

CLAIMS

1. A method for determining a fruit color phenotype of an oil palm plant, the method comprising,
 - 5 providing a sample from the oil palm plant or seed; and
 - detecting presence or absence of a genetic marker linked to a VIR gene alteration within 2,000 kb ~~in~~of a genomic region corresponding to SEQ ID NO: 1 that confers a *virescens* phenotype to fruit of the oil palm plant; wherein the presence of the alteration predicts the presence of the virescens phenotype.
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2. The method of claim 1, wherein the alteration comprises a nucleotide change that results in an encoded amino acid change, a splice site or other alteration resulting in a change in splicing, and/or a stop codon.
- 15 3. The method of claim 1, wherein the alteration comprises a premature stop codon so as to generate a truncated protein compared to the protein encoded by SEQ ID NO:4.
4. The method of claim 1, wherein the alteration is a dominant negative mutation.
- 20 5. The method of claim 1, wherein the alteration is selected from the group corresponding to SEQ ID NOS:7, 9, 11, 13, or 15, or the alteration produces a VIR allele that encodes an amino acid sequence selected from the group consisting of SEQ ID NOS:5, 8, 10, 12, and 14.
- 25 6. The method of claim 1, wherein the altered VIR gene encodes (i) a polypeptide at least 95% identical to SEQ ID NO:4 or (ii) a polypeptide comprising at least 100, 125, 150, 175, 200, or 225 contiguous amino acids that are at least 95% identical to a corresponding fragment of the SEQ ID NO:4.
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7. The method of claim 1, comprising detecting a presence or absence of a genetic marker linked to the alteration within about 1, 10, 20, 50, 100, 200, 500, 1000 kb, or 2000 kb of the genomic region.
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8. The method of claim 1, wherein the plant is less than 5 years old.

9. The method of claim 1, wherein the plant is less than one year old.

~~10. The method of claim 1, wherein the plant is an oil palm.~~

~~11.10.~~ The method of claim 1, wherein the method further comprises predicting a shell thickness phenotype by detecting the presence or absence of a nucleic acid sequence associated with a dura, tenera, or pisifera phenotype.

~~12.11.~~ The method of claim ~~11~~10, wherein the shell thickness phenotype is predicted from the same sample as the fruit color phenotype.

~~13.12.~~ The method of claim ~~11~~10, further comprising selecting the plant or seed for cultivation if the plant is predicted to have the virescens phenotype.

~~14.13.~~ The method of claim ~~13~~12, wherein the plant or seed is discarded if the plant or seed is not predicted to have the virescens phenotype.

~~15.14.~~ A method for segregating a plurality of oil palm plants into different categories based on predicted fruit color phenotype, the method comprising,

providing a sample from each plant in the plurality of plants;
detecting a presence or absence of a genetic marker linked to a VIR gene alteration within 2,000 kb in-of a genomic region corresponding to SEQ ID NO: 1 that confers a virescens phenotype to fruit of the oil palm plants; and
segregating the plants into groups based on the predicted virescens phenotype of the plants;
wherein the presence of the alteration predicts the presence of the virescence phenotype.

~~16.15.~~ The method of claim ~~15~~14, wherein the alteration comprises a premature stop codon so as to generate a truncated protein compared to a protein encoded by SEQ ID NO:4.

~~17.16.~~ The method of claim ~~15~~14, wherein the alteration is a dominant negative mutation.

~~18.17.~~ The method of claim ~~15~~14, wherein the alteration is selected from the group corresponding to SEQ ID NOS:7, 9, 11, 13, or 15, or the alteration produces a VIR allele that encodes an amino acid sequence selected from the group consisting of SEQ ID NOS:5, 8, 10, 12, and 14.

~~19.18.~~ The method of claim ~~15~~14, wherein the altered VIR gene encodes (i) a polypeptide at least 95% identical to SEQ ID NO:4 or (ii) a polypeptide comprising at least 100, 125, 150, 175, 200, or 225 contiguous amino acids that are at least 95% identical to a corresponding fragment of SEQ ID NO:4.

~~20.19.~~ The method of claim ~~15~~14, comprising detecting a presence or absence of a genetic marker linked to the alteration within 1, 10, 20, 50, 100, 200, 500, 1000, or 2000 kb of the genomic region.

~~21.20.~~ The method of claim ~~15~~14, wherein the plant is less than 5 years old.

~~22.21.~~ The method of claim ~~15~~14, wherein the plant is less than one year old.

~~23.22.~~ The method of claim ~~15~~14, wherein the method further comprises predicting a shell thickness phenotype by detecting the presence or absence of a nucleic acid sequence associated with a dura, tenera, or pisifera phenotype.

