provide for an improvement in fungal disease resistance and/or nematode resistance in progeny plants, plant parts, or seeds derived from those treated plants, plant parts, or seeds. In certain embodiments, progeny plants, plant parts, or seeds derived from those treated plants, plant parts, or seeds will exhibit an improvement in fungal disease resistance and/or nematode resistance that result from suppressing expression of an MLO gene. In certain embodiments, the methods and compositions provided herein can provide for an improvement in fungal disease resistance and/or nematode resistance in progeny plants or seeds as a result of epigenetically inherited suppression of MLO expression. In certain embodiments, such progeny plants exhibit an improvement in fungal disease resistance and/or nematode resistance from epigenetically inherited suppression of MLO gene expression that is not caused by a transgene where the polynucleotide is operably linked to a promoter, a viral vector, or a copy of the polynucleotide that is integrated into a non-native location in the chromosomal DNA of the plant. Without seeking to be limited by theory, progeny plants or seeds derived from those treated plants, plant parts, or seeds can exhibit an improvement in an improvement in fungal disease resistance and/or nematode resistance through an epigenetic mechanism that provides for propagation of an epigenetic condition where suppression of MLO gene expression occurs in the progeny plants, plant parts, or plant seeds. In certain embodiments, progeny plants or seeds exhibiting an improvement in fungal disease resistance and/or nematode resistance as a result of epigenetically inherited suppression of MLO gene expression can also exhibit increased methylation, and in particular, increased methylation of cytosine residues, in the endogenous MLO gene of the plant. Plant parts, including seeds, of the progeny plants that exhibit an improvement in an improvement in fungal disease resistance and/or nematode resistance as a result of epigenetically inherited suppression of MLO gene expression, can also in certain embodiments exhibit increased methylation, and in particular, increased methylation of cytosine residues, in the endogenous MLO gene. In certain embodiments,

DNA methylation levels in DNA encoding the endogenous MLO gene can be compared in plants that exhibit an improvement in fungal disease resistance and/or nematode resistance and control plants that do not exhibit an improvement in fungal disease resistance and/or nematode resistance to correlate the presence of the an improvement in fungal disease resistance and/or nematode resistance to epigenetically inherited suppression of MLO gene expression and to identify plants that comprise the epigenetically inherited improvement in fungal disease resistance and/or nematode resistance.

[0092] Various methods of spraying compositions on plants or plant parts can be used to topically apply to a plant surface a composition comprising a polynucleotide that comprises a transfer agent. In the field, a composition can be applied with a boom that extends over the crops and delivers the composition to the surface of the plants or with a boomless sprayer that distributes a composition across a wide area. Agricultural sprayers adapted for directional, broadcast, or banded spraying can also be used in certain embodiments. Sprayers adapted for spraying particular parts of plants including, but not limited to, leaves, the undersides of leaves, flowers, stems, male reproductive organs such as tassels, meristems, pollen, ovules, and the like can also be used. Compositions can also be delivered aerially, such as by a crop dusting airplane. In certain embodiments, the spray can be delivered with a pressurized backpack sprayer calibrated to deliver the appropriate rate of the composition. In certain embodiments, such a backpack sprayer is a carbon dioxide pressurized sprayer with a 11015 flat fan or equivalent spray nozzle with a customized single nozzle assembly (to minimize waste) at a spray pressure of about 0.25 MPa and/or any single nozzle sprayer providing an effective spray swath of 60 cm above the canopy of 3 to 12 inch tall growing plants can be used. Plants in a greenhouse or growth chamber can be treated using a track sprayer or laboratory sprayer with a 11001XR or equivalent spray nozzle to deliver the sample solution at a determined rate. An exemplary and non-limiting rate is about 140 L/ha at about 0.25 MPa pressure.

[0093] In certain embodiments, it is also contemplated that a plant part can be sprayed with the composition comprising a polynucleotide that comprises a transfer agent. Such plant parts can be sprayed either pre-or post-harvest to provide for an improvement in fungal disease resistance and/or nematode resistance in the plant part that results from suppression of MLO gene expression. Compositions can be topically applied to plant parts attached to a plant by a spray as previously described. Compositions can be topically applied to plant parts that are detached from a plant by a spray as previously described or by an alternative method. Alternative methods for applying compositions to detached parts include, but are not limited

to, passing the plant parts through a spray by a conveyor belt or trough, or immersing the plant parts in the composition.

[0094] Compositions comprising polynucleotides and transfer agents can be applied to plants or plant parts at one or more developmental stages as desired and/or as needed. Application of compositions to pre-germination seeds and/or to post-germination seedlings is provided in certain embodiments. Seeds can be treated with polynucleotide compositions provided herein by methods including, but not limited to, spraying, immersion, or any process that provides for coating, imbibition, and/or uptake of the polynucleotide composition by the seed. Seeds can be treated with polynucleotide compositions using seed batch treatment systems or continuous flow treatment systems. Seed coating systems are at least described in U.S. Patent Numbers 6,582,516, 5,891,246, 4,079,696, and 4,023,525. Seed treatment can also be effected in laboratory or commercial scale treatment equipment such as a tumbler, a mixer, or a pan granulator. A polynucleotide composition used to treat seeds can contain one or more other desirable components including, but not limited to liquid diluents, binders to serve as a matrix for the polynucleotide, fillers for protecting the seeds during stress conditions, and plasticizers to improve flexibility, adhesion and/or spreadability of the coating. In addition, for oily polynucleotide compositions containing little or no filler, drying agents such as calcium carbonate, kaolin or bentonite clay, perlite, diatomaceous earth or any other adsorbent material can be added. Use of such components in seed treatments is described in U.S. Patent No. 5,876,739. Additional ingredients can be incorporated into the polynucleotide compositions used in seed treatments. Such ingredients include but are not limited to: conventional sticking agents, dispersing agents such as methylcellulose (Methocel A15LV or Methocel A15C, for example, serve as combined dispersant/sticking agents for use in seed treatments), polyvinyl alcohol (e.g., Elvanol 51-05), lecithin (e.g., Yelkinol P), polymeric dispersants (e.g., polyvinylpyrrolidone/vinyl acetate PVPNA S-630), thickeners (e.g., clay thickeners such as Van Gel B to improve viscosity and reduce settling of particle suspensions), emulsion stabilizers, surfactants, antifreeze compounds (e.g., urea), dyes, colorants, and the like that can be combined with compositions comprising a polynucleotide and a transfer agent. Further ingredients used in compositions that can be applied to seeds can be found in McCutcheon's, vol. 1, "Emulsifiers and Detergents," MC Publishing Company, Glen Rock, N.J., U.S.A., 1996 and in McCutcheon's, vol. 2, "Functional Materials," MC Publishing Company, Glen Rock, N.J., U.S.A., 1996. Methods of applying compositions to seeds and pesticidal compositions that can be used to treat seeds are

described in US Patent Application publication 20080092256, which is incorporated herein by reference in its entirety.

[0095] Application of the compositions in early, mid-, and late vegetative stages of plant development is provided in certain embodiments. Application of the compositions in early, mid-and late reproductive stages is also provided in certain embodiments. Application of the compositions to plant parts at different stages of maturation is also provided.

[0096] The following examples are included to demonstrate examples of certain preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow represent approaches the inventors have found function well in the practice of the invention, and thus can be considered to constitute examples of preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

EXAMPLES

Example 1. Polynucleotides of the invention related to the MLO target gene sequences.

[0097] The amino acid sequences of proteins encoded by targeted MLO genes and transcripts are provided in Table 2 with reference to SEQ ID NOs. 1-27 of the sequence listing. Such protein sequences can be used to identify orthologous MLO genes and transcripts from other plants not provided herewith. Such orthologous genes and their transcripts can then serve as targets of polynucleotides provided herein or as a source of polynucleotides that are specifically designed to target the orthologous genes or transcripts.

[0098] The target MLO polynucleotide molecule at least occurs in the genome of plants provided in Table 2. The MLO genes provided in Table 3, or their corresponding transcripts, can be used as targets of polynucleotide compositions comprising a polynucleotide of at least 18 contiguous nucleotides that are essentially identical or essentially complementary to those genes or transcripts. The proteins and genes respectively provided in Tables 2 and 3, or sequences contained within those proteins or genes can also be used to identify orthologous MLO genes from plants not listed in Tables 2 and 3. Such orthologous genes and their transcripts can then serve as targets of polynucleotides provided herein or as a source of polynucleotides that are specifically designed to target the orthologous genes or transcripts.

[0099] Table 2. Target MLO gene protein sequences

SEQ ID NO:1	*Hordeum vulgare 1*	MLO-like protein from barley
SEQ ID NO:2	*Sorghum bicolor 2*	MLO-like protein from sorghum
SEQ ID NO:3	*Zea mays 3*	MLO-like protein from corn
SEQ ID NO:4	*Gossypium hirsutum*	MLO-like protein from cotton
SEQ ID NO:5	*Glycine max 3*	MLO-like protein from soybeans
SEQ ID NO:6	*Glycine max 4*	MLO-like protein from soybeans
SEQ ID NO:7	*Cucumis sativus 2*	MLO-like protein from cucumber
SEQ ID NO:8	*Cucumis sativus 4*	MLO-like protein from cucumber
SEQ ID NO:9	*Cucumis sativus 5*	MLO-like protein from cucumber
SEQ ID NO:10	*Cucumis sativus 6*	MLO-like protein from cucumber
SEQ ID NO:11	*Vitis vinifera 1*	MLO-like protein from grape
SEQ ID NO:12	*Vitis vinifera 7*	MLO-like protein from grape
SEQ ID NO:13	*Arabidopsis thaliana 3*	MLO-like protein from *Arabidopsis*
SEQ ID NO:14	*Arabidopsis thaliana 9*	MLO-like protein from *Arabidopsis*
SEQ ID NO:15	*Arabidopsis thaliana 4*	MLO-like protein from *Arabidopsis*
SEQ ID NO:16	*Arabidopsis thaliana 8*	MLO-like protein from *Arabidopsis*
SEQ ID NO:17	*Arabidopsis thaliana 7*	MLO-like protein from *Arabidopsis*
SEQ ID NO:18	*Arabidopsis thaliana 2*	MLO-like protein from *Arabidopsis*
SEQ ID NO:19	*Arabidopsis thaliana 10*	MLO-like protein from *Arabidopsis*
SEQ ID NO:20	*Arabidopsis thaliana 11*	MLO-like protein from *Arabidopsis*
SEQ ID NO:21	*Arabidopsis thaliana 6*	MLO-like protein from *Arabidopsis*
SEQ ID NO:22	*Arabidopsis thaliana 13*	MLO-like protein from *Arabidopsis*
SEQ ID NO:23	*Arabidopsis thaliana 14*	MLO-like protein from *Arabidopsis*
SEQ ID NO:24	*Arabidopsis thaliana 12*	MLO-like protein from *Arabidopsis*
SEQ ID NO:25	*Arabidopsis thaliana 1*	MLO-like protein from *Arabidopsis*
SEQ ID NO:26	*Arabidopsis thaliana 15*	MLO-like protein from *Arabidopsis*
SEQ ID NO:27	*Arabidopsis thaliana 5*	MLO-like protein from *Arabidopsis*

