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 genetic marker linked to a VIR gene alteration within 2,000 kb 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.

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, 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.

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 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.

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

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

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

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 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.

15. The method of claim 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.

16. The method of claim 14, wherein the alteration is a dominant negative mutation.

17. The method of claim 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.

18. The method of claim 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.

19. The method of claim 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.

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

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

22. The method of claim 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.

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