

CLAIMS

1. A method for determining a fruit color phenotype of an oil palm plant, the method comprising, providing a sample from the oil palm plant or seed; and detecting presence or absence of a VIR gene alteration in 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.
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.
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.
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.
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.
7. The method of claim 1, wherein the plant is less than 5 years old.
8. The method of claim 1, wherein the plant is less than one year old.

9. 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.
10. The method of claim 9, wherein the shell thickness phenotype is predicted from the same sample as the fruit color phenotype.
11. The method of claim 1, further comprising selecting the plant or seed for cultivation if the plant is predicted to have the *virescens* phenotype.
12. The method of claim 11, wherein the plant or seed is discarded if the plant or seed is not predicted to have the *virescens* phenotype.
13. 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 VIR gene alteration in 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 *virescens* phenotype.
14. The method of claim 13, 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.
15. The method of claim 13, wherein the alteration is a dominant negative mutation.
16. The method of claim 13, 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.
17. The method of claim 13, 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.

18. The method of claim 13, wherein the plant is less than 5 years old.
19. The method of claim 13, wherein the plant is less than one year old.
20. The method of claim 13, 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.
21. The method of claim 20, wherein the shell thickness phenotype is predicted from the same sample as the fruit color phenotype in each of the plurality of plants.
22. 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.
23. An isolated nucleic acid comprising a polynucleotide encoding a polypeptide comprising a sequence at least 95% identical to SEQ ID NO:4.
24. An oil palm plant comprising a heterologous expression cassette, the expression cassette comprising a heterologous promoter operably linked to a polynucleotide 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.

25. The plant of claim 24, wherein the polypeptide comprises SEQ ID NO:4.
26. An oil palm plant having a virescens phenotype, the oil palm plant comprising the expression cassette of any of claims 24-25.
27. An oil palm plant having a nigrescens phenotype, the oil palm plant comprising the expression cassette of any of claims 24-25.
28. 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.
29. An isolated nucleic acid comprising an expression cassette comprising a promoter operably linked to a polynucleotide, which polynucleotide, when expressed in an oil palm plant, reduces expression of a VIR polypeptide corresponding to SEQ ID NO: 4 in the oil palm plant (compared to a control plant lacking the expression cassette).
30. The nucleic acid of claim 29, 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.
31. The nucleic acid of claim 30, 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.
32. The nucleic acid of any of claims 29-31, 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.

33. An oil palm plant having a virescens phenotype, the plant comprising the expression cassette of any of claims 29-32.
34. 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.
35. The nucleic acid of claim 34, wherein the polypeptide comprises the polypeptide encoded by SEQ ID NOS:7, 9, 11, 13, or 15.
36. An oil palm plant having a virescens phenotype, the plant comprising the expression cassette of any of claims 34 or 35.
37. A method of making the oil palm plant of any of claims 24-27, 33, or 36, the method comprising introducing the expression cassette into the plant.
38. A method of cultivating the oil palm plant of any of claims 24-27, 33, or 36.