[00100] Table 3. Target gene sequences

SEQ ID NO:28	*Hordeum vulgare*	MLO protein from barley
SEQ ID NO:29	*Hordeum vulgare*	MLO cDNA from barley
SEQ ID NO:30	*Cucumis sativus 1*	MLO-like protein from cucumber
SEQ ID NO:31	*Cucumis sativus 1*	MLO-like cDNA from cucumber
SEQ ID NO:32	*Cucumis sativus 3*	MLO-like protein from cucumber
SEQ ID NO:33	*Cucumis sativus 3*	MLO-like cDNA from cucumber
SEQ ID NO:34	*Cucumis sativus 7*	MLO-like protein from cucumber
SEQ ID NO:35	*Cucumis sativus 7*	MLO-like cDNA from cucumber
SEQ ID NO:36	*Cucumis sativus 8*	MLO-like protein from cucumber
SEQ ID NO:37	*Cucumis sativus 8*	MLO-like cDNA from cucumber
SEQ ID NO:38	*Lactuca sativa*	MLO-like protein from lettuce
SEQ ID NO:39	*Lactuca sativa*	MLO-like cDNA from lettuce
SEQ ID NO:40	*Pisum sativum 1*	MLO-like protein from pea
SEQ ID NO:41	*Pisum sativum 1*	MLO-like cDNA from pea
SEQ ID NO:42	*Medicago truncatula*	MLO-like protein from barrel clover
SEQ ID NO:43	*Medicago truncatula*	MLO-like cDNA from barrel clover
SEQ ID NO:44	*Glycine max 1*	MLO-like protein from soybean

SEQ ID NO:45	*Glycine max 1*	MLO-like cDNA from soybean
SEQ ID NO:46	*Glycine max 2*	MLO-like protein from soybean
SEQ ID NO:47	*Glycine max 2*	MLO-like cDNA from soybean
SEQ ID NO:48	*Capsicum annuum*	MLO-like protein from pepper
SEQ ID NO:49	*Capsicum annuum*	MLO-like cDNA from pepper
SEQ ID NO:50	*Solanum lycopersicum 1*	MLO-like protein from tomato
SEQ ID NO:51	*Solanum lycopersicum 1*	MLO-like cDNA from tomatos
SEQ ID NO:52	*Solanum lycopersicum 2*	MLO-like protein from tomato
SEQ ID NO:53	*Solanum lycopersicum 2*	MLO-like cDNA from tomato
SEQ ID NO:54	*Triticum aestivum*	MLO-like protein from wheat
SEQ ID NO:55	*Triticum aestivum*	MLO-like cDNA from wheat
SEQ ID NO:56	*Triticum aestivum 1*	MLO-like protein from wheat
SEQ ID NO:57	*Triticum aestivum 1*	MLO-like cDNA from wheat
SEQ ID NO:58	*Triticum aestivum 2*	MLO-like protein from wheat
SEQ ID NO:59	*Triticum aestivum 2*	MLO-like cDNA from wheat
SEQ ID NO:60	*Vitis vinifera 17*	MLO-like protein from grape
SEQ ID NO:61	*Vitis vinifera 17*	MLO-like cDNA from grape
SEQ ID NO:62	*Vitis vinifera 13*	MLO-like protein from grape
SEQ ID NO:63	*Vitis vinifera 13*	MLO-like cDNA from grape
SEQ ID NO:64	*Vitis vinifera 6*	MLO-like protein from grape
SEQ ID NO:65	*Vitis vinifera 6*	MLO-like cDNA from grape
SEQ ID NO:66	*Vitis vinifera 3*	MLO-like protein from grape
SEQ ID NO:67	*Vitis vinifera 3*	MLO-like cDNA from grape
SEQ ID NO:68	*Zea mays 1*	MLO-like protein from corn
SEQ ID NO:69	*Zea mays 1*	MLO-like cDNA from corn
SEQ ID NO:70	*Sorghum bicolor 1*	MLO-like protein from sorghum
SEQ ID NO:71	*Sorghum bicolor 1*	MLO-like cDNA from sorghum
SEQ ID NO:72	*Oryza sativa japonica 1*	MLO-like protein from rice
SEQ ID NO:73	*Oryza sativa japonica 1*	MLO-like cDNA from rice
SEQ ID NO:74	*Oryza sativa japonica 2*	MLO-like protein from rice
SEQ ID NO:75	*Oryza sativa japonica 2*	MLO-like cDNA from rice
SEQ ID NO:76	*Oryza sativa japonica 3*	MLO-like protein from rice
SEQ ID NO:77	*Oryza sativa japonica 3*	MLO-like cDNA from rice
SEQ ID NO:78	*Oryza sativa indica*	MLO-like protein from rice
SEQ ID NO:79	*Oryza sativa indica*	MLO-like cDNA from rice

[00101] The sequence listing contains the target MLO DNA sequences from the indicated plant species of Table 3. For each gene having a DNA sequence provided in the sequence listing and listed in Table 3, polynucleotides such as single stranded or double stranded DNA or RNA fragments in sense and/or antisense orientation will be mixed with an organosilicone preparation. These compositions will be topically applied to plants to effect expression of the target genes in the specified plant to obtain the plants that exhibit disease resistance. In particular, plants that are resistant to powdery mildew, downy mildew, and/or

rust infection and/or nematodes will be obtained through the application of such compositions.

Example 2. Identification of Orthologous MLO genes

[00102] A bootstrapped phylogenetic tree is provided in Figure 1. The phylogenetic tree shown in Figure 1 was generated with ClustalX version 2.0.12 using default parameters. First, a multiple sequence alignment was generated with ClustalX using the default parameters, except that iteration at each alignment step was done. The bootstrapped phylogenetic tree was then assembled using the Neighbor-Joining method. The protein sequences disclosed in SEQ ID NOS: 1-27 are a useful basis set for determining whether MLO-like proteins are functional orthologs and likely to be useful targets for suppression in order to control fungal diseases such as powdery mildew, downy mildew and rust infections. Specifically, MLO homologs useful for the control of powdery mildews fall into one of two clades: 1) the clade with A. thaliana MLO2 (SEQ ID NO: 18), such as A. thaliana MLO6 (SEQ ID NO: 21), A. thaliana MLO12 (SEQ ID NO: 24) and Pisum sativum MLO1 (SEQ ID NO: 40) but not A. thaliana MLO11 (SEQ ID NO: 20) or 2) in the clade with Hordeum vulgare MLO (SEQ ID NO: 28), Zea mays MLO1 (SEQ ID NO: 68) and Sorghum bicolor MLO1 (SEQ ID NO: 70) but not Sorghum bicolor MLO2 (SEQ ID NO: 2)

[00103] The sequences disclosed in SEQ ID NO: 1 through 79, along with the phylogentic method for functional assignment described above, can be used to efficiently identify and clone MLO homologs useful for the control of pathogens causing powdery mildews, downy mildews or rusts, from other plant species not explicitly described herein.

Example 3. Polynucleotides that can be used to reduce MLO expression in various plants

[00104] Examples of polynucleotides that can be used to reduce expression of MLO genes in various plants is provided herewith as SEQ ID NOS: 80 - 195. The SEQ ID NOS: 80 - 195 describe sense/antisense double stranded RNA targeted to the coding regions of Mildew Resistance Locus O (MLO) sequences from a variety of dicot and monocot plants and are useful for downregulating MLO expression using methods described herein. Other regions of MLO genes can also be targeted to modify expression including coding regions and/or promoter regions. Polynucleotides that can be used to reduce MLO expression include sense/antisense dsRNA, antisense RNA, sense or antisense ssDNA as well as sense/antisense double stranded DNA. For example, a polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31,

33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79 can be used to downregulate expression of those MLO genes.

Example 4. Topical Polynucleotide application and powdery mildew testing methods

[00105] Barley seeds are planted in 2 inch pots in the greenhouse. Five days later, barley seedlings are sprayed with polynucleotides such as ssDNA and/or dsRNA polynucleotides directed to the promoter and/or the coding region of a target gene of interest. For example, polynucleotides directed to MLO include polynucleotides that comprise at least 18 contiguous nucleotides that are essentially identical or complementary to SEQ ID NO:28 or 29. Other examples of polynucleotides that target MLO for down regulation include polynucleotides of SEQ ID NO:80 to 83. A nucleotide solution of 6-20nm of each ssDNA or 0.5-4 nm dsRNA, 0.1 to 0.3 % L77 silwet, 50mM $NaPO_4$ in a final volume of 40 microliters of water is applied. Two to 4 days post spraying, seedlings will be infected with dry spores of barley powdery mildew (*Blumeria graminis* f. sp. *hordei*) and 7 days post infection, disease development is determined by scoring for the percentage of leaf area covered with powdery mildew.

[00106] Cucumber seeds are planted in 3-inch square pots and thinned to one plant per pot after emergence. When the first true leaf is fully expanded and the second leaf is opening, a polynucleotide solution, such as ssDNA and/or dsRNA polynucleotides directed to the promoter and/or the coding region of a target gene of interest, is applied to the first true leaf or the cotyledons. For example, polynucleotides directed to MLO include polynucleotides that comprise at least 18 contiguous nucleotides that are essentially identical or complementary to SEQ ID NO:38 or 39. Examples of polynucleotides also include polynucleotides of SEQ ID NO:100 to 103. A nucleotide solution of 6-20nm of each ssDNA or 0.5-4 nm dsRNA, 0.1 to 0.3 % L77 Silwet, 50mM $NaPO_4$ in a final volume of 40 microliters of water is applied. Two days later the entire cucumber plant is inoculated with a shower of dry spores of cucumber powdery mildew (*Sphaerotheca fuliginea*) shaken off diseased plants. Disease severity will be evaluated on the treated leaf and succeeding leaves 10 days later and at subsequent intervals.

