Claims

1. A method for predicting palm oil yield of a test oil palm plant, the method comprising the steps of:

(i) determining, from a sample of a test oil palm plant of a population of oil palm plants, at least a first single nucleotide polymorphism (SNP) genotype of the test oil palm plant, the first SNP genotype corresponding to a first SNP marker, the first SNP marker (a) being located in a first candidate gene region for a high-oil-production trait and (b) being associated, after stratification and kinship correction, with the high-oil-production trait with a *p-value* < 0.001 in the population or having a linkage disequilibrium r^2 value of at least 0.2 with respect to a first other SNP marker that is linked thereto and associated, after stratification and kinship correction, with the high-oil-production trait with a *p-value* < 0.001 in the population;

(ii) comparing the first SNP genotype of the test oil palm plant to a corresponding first reference SNP genotype indicative of the high-oil-production trait in the same genetic background as the population; and

(iii) predicting palm oil yield of the test oil palm plant based on the extent to which the first SNP genotype of the test oil palm plant matches the corresponding first reference SNP genotype,

wherein

the high-oil-production trait comprises increased oil-to-dry mesocarp; and

the first candidate gene region is a region of the oil palm genome corresponding to:

(1) candidate gene region 1, comprising a gene encoding CBL-Interacting Protein Kinase 32 and extending from 4 kb upstream to 4 kb downstream of the gene encoding CBL-Interacting Protein Kinase 32;

(2) candidate gene region 2, comprising a gene encoding Shaggy-Related Protein Kinase and extending from 4 kb upstream to 4 kb downstream of the gene encoding Shaggy-Related Protein Kinase;

(3) candidate gene region 3, comprising a gene encoding Probable Receptor-Like Protein Kinase and extending from 4 kb upstream to 4 kb downstream of the gene encoding Probable Receptor-Like Protein Kinase;

(4) candidate gene region 4, comprising a gene encoding Tau Class Glutathione S-Transferase and extending from 4 kb upstream to 4 kb downstream of the gene encoding Tau Class Glutathione S-Transferase;

(5) candidate gene region 5, comprising a gene encoding Cinnamoyl-CoA Reductase and extending from 4 kb upstream to 4 kb downstream of the gene encoding Cinnamoyl-CoA Reductase;

(6) candidate gene region 6, comprising a gene encoding 1-Aminocyclopropane-1-Carboxylate Synthase 7 and extending from 4 kb upstream to 4 kb downstream of the gene

encoding 1-Aminocyclopropane-1-Carboxylate Synthase 7;

(7) candidate gene region 7, comprising a gene encoding Mitochondrial Trans-2-Enoyl-CoA Reductase and extending from 4 kb upstream to 4 kb downstream of the gene encoding Mitochondrial Trans-2-Enoyl-CoA Reductase; or

(8) candidate gene region 8, comprising a gene encoding Chloroplastic Biotin Carboxyl Carrier Protein of Acetyl CoA Carboxylase and extending from 4 kb upstream to 4 kb downstream of the gene encoding Chloroplastic Biotin Carboxyl Carrier Protein of Acetyl CoA Carboxylase.

2. The method according to claim 1, wherein the population of oil palm plants comprises a *Ulu Remis dura* x AVROS *pisifera* population, a *Johor Labis dura* x AVROS *pisifera* population, a *Ulu Remis dura* x Dumpy AVROS *pisifera* population, a Dumpy AVROS population, or a combination thereof.

3. The method according to claim 1 or 2, wherein:

the first candidate gene region is candidate gene region 1; and

the population of oil palm plants comprises a *Ulu Remis dura* x AVROS *pisifera* population, a *Johor Labis dura* x AVROS *pisifera* population, a *Ulu Remis dura* x Dumpy AVROS *pisifera* population, or a combination thereof.

4. The method according to claim 1 or 2, wherein:

the first candidate gene region is candidate gene region 2; and

the population of oil palm plants comprises a *Ulu Remis dura* x AVROS *pisifera* population, a *Ulu Remis dura* x Dumpy AVROS *pisifera* population, or a combination thereof.

5. The method according to claim 1 or 2, wherein:

the first candidate gene region is candidate gene region 3; and

the population of oil palm plants comprises a Dumpy AVROS population.

6. The method according to claim 1 or 2, wherein:

the first candidate gene region is candidate gene region 4; and

the population of oil palm plants comprises a *Ulu Remis dura* x AVROS *pisifera* population, a *Johor Labis dura* x AVROS *pisifera* population, or a combination thereof.

7. The method according to claim 1 or 2, wherein:

the first candidate gene region is candidate gene region 5; and

the population of oil palm plants comprises a *Ulu Remis dura* x AVROS *pisifera*

population.

8. The method according to claim 1 or 2, wherein:
the first candidate gene region is candidate gene region 6; and
the population of oil palm plants comprises a Dumpy AVROS population.

9. The method according to claim 1 or 2, wherein:
the first candidate gene region is candidate gene region 7; and
the population of oil palm plants comprises a Dumpy AVROS population.

10. The method according to claim 1 or 2, wherein:
the first candidate gene region is candidate gene region 8; and
the population of oil palm plants comprises a *Ulu Remis dura* x AVROS *pisifera* population, a *Johor Labis dura* x AVROS *pisifera* population, or a combination thereof.

11. The method according to any of claims 1 to 10, wherein:
the first SNP marker comprises one or more SNP marker(s) of either of the two following Tables, wherein said SNP marker(s) is/are associated with the high-oil-production trait:

SNP No.	SNP ID	Candidate gene region
1	S_00002156_00008396	1
2	S_000023169_00001770	2
3	S_000023169_00004772	2
4	S_000004932_00093119	3
5	S_000004932_00094229	3
6	S_000004932_00094970	3
7	S_00004932_00097689	3
8	S_00004607_00009651	4
9	S_00007694_00038606	5

SNP No.	SNP ID	Candidate gene region
10	S_00000302_00166120	6
11	S_00002174_00010170	7
12	S_00018257_00003287	8
13	S_00018257_00006313	8