~~24.23.~~ The method of claim ~~23~~22, wherein the shell thickness phenotype is predicted from the same sample as the fruit color phenotype in each of the plurality of plants.

~~25.24.~~ A method for determining a fruit color phenotype of an oil palm plant, the method comprising,
providing a sample from a plant or seed; and detecting presence or absence of an alteration in a VIR polypeptide corresponding to SEQ ID NO:4 that confers a virescens phenotype to fruit of the oil palm plant, wherein the presence of the alteration predicts the presence of the virescens phenotype.

~~26.~~ A nucleic acid comprising a polynucleotide encoding a polypeptide comprising a sequence at least 95% identical to SEQ ID NO:4.

encoding (i) a polypeptide comprising a sequence at least 95% identical to SEQ ID NO:4 or (ii) a polypeptide comprising at least 100, 125, 150, 175, 200, or 225 contiguous amino acids that are at least 95% identical to a corresponding fragment of SEQ ID NO:4.

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~~28.26.~~ The plant of claim ~~2725~~, wherein the polypeptide comprises SEQ ID NO:4.

~~29.27.~~ A plant having a virescens phenotype, the plant comprising the expression cassette of any of claims ~~2725-2826~~.

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~~30.28.~~ A plant having a nigrescens phenotype, the plant comprising the expression cassette of any of claims ~~2725-2826~~.

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~~31.~~ ~~An isolated nucleic acid comprising an expression cassette, the expression cassette comprising a heterologous promoter operably linked to a polynucleotide encoding a polypeptide comprising (i) a sequence at least 95% identical to SEQ ID NO:4 or (ii) a polypeptide comprising at least 100, 125, 150, 175, 200, or 225 contiguous amino acids that are at least 95% identical to a corresponding fragment of SEQ ID NO:4.~~

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~~32.29.~~ An isolated nucleic acid comprising an expression cassette comprising a promoter operably linked to a polynucleotide, which polynucleotide, when expressed in the plant, reduces expression of a VIR polypeptide corresponding to SEQ ID NO: 4 in a plant ~~(compared to a control plant lacking the expression cassette)~~.

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~~33.30.~~ The nucleic acid of claim ~~3229~~, wherein the polynucleotide comprises at least 20 contiguous nucleotides, the complement, or the reverse complement thereof, of an endogenous nucleic acid encoding a VIR polypeptide at least 95% identical to SEQ ID NO:4, such that expression of the polynucleotide in a plant inhibits expression of the endogenous VIR gene.

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~~34.31.~~ The nucleic acid of claim ~~3330~~, wherein the polynucleotide comprises at least 20, 30, 40, 50, 75, or 100 contiguous nucleotides, the complement, or the reverse complement thereof, of SEQ ID NO: 1 or SEQ ID NO:3.

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~~35.32.~~ The nucleic acid of any of claims ~~3229-3430~~, wherein the polynucleotide encodes an siRNA, antisense polynucleotide, a microRNA, or a sense suppression nucleic acid, which when expressed in a plant suppresses expression of an endogenous VIR gene.

~~36-33.~~ An oil palm plant having a virescens phenotype, the plant comprising the expression cassette of any of claims ~~3229-3532~~.

~~37. An isolated nucleic acid comprising an expression cassette comprising a promoter operably linked to a polynucleotide encoding a polypeptide comprising an amino acid sequence at least 95% identical to at least 100, 125, 150, 175, 200, or 225 contiguous amino acids of SEQ ID NO:4 but lacking at least a corresponding 3' terminal portion {e.g., at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150 carboxyl terminal amino acids } of SEQ ID NO:4.~~

~~38. The nucleic acid of claim 37, wherein the polypeptide comprises the polypeptide encoded by SEQ ID NOS:7, 9, 11, 13, or 15.~~

~~39-34.~~ An oil palm plant having a virescens phenotype, the plant comprising ~~the an~~ expression cassette ~~of any of claims 37 or 38~~ comprising a promoter operably linked to a polynucleotide encoding a polypeptide comprising an amino acid sequence at least 95% identical to at least 100, 125, 150, 175, 200, or 225 contiguous amino acids of SEQ ID NO:4 but lacking at least a corresponding 3' terminal portion {e.g., at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150 carboxyl terminal amino acids } of SEQ ID NO:4.

35. The oil palm plant having a virescent phenotype of claim 34, wherein the polypeptide comprises the polypeptide encoded by SEQ ID NOS: 7, 9, 11, 13, or 15.

~~40-36.~~ A method of making the oil palm plant of any of claims ~~2725-3028~~, ~~3633~~, or ~~3934~~, the method comprising introducing the expression cassette into the plant.

~~41-37.~~ A method of cultivating the oil palm plant of any of claims ~~2725-3028~~, ~~3633~~, or ~~3934~~.