[00107] Tomato seeds are planted in a 3-inch square pots and thinned to one plant per pot after emergence. Two weeks old tomato seedlings are treated with 6-20nm of each ssDNA or 0.5- 4 nm dsRNA, 0.2 – 0.5% L77 silwet, 50mM $NaPO_4$, 1% ammonium sulfate in a final volume of 30 microliters of water. For example, polynucleotides directed to MLO include polynucleotides that comprise at least 18 contiguous nucleotides that are essentially identical

or complementary to SEQ ID NO:50, 51, 52, or 53. Examples of polynucleotides also include polynucleotides of SEQ ID NO:126 to 131. Two to 4 days post spraying plants are inoculated with dry spores of tomato powdery mildew (*Oidium neolycopersici*) and 13 days post infection, disease development is scored for the percentage of leaf area covered with powdery mildew.

Example 5. Protection of Barley from powdery mildew by topical polynucleotide application

[00108] Barley seeds were planted in 2 inch pots in the greenhouse. Five days later, barley seedlings were sprayed with the indicated polynucleotides or a control formulation according to either the Treatment 1 or Treatment 2 methods of Tables 4 and 5, respectively. The liquids applied to the plants are provided in Table 6 and the description of nucleic acid sequences of the ssDNA polynucleotides used is provided in Table 7. Post spraying, the seedlings were infected with dry spores of barley powdery mildew (*Blumeria graminis* f. sp. *hordei*) and 7 days post infection, disease development was scored for the percentage of leaf area covered with powdery mildew. The average leaf length was also scored. Results of this analysis are shown in Figure 2.

[00109] Table 4. Treatment 1

Treatment 1	5mM NaPO4
	0.3% Silwet
	2X5ul/leaf
	Disease infection 3 days later

[00110] Table 5. Treatment 2

Treatment 2	**5mM NaPO4**
	1%AMS
	0.2% Silwet
	2 X 7.5ul/leaf
	Disease infection 2 day later

[00111] Table 6. Liquids Tested

Liquid	trigger type	nucleotide ID #	conc	silwet		Treatment #
S	Formulation			0.30%	first leaf	Treatment 1

C	DNA GFP	GFP_as	1X12nmol	0.30%	first leaf	Treatment 1
1	DNA mlo	T4213as, T4214as, T4215as	3X12nmol	0.30%	first leaf	Treatment 1
2	DNA mlo	T4216as,T4217as,T4218as	3X12nmol	0.30%	first leaf	Treatment 1
3	DNA mlo	T4211as, T4219as, T4220as	3X36nmol	0.20%	first leaf	Treatment 2
4	DNA mlo	T4212as, T4214as, T4222as	3X36nmol	0.20%	first leaf	Treatment 2
5	Formulation			0.20%	first leaf	Treatment 2
6	DNA GFP	GFP_as	1X36nmol	0.20%	first leaf	Treatment 2

Table 7. Polynucleotides used

Target Plant and Gene	Type	Name	Sequence	SEQ ID	Length	Target
barley MLO	antisense DNA	T4211_AS	GGGGTGCTGGAGAGGCCCAGGTGG	184	24	ORF
barley MLO	antisense DNA	T4212_AS	CGACGTCTGGTGCGTGAACCGGA	185	23	ORF
barley MLO	antisense DNA	T4213_AS	CTGGTATTCCAAGGAGGTGGTCT	186	23	ORF
barley MLO	antisense DNA	T4214_AS	GATGAGGAGCAGGGATATGAAGC	187	23	ORF
barley MLO	antisense DNA	T4215_AS	ATGAGCTCCGCCTTCATCTTCTC	188	23	ORF
barley MLO	antisense DNA	T4216_AS	GGCCTTCTTGTGCCGGTGCTGGA	189	23	ORF
barley MLO	antisense DNA	T4217_AS	CTGTCCACACAAAATGCGCCATC	190	23	ORF
barley MLO	antisense DNA	T4218_AS	GTTCTGGAACAACGTCAGGTGT	191	22	ORF
barley MLO	antisense DNA	T4219_AS	GTCGGGGCGGTGGAACCAGAAG	192	22	ORF
barley MLO	antisense DNA	T4220_AS	AAAAATCTGCACTGGGGATGT	193	21	ORF
barley MLO	antisense DNA	T4221_AS	GATTTAGTCTGTGCACCGGGTGCG	194	24	ORF
barley MLO	antisense DNA	T4222_AS	AACCGGGTACATGTCCCTAGCCTC	195	24	ORF

[00112] Figure 2 shows that the percentage disease area was significantly deceased in plants treated with Silwet formulations containing the barley MLO antisense DNA polynucleotides relative to both the Silwet formulation alone or the Silwet formulation combined with a control GFP (Green Fluorescent Protein) polynucleotide (SEQ ID NO:196).

Example 6. Protection of Barley from powdery mildew by topical polynucleotide application

[00113] Barley seeds were planted in 2 inch pots in the greenhouse. Five days later, barley seedlings were sprayed with the indicated polynucleotides or a control formulation according to either the Treatment 1 or Treatment 2 methods of Tables 8 and 9, respectively. The liquids applied to the plants are provided in Table 10 and the description of nucleic acid sequences of the ssDNA polynucleotides used is provided in Table 7. Post spraying, the seedlings were infected with dry spores of barley powdery mildew (*Blumeria graminis* f. sp. *hordei*) and 7 days post infection, disease development was scored for the percentage of leaf area covered with powdery mildew. The average leaf length was also scored. Results of this analysis are shown in Table 11.

[00114] Table 8. Treatment 1

Treatment 1	**5mM NaPO4**
	1%AMS
	0.25% Silwet
	2X5ul
	Disease infection 2 days later

[00115] Table 9. Treatment 2

Treatment 2	5mM NaPO4
	1%AMS
	0.25% Silwet
	2X6ul
	Disease infection 1 day later

[00116] Table 10. Liquids Tested

Liquid	trigger type	polynucleotide ID #	Concentration of polynucleotides	Treatment #
0	0			Treatment 1
7	DNA GFP	GFP_as	40nmol	Treatment 1
8	DNA GFP	GFP_as	80nmol	Treatment 1
9	DNA mlo, antisense	T4211as,13, 15, 22	4X10nmol	Treatment 1
10	DNA mlo, antisense	T4212as, T4219as, T4220as, T4221as	4X20nmol	Treatment 1
11	DNA GFP	GFP_as	48nmol	Treatment 2
12	DNA GFP	GFP_as	96nmol	Treatment 2
13	DNA mlo, antisense	T4211as, T4215as, T4216as, T4218as	4X12nmol	Treatment 2
14	DNA mlo, antisense	T4219as, T4220as, T4221as, T4222as	4X24nmol	Treatment 2
15	0			Treatment 2

[00117] Table 11 shows that the percentage disease area was significantly decreased in plants treated with Silwet formulations containing the barley MLO antisense DNA polynucleotides relative to both the non-treated control or the Silwet formulation combined with a control GFP (Green Fluorescent Protein) polynucleotide.

[00118] Table 11. Percentage of disease area

Liquid	trigger type	R1	R2	R3	R4	R5	R6	avr	stdev
NT	NT	10	25	10	5			13	8.7
15	Blank	25	5	5	5			10	10

Liquid	trigger type	R1	R2	R3	R4	R5	R6	avr	stdev
11	DNA GFP	5	5	10	5	1	10	6	3.5
12	DNA GFP	5	1	1	5	5		3.4	2.2
13	DNA MLO	1	1	1	1	1	5	1.7	1.6
14	DNA MLO	1	1	1	5	1		1.8	1.8
7	DNA GFP	25	10	10	10	10	10	12.5	7.1
8	DNA GFP	10	5	5	5	10		5	3.5
9	DNA MLO	5	1	1	5	1		2.6	2.1
10	DNA MLO	5	5	5	5	1		4.1	1.7

R1-R6 are replicates 1 through 6.

Example 7. Topical polynucleotide application and nematode testing methods

Application of polynucleotides to leaves for nematode control

[00119] Ten day old cucumber plants grown in sand are spotted with nucleotides, either ssDNA and/or dsRNA polynucleotides, directed to the promoter and/or the coding region of a target gene of interest. A nucleotide solution of 6-20nm of each ssDNA or 0.5-1 nm dsRNA, 0.1% L77 silwet, 50mM NaPO4 in a final volume of 40uL water is applied. Two cotyledon or leaves are spotted with 20uL of the nucleotide solution for a total of 40uL per plant. After 6-24 hours, 1000 vermiform eggs or 1000 J2 *Meloidogyne incognita* (RKN) are inoculated into each pot. Watering of the test plants is then restricted to only water as needed to prevent wilt for a period of 24 hours. After the 24 hour restricted watering, normal sub-irrigation watering is done for the duration of the test. Cucumber plants are harvested approximately 14 days after inoculation by washing sand off the roots. A root gall rating and visual phytotoxicity rating is assigned using the following scales: Gall rating scale (Gall: % root mass galled): 0 = 0-5%; 1 = 6-20%; 2 = 21-50%; and 3 = 51-100%. Visual phytotoxicity scale is also assigned (Vis. tox; visual reduction in root mass compared to the control): rs1 = mild stunting; rs2 = moderate stunting; rs3 = severe stunting.

[00120] Experiments in soybeans using soy cyst nematodes (SCN) are similar to the cucumber RKN assay except for the following changes. Soybean seeds are planted in 100% sand in two inch square plastic pots. The polynucleotide solution is applied when the soybeans show the first trifoliate beginning to emerge, about 10 to 12 days after planting. At

least six hours after application of the polynucleotide solution, the nematode soybean cyst nematode (SCN) inoculum (1000 vermiform eggs or 1000 J2s) is applied to the pots. Watering of the test plants is then restricted to only water as needed to prevent wilt for a period of 24 hours. After the 24 hour restricted watering, normal sub-irrigation watering is done for the duration of the test. Twenty eight days after inoculation the plants are harvested and cysts counted.

[00121] Experiments in corn using lesion nematodes are similar to above except for the following changes. Corn plants growing in a sand:Turface mix 2:1 in 4 inch deep pots (Turface™ MVP, Profile Products, LLC., Buffalo Grove, IL) . Treatment with polynucleotide solution is done when the plants are approximately 8-10 days old. At least six hours after inoculation of the polynucleotide solution, plants are inoculated with 2 gm of *P. scribneri* infested corn roots which are then removed from the pot after 7 days. Watering of the test plants is then restricted to only water as needed to prevent wilt for a period of 24 hours after inoculation. After the 24 hour restricted watering, normal sub-irrigation watering as needed is done for the duration of the test. 12-14 days post inoculation, plants are harvested and nematodes extracted for 6 days from the cut up roots in a mist tent.

Application of polynucleotides to seeds for nematode control

[00122] Cucumber seeds are soaked approximately 5 - 72 hours in nucleotides, either ssDNA and/or dsRNA polynucleotides directed to the promoter and/or targeting the coding region of a target of interest. Seeds can also be soaked in water for a few hours prior to soaking in polynucleotide solution. Soaking solution consists of 20nm of each ssDNA or 0.03-1nm dsRNA, .1% silwet L77, 50mM NaPO4 in a final volume 200uL in water. The radicals of the cucumber seeds emerge within 72 hours, after which the seeds are placed on germination paper until root length is approximately 2 inches. Seedlings are transplanted to sand vials for RKN inoculation 24 hours later. Ten mL dry sand is added to each vial and seedlings are planted by tilting the vial and laying the seedling in the correct orientation so that the cotyledons are just above the sand and then tilting back to cover the radicles with sand. 3.3 ml water is added to each vial and the vials placed in racks under fluorescent light banks. 500 vermiform eggs or 300 J2 RKN are inoculated in each tube in 50 uL of deionized or spring water. Harvest of the cucumber plants is performed 10 to 12 days after inoculation by washing sand off the roots. A root gall rating and visual phytotoxicity rating is assigned using the following scales: Gall rating scale (Gall: % root mass galled): 0 = 0-5%; 1 = 6-20%; 2 = 21-50%; and 3 = 51-100%. The average of the triplicate gall rating is then calculated:

green = 0.00-0.33 (no galls); yellow = 0.67-1.33 (mild galling); orange = 1.67-2.33 (moderate galling); red = 2.67-3.00 (severe galling). Visual phytotoxicity scale is also assigned (Vis. tox; visual reduction in root mass compared to the control): rs1 = mild stunting; rs2 = moderate stunting; rs3 = severe stunting.

[00123] Experiments in soybeans using soy cyst nematodes (SCN) are similar to RKN assays except for the following changes. After 5 - 72 hours of soaking soybean seeds are planted in 100% sand in two inch square plastic pots. Seeds can also be soaked in water for a few hours prior to soaking in polynucleotide solution. Seven days after planting the soybean seed, the nematode soybean cyst nematode (SCN) inoculum (1000 vermiform eggs or 1000 J2s) are applied to the pot. Watering of the test plants is then restricted to only water as needed to prevent wilt for a period of 24 hours. After the 24 hour restricted watering, normal sub-irrigation watering is done for the duration of the test. Twenty eight days after inoculation the test is harvested and cysts counted.

[00124] Experiments in corn using lesion nematodes are similar to above except for the following changes. After 5 - 72 hours of soaking corn seeds are planted in a sand:turface mix 2:1 in 4 inch deep pots. Seeds can also be soaked in water for a few hours prior to soaking in polynucleotide solution. Inoculum of 2gm of roots *P. scribneri* infested corn roots are applied at seeding and removed from the pot after 7 days. Watering of the test plants is then restricted to only water as needed to prevent wilt for a period of 24 hours after inoculation. After the 24 hour restricted watering, normal sub-irrigation watering as needed is done for the duration of the test. 12-14 days post inoculation, plants are harvested and nematodes extracted for 6 days from the cut up roots in a mist tent.

[00125] RKN and SCN J2s are prepared from hatchbowls using the following solutions: RKN solution: 1L aerated tap water, 1ml of 50mg/ml kanamycin, 0.5ml of 20mg/ml imazalil sulfate; SCN solution: 1L aerated tap water, 1ml of 50mg/ml kanamycin, 0.5ml of 20mg/ml imazalil sulfate, 1430mg zinc sulfate.

[00126] Hatchbowls are autoclaved 6 oz bowls, lined with screen mesh and paper filter. Approximately 20ml of appropriate hatch solution is poured into each bowl. Eggs are then place in the bowls and covered with foil. The bowls are then placed in a 25 °C incubator overnight. The next day the hatched J2's are extracted, additional solution added as needed and replaced in the incubator. Each bowl is used for 2 weeks and then disposed.

Example 8. Protection of Barley from powdery mildew by topical polynucleotide application

[00127] Barley seeds were planted in 2 inch pots in the greenhouse. Five days later, barley seedlings were sprayed with the indicated polynucleotides or a control formulation according to the methods of Table 12. The description of nucleic acid sequences of the ssDNA polynucleotides used is provided in Table 13. Post spraying, the seedlings were infected with dry spores of barley powdery mildew (*Blumeria graminis* f. sp. *hordei*) and 7 days post infection, disease development was scored for the percentage of leaf area covered with powdery mildew. Results of these experiments are shown in Table 14, ANOVA statistical calculations are shown in Table 15 and a corresponding graph with LSD bar is shown in Figure 3.

[00128] Table 12. Treatment Protocols

Trt	trigger type	nucleotide ID #	ratio	nmol/plant*
1	DNA GFP	GFP		13.4
2	DNA mlo	T4211		13.4
3	DNA mlo	T4219		13.4
4	DNA mlo	T4221		13.4
5	DNA mlo	T4211/T4219	1 to 1	6.7/6.7
6	DNA mlo	T4211/T4221	1 to 1	6.7/6.7
7	DNA mlo	T4219/T4221	1 to 1	6.7/6.7
8	DNA mlo	T4211/19as/21	1 to 1 to 1	4.5 each
9	DNA mlo	T4211/T4221	1 to 3	3.3/10
10	DNA mlo	T4211/GFP	1 to 1	6.7/6.7
11	DNA mlo	T4211/TGFP	1 to 3	3.3/10
12	DNA mlo	T4211		3.3/11

*The indicated amounts of polynucleotides were provided in 5mM $NaPO_4$, 1% Ammonium Sulfate, and 0.25% Silwet^{TM} (wt percent).

[00129] Table 13. Polynucleotides used

Seq Name	Sequence Composition	# nucleotides	SEQ ID NO	Organism
T4211	GGGGTGCTGGAGAGGCCCAGGTGG	24	184	barley
T4212	CGACGTCTGGTGCGTGAACCGGA	23	185	barley
T4213	CTGGTATTCCAAGGAGGTGGTCT	23	186	barley
T4214	GATGAGGAGCAGGGATATGAAGC	23	187	barley
T4215	ATGAGCTCCGCCTTCATCTTCTC	23	188	barley
T4216	GGCCTTCTTGTGCCGGTGCTGGA	23	189	barley
T4217	CTGTCCACACAAAATGCGCCATC	23	190	barley
T4218	GTTCTGGAACAACGTCAGGTGT	22	191	barley

Seq Name	Sequence Composition	# nucleotides	SEQ ID NO	Organism
T4219	GTCGGGGCGGTGGAACCAGAAG	22	192	barley
T4220	AAAAATCTGCACTGGGGATGT	21	193	barley
T4221	GATTTAGTCTGTGCACCGGGTGCG	24	194	barley
T4222	AACCGGGTACATGTCCCTAGCCTC	24	195	barley
GFP	GTTGTAGTTGTACTCCATCTTATTG	25	196	*A.victoria*

[00130] Table 14. Percent Leaf Infection Area Results

Treatment No.	nucleotide ID #	Average Percent Infection Area	STDEV	N	Variance
	NT	28.6	9.45	7	89.29
	Formulation	17.5	8.22	6	67.50
1	GFP	10.6	6.23	8	38.84
2	T4211	1.38	2.26	8	5.13
4	T4219	2.33	2.07	6	14.17
5	T4221	4.16	2.04	6	4.27
6	T4211/T4219 1:1	2.2	2.59	6	4.17
7	T4211/T4221 1:1	2.2	2.59	5	6.70
8	T4219/T4221 1:1	4.2	1.79	5	6.70
10	T4211/T4221 1:3	2.4	2.4	5	3.20
11	T4211/GFP 1:1	2.4	2.4	5	4.30
12	T4211/TGFP 1:3	2.6	2.19	5	5.80
	T4211	1.75	2.22	5	5.80

[00131] Table 15. ANOVA

ANOVA						
Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	5351.475	15	356.765	17.96064	7.29E-19	1.581213
Within Groups	1469.914	74	19.86371			
Total	6821.389	89				

Example 9. Topical application of short dsRNA polynucleotides provides protection of Barley from powdery mildew.

Barley seeds were planted in 2 inch pots in the greenhouse. Five days later, barley seedlings were treated by hand application of dsRNA polynucleotides or a control formulation as

indicated in Table 16. 1.7-6.7nm of the dsRNA polynucleotide, as indicated in Table 16, was provided in 5mM $NaPO_4$, 1% Ammonium Sulfate, and 0.25% L77-Silwet^{TM} (wt percent). Two cotyledon or leaves were spotted with 20uL of the nucleotide solution for a total of 40uL per plant. The nucleotide sequence of the dsRNA polynucleotides is provided in Table 17. Post application, the seedlings were infected with dry spores of barley powdery mildew (*Blumeria graminis* f. sp. *hordei*) and disease development was scored at both 7 days and 14 days post infection for the percentage of leaf area covered with powdery mildew. Results of these experiments are shown in Table 18, ANOVA statistical calculations are shown in Table 19 and corresponding graph with LSD bar is shown in Figure 4. Figure 5 shows the results in graph format for 14 days post-infection.

Table 16. Treatment Protocols for dsRNA polynucleotides

Trt	**Trigger type**	**Nucleotide ID#**	**nmol/plant***
NT	None		
F	None		
1	dsRNA	T4211_dsRNA	6.7
2	dsRNA	T4114_dsRNA	6.7
3	dsRNA	T4217_dsRNA	6.7
4	dsRNA	T4219_dsRNA	6.7
5	dsRNA	T4220_dsRNA	6.7
6	dsRNA	T5910_dsRNA	6.7
7	dsRNA	T5917_dsRNA	6.7
8	dsRNA	T5923_dsRNA	6.7
9	dsRNA	M4214_7_9: a mix of T4214, T4217, T4219	2.2 each
10	dsRNA	T4220_5910_17_23: a mix of T4220, T5910, T5917, and T5923	1.7 each
11	dsRNA	GFP_dsRNA	6.7

*The indicated amounts of polynucleotides were provided in 5mM $NaPO_4$, 1% Ammonium Sulfate, and 0.25% Silwet^{TM} (wt percent).

Table 17. dsRNA polynucleotides used

Seq Name	Sequence Composition	# nucleotides	SEQ ID NO	Organism
T4211_dsRNA	GGGGUGCUGGAGAGGCCCAGGUGG	24	197	barley
T4114_dsRNA	GAUGAGGAGCAGGGAUAUGAAGC	23	198	barley
T4217_dsRNA	CUGUCCACACAAAAUGCGCCAUC	23	199	barley
T4219_dsRNA	GUCGGGGCGGUGGAACCAGAAG	22	200	barley
T4220_dsRNA	AAAAAUCUGCACUGGGGAUGU	21	201	barley
T5910_dsRNA	CGCCUUCAUCUUCUCCAGCGCCUCC	25	202	barley
T5917_dsRNA	GUCGUCCUCCAUCGACCUCUUGAUG	25	203	barley
T5923_dsRNA	UCAGCCCGAUCUGCGUGUGGUAGCA	25	204	barley
GFP_dsRNA	GUUGUAGUUGUACUCCAUCUUAUUG	25	205	*A.victoria*

Table 18. Percent Infection Area on treated plants

Treatment No.	nucleotide ID #	Average Percent Infection Area	STDEV	N	Variance (LSD)
1	T4211_dsRNA	0.285714286	0.487950036	7	3
2	T4114_dsRNA	3.857142857	3.484660262	7	3
3	T4217_dsRNA	3.285714286	2.138089935	7	3
4	T4219_dsRNA	8.71428571	7.846746368	7	3
5	T4220_dsRNA	9.428571429	7.678045386	7	3
6	T5910_dsRNA	6.285714286	8.920281866	7	3
7	T5917_dsRNA	5.142857143	2.60950643	7	3
8	T5923_dsRNA	7.428571429	8.323804075	7	3
9	T4214, T4217, T4219 all dsRNA	12	7.582875444	5	3
10	T4220, T5910, T5917, T5923 all dsRNA	10	7.745966692	6	3
11	GFP_dsRNA	13.57142857	8.017837257	7	3

Table 18 shows the percentage disease area was significantly reduced in plants treated with the Silwet formulation containing the barley MLO dsRNA triggers.

Table 19. ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	5242.448052	12	436.870671	9.63	5.29233E-11	1.63
Within Groups	3403.142857	75	45.3752381			
Total	8645.590909	87				

Figure 4 shows that at six days post infection, of the eight dsRNA triggers tested, six showed a significant reduction in the percent disease area when compared to the GFP dsRNA control (dsR-4211, dsR-4217, dsR-4219, dsR5910, dsR-5917, and dsR5923). Similarly, as shown in Figure 5, at thirteen days post infection, four dsRNA treatments showed significant disease reduction when compared to the GFP dsRNA trigger (dsR-4211, dsR-4217, dsR-5910 and dsR-5923). The most efficacious trigger appeared to be T4211_dsRNA, similar to the results obtained using T4211_ssDNA, the dsRNA form of this polynucleotide reduced mildew infection by about 96%.

Example 10. Topical application of long dsRNA polynucleotides provides protection of Barley from powdery mildew.

Barley seeds were planted in 2 inch pots in the greenhouse. Five days later, barley seedlings were treated by hand application with dsRNA polynucleotides or a control formulation as indicated in Table 20. 13.5-28pmol of dsRNA polynucleotide as indicated in Table 20 was provided in 5mM $NaPO_4$, 1% Ammonium Sulfate, and 0.25% L77-Silwet^{TM} (wt percent). Two cotyledon or leaves were spotted with 20uL of the nucleotide solution for a total of 40uL per plant. The description of the nucleotide sequences of the dsRNA polynucleotides is provided in Table 21. Following application of the dsRNA polynucleotides, the seedlings were infected with dry spores of barley powdery mildew (*Blumeria graminis* f. sp. *hordei*) and disease development was scored at 6 days post infection for the percentage of leaf area

covered with powdery mildew. Results of these experiments are shown in Table 22, ANOVA statistical calculations are shown in Table 23 and corresponding graph with LSD bar is shown in Figure 5.

Table 20. Treatment Protocol for long dsRNA polynucleotides

Trt	**Trigger type**	**Nucleotide ID#**	**pmol/plant***
NT	None		
F	None		
1	Long dsRNA	5946_150a	18.6
2	Long dsRNA	5947_150a	18.6
3	Long dsRNA	5948_150a	18.6
4	Long dsRNA	5946_100a	28
5	Long dsRNA	5947_100a	28
6	Long dsRNA	5948_100a	28
7	Long dsRNA	5946_80b	16.9
8	Long dsRNA	dsGFP_100b	28
9	Long dsRNA	dsGFP_100b	13.5

Table 21. Polynucleotides used

Seq Name	Seq Composition	# nucleotides	SEQ ID NO	Organism
5946_150a	AUGUCGGACAAAAAAGGGGUGCCGGCGCGGGA GCUGCCGGAGACGCCGUCGUGGGCGGUGGCGG UGGUCUUCGCCGCCAUGGUGCUCGUGUCCGUCC UCAUGGAACACGGCCUCCACAAGCUCGGCCAUU GGUUCCAGCACCGGCACAAG	150	206	Barley
5947_150a	CGUCGUCGGCCCUCGAAGCCGACAUCCCCAGUG CAGAUUUUUCCUUCAGCCAGGGAUGAGACAAG UUUCUGUAUUCAUGUUAGUCCCAAUGUAUAGC CAACAUAGGAUGUGAUGAUUCGUACAAUAAGA AAUACAAUUUUUUACUGAGUC	150	207	Barley
5948_150a	UGGUGGUGGGGCUAGCUCUCCAGUUCCUCUGC AGCUAUAUGACCUUCCCCCUCUACGCGCUCGUC ACACAGAUGGGAUCAAACAUGAAGAGGUCCAU CUUCGACGAGCAGACGUCCAAGGCGCUCACCAA	150	208	Barley

	CUGGCGGAACACGGCCAAGG			
5946_100a	GUGGGCGGUGGCGGUGGUCUUCGCCGCCAUGG UGCUCGUGUCCGUCCUCAUGGAACACGGCCUCC ACAAGCUCGGCCAUUGGUUCCAGCACCGGCACA AG	100	209	Barley
5947_100a	CAGGGAUGAGACAAGUUUCUGUAUUCAUGUUA GUCCCAAUGUAUAGCCAACAUAGGAUGUGAUG AUUCGUACAAUAAGAAAUACAAUUUUUUACUG AGUC	100	210	Barley
5948_100a	CUCUACGCGCUCGUCACACAGAUGGGAUCAAA CAUGAAGAGGUCCAUCUUCGACGAGCAGACGU CCAAGGCGCUCACCAACUGGCGGAACACGGCCA AGG	100	211	Barley
5946_80b	UCGCCGCCAUGGUGCUCGUGUCCGUCCUCAUGG AACACGGCCUCCACAAGCUCGGCCAUUGGUUCC AGCACCGGCACAAG	80	212	Barley
dsGFP_100a	UCAAGGAGGAUGGCAACAUCCUGGGCAAUAAG AUGGAGUACAACUACAACGCCCACAAUGUGUA CAUCAUGACCGACAAGGCCAAGAAUGGCAUCA AGGUGAACUUCAAGAUCCGCCACAACAUCGAG GAUGGCAGCGUGCAGCUGGCCGAC	100	213	*A.victoria*

Table 22. Percent Leaf Infection Area Results

Trt No.	Nucleotide ID	N	Avg Percent Infection	STDEV	LSD
	NT	8	23.125	5.303301	2.82
	Formulation	8	19.375	7.763238	2.82
1	dsGFP_100a	8	13.125	7.529703	2.82
2	5946_150a	9	5.777778	3.562926	2.82
3	5947_150a	9	9	6.819091	2.82
4	5948_150a	9	8.444444	6.930208	2.82
5	5946_100a	8	10	6.546537	2.82
6	5947_100a	9	12.77778	7.120003	2.82
7	5948_100a	9	12.22222	7.546154	2.82
8	dsGFP_100b	9	12.77778	7.120003	2.82
9	5946_80b	8	13.75	6.943651	2.82

Table 23. ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	2013.068853	10	201	4.4	0	1.7
Within Groups	3777.569444	83	46			
Total	5790.638298	93				

Figure 5 shows that at six days post infection of the eight dsRNAs tested, T5946 (150-mer) had significantly lower infection compared to the GFP dsRNA control. The other two 150-mer dsRNAs (T5947 and T5948) also trended lower compared to the control.

What is claimed is:

1. A method for producing a plant exhibiting an improvement in fungal disease resistance comprising topically applying to a plant surface a composition that comprises:

a. at least one polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or to a transcript of said gene; and

b. a transfer agent, wherein said plant exhibits an improvement in fungal disease resistance that results from suppression of said Mildew Resistance Locus O (MLO) gene.

2. The method of claim 1, wherein said polynucleotide molecule comprises sense ssDNA, sense ssRNA, dsRNA, dsDNA, a double stranded DNA/RNA hybrid, anti-sense ssDNA, or anti-sense ssRNA.

3. The method of claim 1, wherein said polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79.

4. The method of claim 3, wherein:

(a) said plant is a corn plant, said gene or said transcript is a corn Mildew Resistance Locus O (MLO) Gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69;

(b) said plant is a soybean plant, said gene or said transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47;

(c) said plant is a cotton plant, said gene or said transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and or said polynucleotide comprises at least 18

contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4;

(d) said plant is a barley plant, said gene or said transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, and SEQ ID NO:194, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29;

(e) said plant is a cucumber plant, said gene or said transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;

(f) said plant is a lettuce plant, said gene or said transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39;

(g) said plant is a pea plant, said gene or said transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;

(h) said plant is a *Medicago* plant, said gene or said transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43;

(i) said plant is a pepper plant, said gene or said transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49;

(j) said plant is a tomato plant, said gene or said transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the

group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53;

(k) said plant is a wheat plant, said gene or said transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59;

(l) said plant is a grape plant, said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67;

(m) said plant is a sorghum plant, said gene or said transcript is a sorghum Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or,

(n) said plant is a rice plant, said gene or said transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:183, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79.

5. The method of claim 1, wherein said composition comprises any combination of two or more polynucleotide molecules.

6. The method of claim 1, wherein said polynucleotide is at least 18 to about 24, about 25 to about 50, about 51 to about 100, about 101 to about 300, about 301 to about 500, or at least about 500 or more residues in length.

7. The method of claim 1, wherein said composition further comprises a non-polynucleotide herbicidal molecule, a polynucleotide herbicidal molecule, a polynucleotide that suppresses an herbicide target gene, an insecticide, a fungicide, a nematocide, or a combination thereof.

8. The method of claim 1, wherein said composition further comprises a non-polynucleotide herbicidal molecule and said plant is resistant to said herbicidal molecule.

9. The method of any one of claims 1-8, wherein said transfer agent comprises an organosilicone preparation.

10. The method of claim 1-8, wherein said polynucleotide is not operably linked to a viral vector.

11. The method of any one of claims 1-8, wherein said polynucleotide is not integrated into the plant chromosome.

12. A plant obtained by the method of any one of claims 1-8.

13. The plant obtained by the method of claim 12, wherein a progeny plant or a plant part derived therefrom exhibits an improvement in fungal disease resistance.

14. A progeny plant of said plant of claim 12, wherein said progeny plant exhibits said improvement in fungal disease resistance.

15. A seed of said plant of claim 12, wherein said seed exhibits said improvement in fungal disease resistance.

16. A processed product of said plant of claim 12, wherein said processed product exhibits an improved attribute relative to a processed product of an untreated control plant and wherein said improved attribute results from said fungal disease resistance.

17. A processed product of said progeny plant of claim 14, wherein said processed product exhibits an improved attribute relative to a processed product of an untreated control plant and wherein said improved attribute results from said fungal disease resistance.

18. A processed product of said seed of claim 15, wherein said processed product exhibits an improved attribute relative to a processed product of an untreated control plant and wherein said improved attribute results from said fungal disease resistance.

19. A composition comprising a polynucleotide molecule that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of said gene, wherein said polynucleotide is not operably linked to a promoter; and, b) a transfer agent.

20. The composition of claim 19, wherein said polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79.

21. The composition of claim 19, wherein:
(a) said gene or said transcript is a corn Mildew Resistance Locus O (MLO) Gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69;
(b) said gene or said transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47;
(c) said gene or said transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4;
(d) said gene or said transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, and SEQ ID NO:194, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29;

(e) said gene or said transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;

(f) said gene or said transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39;

(g) said gene or said transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;

(h) said gene or said transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43;

(i) said gene or said transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, , or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49;

(j) said gene or said transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53;

(k) said gene or said transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59;

(l) said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or said polynucleotide comprises at least 18 contiguous

nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67;

(m) said gene or said transcript is a sorghum Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or,

(n) said gene or said transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:195, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79.

22. The composition of claim 19, wherein said polynucleotide is at least 18 to about 24, about 25 to about 50, about 51 to about 100, about 101 to about 300, about 301 to about 500, or at least about 500 or more residues in length.

23. The composition of claim 19, wherein said composition further comprises a non-polynucleotide herbicidal molecule, a polynucleotide herbicidal molecule, a polynucleotide that suppresses an herbicide target gene, an insecticide, a fungicide, a nematocide, or a combination thereof.

24. The composition of claim 19, wherein said transfer agent is an organosilicone preparation.

25. The composition of any one of claims 19-24, wherein said polynucleotide is not physically bound to a biolistic particle.

26. A method of making a composition comprising the step of combining at least:

a) a polynucleotide molecule comprising at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of a plant, wherein said polynucleotide is not operably linked to a promoter or a viral vector; and,

b) a transfer agent.

27. The method of claim 26, wherein said polynucleotide is obtained by *in vivo* biosynthesis, *in vitro* enzymatic synthesis, or chemical synthesis.

28. The method of claim 26, wherein said method further comprises combining with said polynucleotide and said transfer agent at least one of a non-polynucleotide herbicidal molecule, a polynucleotide herbicidal molecule, an insecticide, a fungicide, and/or a nematocide.

29. The method of any one of claims 26-28, wherein said transfer agent is an organosilicone preparation.

30. A method of identifying a polynucleotide for improving fungal disease resistance in a plant comprising;

a) selecting a population of polynucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of a plant;

b) topically applying to a surface of at least one of said plants a composition comprising at least one polynucleotide from said population and an transfer agent to obtain a treated plant; and,

c) identifying a treated plant that exhibits suppression of the Mildew Resistance Locus O (MLO) gene or exhibits an improvement in fungal disease resistance or exhibits an improvement in nematode resistance, thereby identifying a polynucleotide that improves fungal disease resistance in said plant.

31. The method of claim 30, wherein said polynucleotide is selected from the group consisting of wherein said polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79.

32. The method of claim 30, wherein:

(a) said plant is a corn plant, said gene or said transcript is a corn Mildew Resistance Locus O (MLO) Gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or said polynucleotide comprises

at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69;

(b) said plant is a soybean plant, said gene or said transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47;

(c) said plant is a cotton plant, said gene or said transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4;

(d) said plant is a barley plant, said gene or said transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, and SEQ ID NO:194, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29;

(e) said plant is a cucumber plant, said gene or said transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;

(f) said plant is a lettuce plant, said gene or said transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39;

(g) said plant is a pea plant, said gene or said transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;

(h) said plant is a *Medicago* plant, said gene or said transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or said

polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43;

(i) said plant is a pepper plant, said gene or said transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49;

(j) said plant is a tomato plant, said gene or said transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53;

(k) said plant is a wheat plant, said gene or said transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59;

(l) said plant is a grape plant, said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67;

(m) said plant is a sorghum plant, said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or,

(n) said plant is a rice plant, said gene or said transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:195, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79.

33. A plant comprising an exogenous polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of said gene, wherein said exogenous polynucleotide is not operably linked to a promoter or to a viral vector, is not integrated into the chromosomal DNA of the plant, and is not found in a non-transgenic plant; and, wherein said plant exhibits an improvement in fungal disease resistance that results from suppression of the Mildew Resistance Locus O (MLO) gene.

34. The plant of claim 33, wherein said plant further comprises an organosilicone compound or a component thereof.

35. The plant of claim 33 or claim 34, wherein said polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79.

36. The plant of claim 33 or claim 34, wherein:

(a) said plant is a corn plant, said gene or said transcript is a corn Mildew Resistance Locus O (MLO) Gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69;

(b) said plant is a soybean plant, said gene or said transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47;

(c) said plant is a cotton plant, said gene or said transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a cotton gene or transcript that encodes SEQ ID NO:4;

(d) said plant is a barley plant, said gene or said transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the

group consisting of SEQ ID NO:80-83, 184, 192, and SEQ ID NO:194, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29;

(e) said plant is a cucumber plant, said gene or said transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;

(f) said plant is a lettuce plant, said gene or said transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39;

(g) said plant is a pea plant, said gene or said transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;

(h) said plant is a *Medicago* plant, said gene or said transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43;

(i) said plant is a pepper plant, said gene or said transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49;

(j) said plant is a tomato plant, said gene or said transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53;

(k) said plant is a wheat plant, said gene or said transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59;
(l) said plant is a grape plant, said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67;
(m) said plant is a sorghum plant, said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or,
(n) said plant is a rice plant, said gene or said transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:195, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:73, 75, 77, or 79.

37. A plant part comprising an exogenous polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO) gene or transcript of said gene, wherein said exogenous polynucleotide is not operably linked to a promoter or to a viral vector and is not found in a non-transgenic plant; and, wherein said plant part exhibits an improvement in fungal disease resistance that results from suppression of the Mildew Resistance Locus O (MLO) gene.

38. The plant part of claim 37, wherein said plant part further comprises an organosilicone compound or a metabolite thereof.

39. The plant part of claim 37 or claim 38, wherein said polynucleotide is selected from the group consisting of SEQ ID NO: 80-195, or wherein said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ

ID NO: 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, or 79.

40. The plant part of claim 37 or claim 38, wherein:

(a) said plant part is a corn plant part, said gene or said transcript is a corn Mildew Resistance Locus O (MLO) Gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 160-162, and SEQ ID NO: 163, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:68-69;

(b) said plant part is a soybean plant part, said gene or said transcript is a soybean Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO: 112-118, and SEQ ID NO: 119, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:45 or 47;

(c) said plant part is a cotton plant part, said gene or said transcript is a cotton Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:4;

(d) said plant part is a barley plant part, said gene or said transcript is a barley Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:80-83, 184, 192, and SEQ ID NO:194, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:29;

(e) said plant part is a cucumber plant part, said gene or said transcript is a cucumber Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:84-98, and SEQ ID NO:99, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:31, 33, 35, or 37;

(f) said plant part is a lettuce plant part, said gene or said transcript is a lettuce Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:100-102, and SEQ ID NO:103, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:39;

(g) said plant part is a pea plant part, said gene or said transcript is a pea Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:104-106, and SEQ ID NO:107, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:41;

(h) said plant part is a *Medicago* plant part, said gene or said transcript is a *Medicago* Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:108-110, and SEQ ID NO:111, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:43;

(i) said plant part is a pepper plant part, said gene or said transcript is a pepper Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:120-122, and SEQ ID NO:123, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:49;

(j) said plant part is a tomato plant part, said gene or said transcript is a tomato Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:124-130, and SEQ ID NO:131, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:51 or 53;

(k) said plant part is a wheat plant part, said gene or said transcript is a wheat Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:132-142, and SEQ ID NO:143, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:55, 57 or 59;

(l) said plant part is a grape plant part, said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:144-158, and SEQ ID NO:159 or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:61, 63, 65, or 67;

(m) said plant part is a sorghum plant part, said gene or said transcript is a grape Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:164-166, and SEQ ID NO:167, or said

polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO:71; or,

(n) said plant part is a rice plant part, said gene or said transcript is a rice Mildew Resistance Locus O (MLO) gene or transcript, and said polynucleotide molecule is selected from the group consisting of SEQ ID NO:168-182, and SEQ ID NO:183, or said polynucleotide comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to SEQ ID NO: 73, 75, 77, or 79.

41. The plant part of any one of claims 37-38, wherein said plant part is a flower, meristem, ovule, stem, tuber, fruit, anther, pollen, leaf, root, or seed.

42. The plant part of claim 41, wherein said plant part is a seed.

43. A processed plant product obtained from the plant part of claim 33 exhibiting an improved attribute relative to a processed plant product of an untreated control plant and wherein said improved attribute results from said improved disease tolerance.

44. The processed plant product of claim 43, wherein said product is a meal, a pulp, a feed, or a food product.

45. A plant that exhibits an improvement in fungal disease resistance, wherein said plant was topically treated with a composition that comprises:

a. at least one polynucleotide that comprises at least 18 contiguous nucleotides that are essentially identical or essentially complementary to a Mildew Resistance Locus O (MLO)gene or to a transcript of said gene; and,

b. a transfer agent; and,

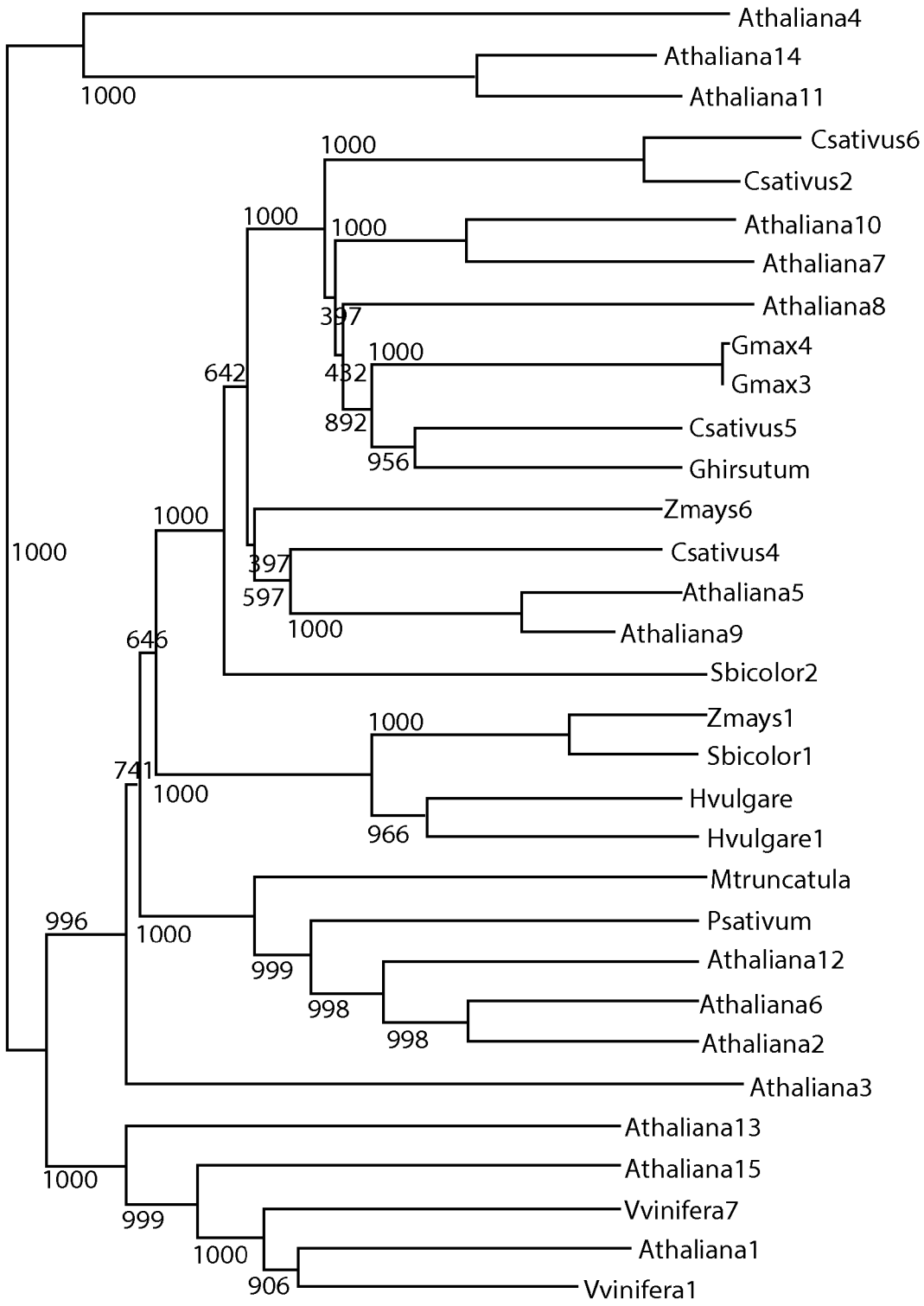
wherein said plant exhibits an improvement in fungal disease resistance that results from suppression of the Mildew Resistance Locus O (MLO) gene.

46. The plant of claim 45, wherein said transfer agent is an organosilicone preparation.

47. A plant obtained by the method of claim 9.

48. A plant obtained by the method of claim 10.

49. A plant obtained by the method of claim 11.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Athaliana10
Athaliana7
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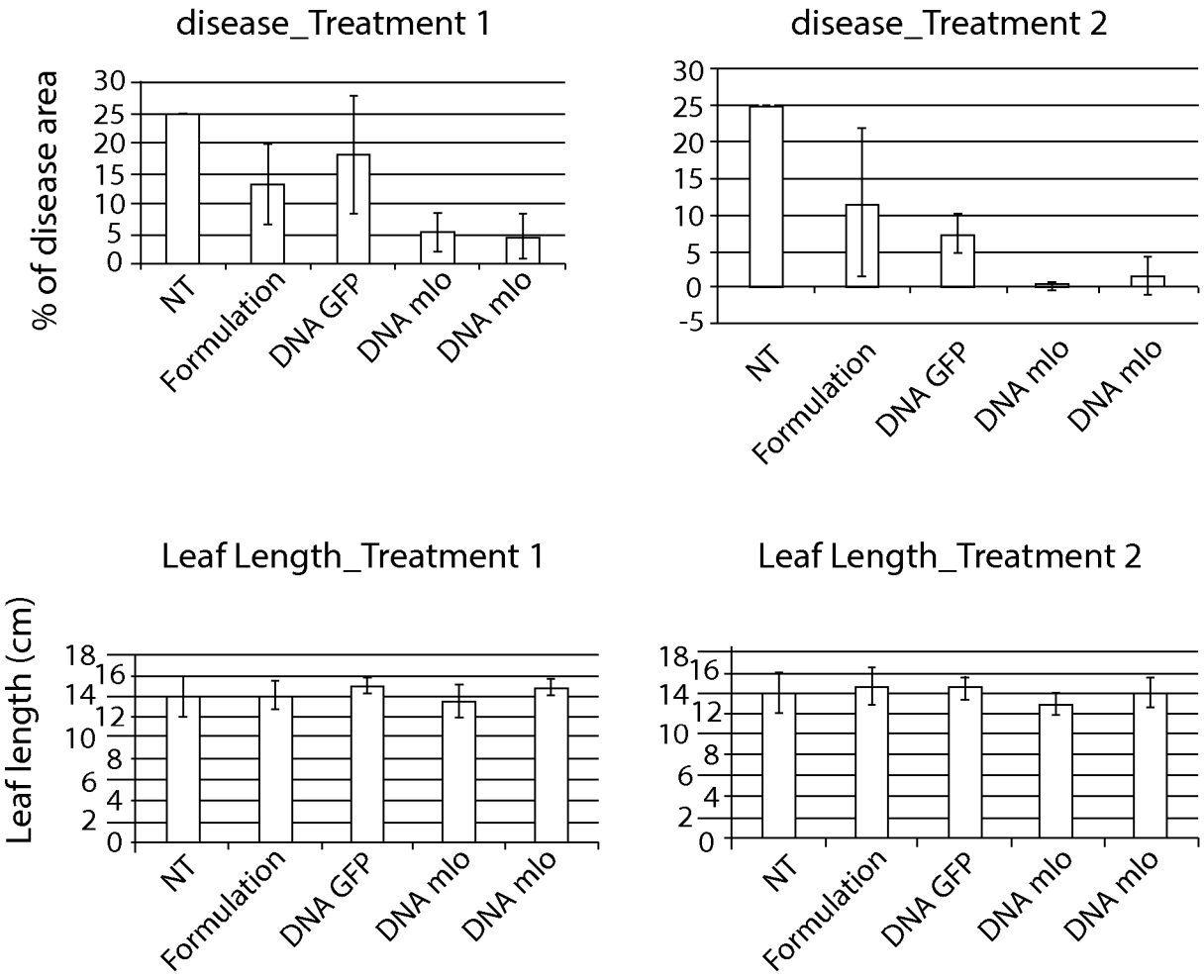
1000
Athaliana8
397
Gmax4
Gmax3
1000
642
432
892
Csativus5
956
Ghirsutum
Zmays6
1000
Csativus4
1000
397
597
Athaliana5
1000
Athaliana9
646
Sbicolor2
Zmays1
1000
Sbicolor1
741
1000
Hvulgare
966
Hvulgare1
Mtruncatula
996
Psativum
1000
Athaliana12
999
998
Athaliana6
998
Athaliana2
Athaliana3
Athaliana13
Athaliana15
1000
999
Vvinifera7
1000
Athaliana1
906
Vvinifera1

FIGURE 1



Leaf length were measured when disease was scored.

FIGURE 2

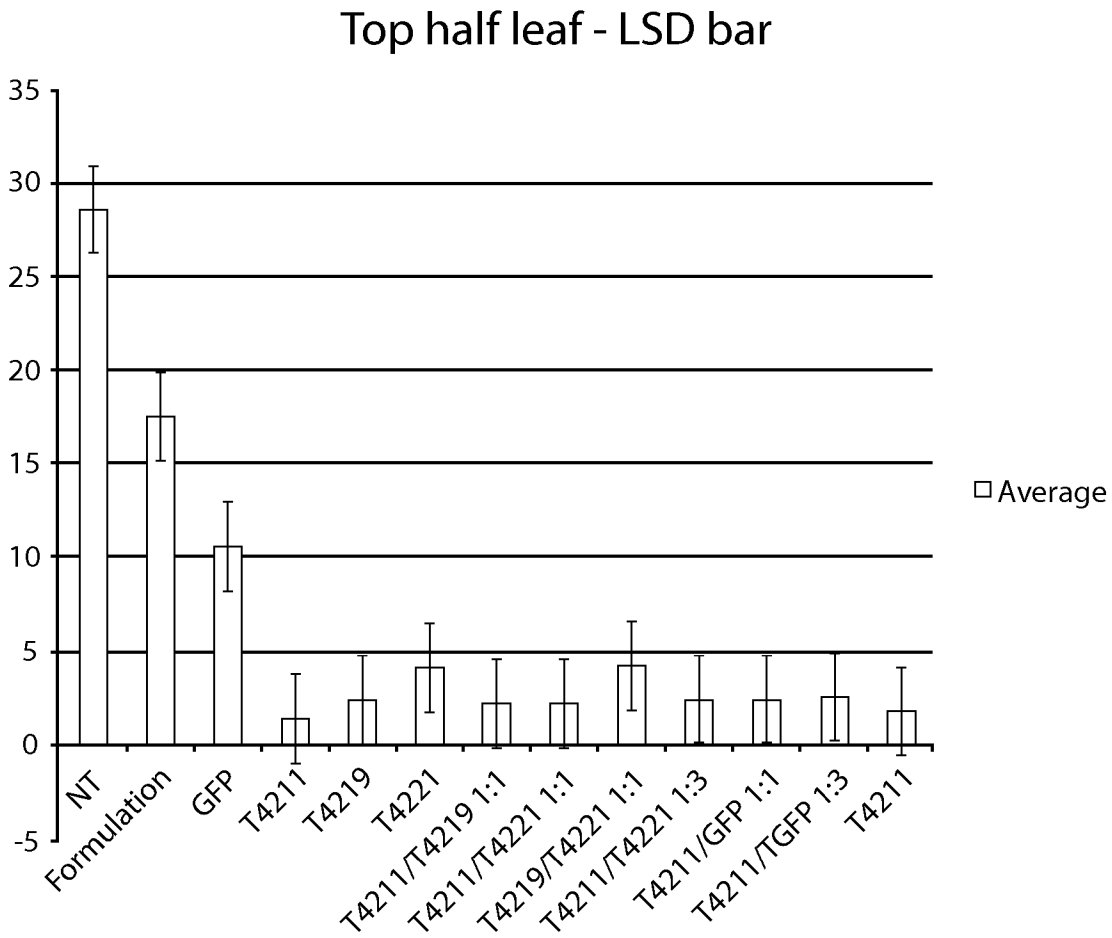

Top half leaf - LSD bar
35
30
25
20
15
10
5
0
-5
NT
Formulation
GFP
T4211
T4219
T4221
T4211/T4219 1:1
T4211/T4221 1:1
T4219/T4221 1:1
T4211/T4221 1:3
T4211/GFP 1:1
T4211/TGFP 1:3
T4211
Average

FIGURE 3

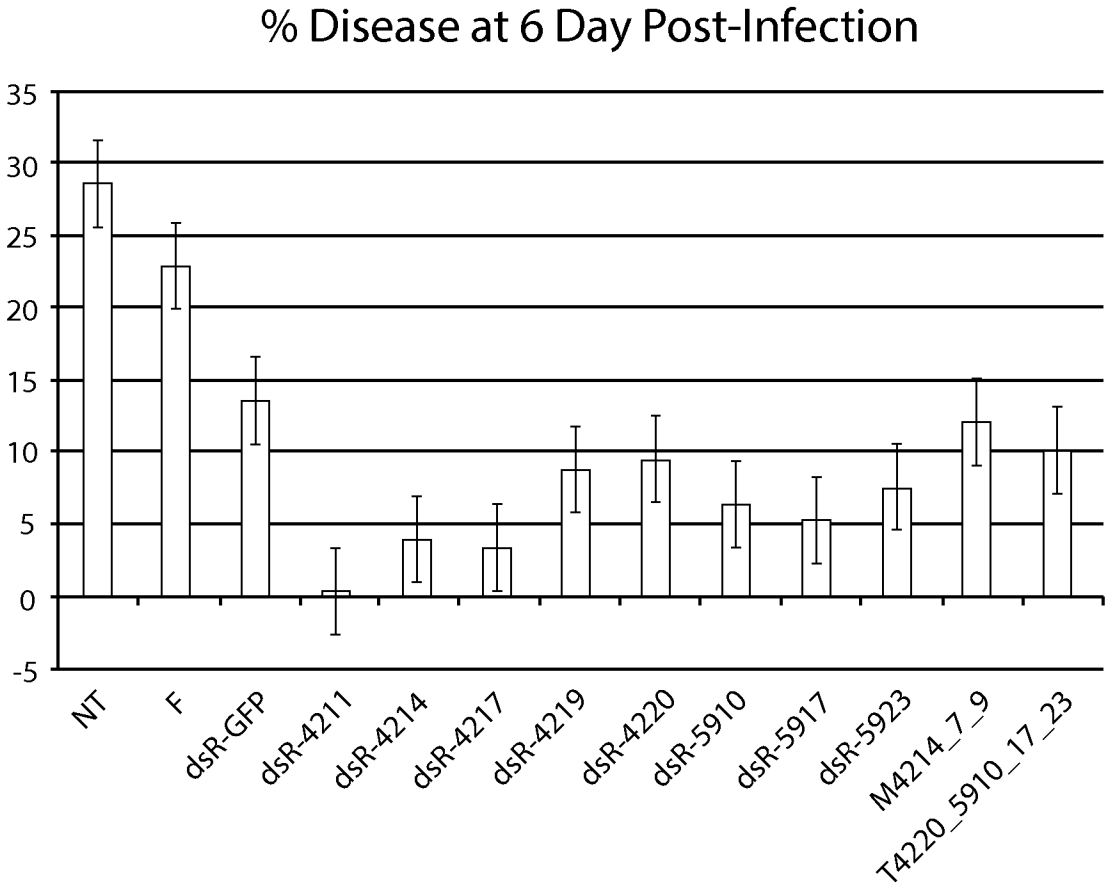

% Disease at 6 Day Post-Infection
35
30
25
20
15
10
5
0
-5
NT
F
dsR-GFP
dsR-4211
dsR-4214
dsR-4217
dsR-4219
dsR-4220
dsR-5910
dsR-5917
dsR-5923
M4214_7_9
T4220_5910_17_23

FIGURE 4

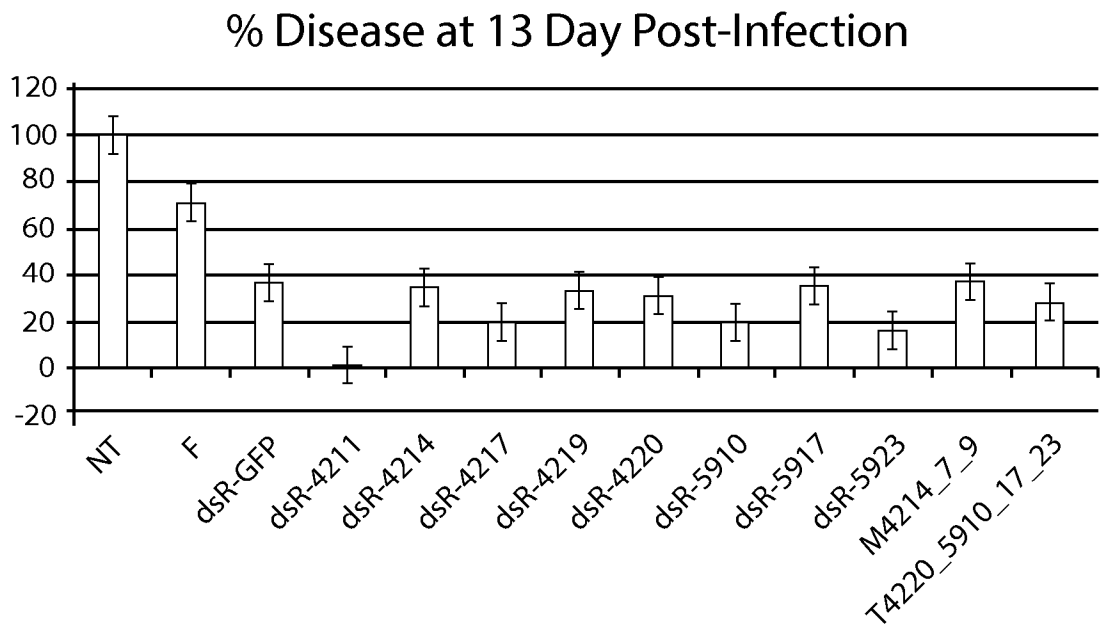

% Disease at 13 Day Post-Infection
120
100
80
60
40
20
0
-20
NT
F
dsR-GFP
dsR-4211
dsR-4214
dsR-4217
dsR-4219
dsR-4220
dsR-5910
dsR-5917
dsR-5923
M4214_7_9
T4220_5910_17_23

FIGURE 5

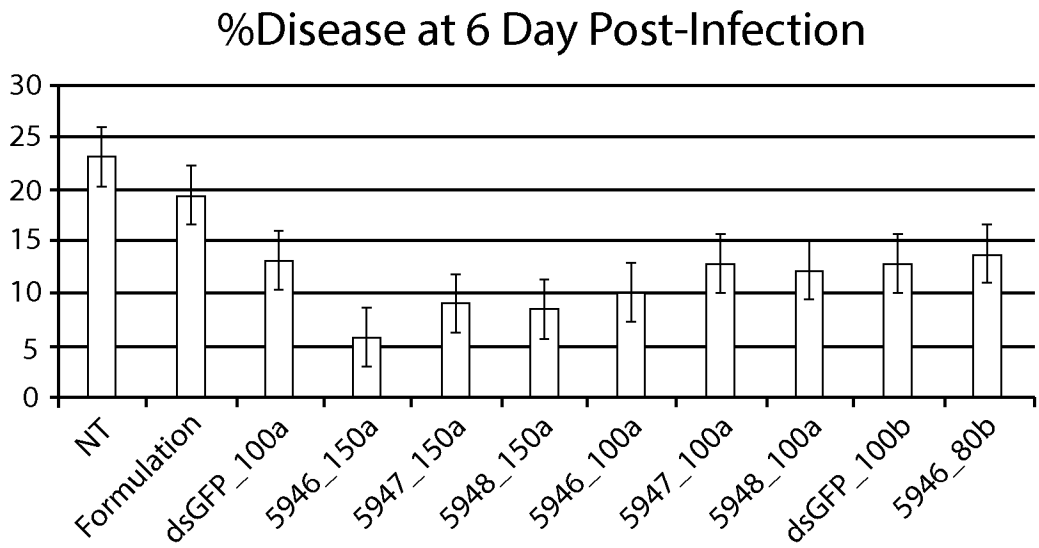

%Disease at 6 Day Post-Infection
30
25
20
15
10
5
0
NT
Formulation
dsGFP_100a
5946_150a
5947_150a
5948_150a
5946_100a
5947_100a
5948_100a
dsGFP_100b
5946_80b

FIGURE 6