1. A method of detecting the genotype of a polymorphic marker in the SHELL gene of *Elaeis guineensis* (*E. guineensis*) palm plants or seeds, wherein the method comprises detecting the genotype of the polymorphic marker corresponding to:

(i) nucleotide 67 of exon 1 of the SHELL gene, wherein an A to C mutation corresponding to nucleotide 67 of exon 1 of the SHELL gene as shown in SEQ ID NO: 13, indicates the presence of a *pisifera* allele; or

(ii) nucleotide 69 of exon 1 of the SHELL gene, wherein an A to T mutation corresponding to nucleotide 69 of exon 1 of the SHELL gene as shown in SEQ ID NO: 15, indicates the presence of a *pisifera* allele; or

(iii) nucleotide 70 of exon 1 of the SHELL gene, wherein a C to G mutation corresponding to nucleotide 70 of exon 1 of the SHELL gene as shown in SEQ ID NO: 19, indicates the presence of a *pisifera* allele; or

(iv) nucleotide 71 of exon 1 of the SHELL gene, wherein a G to A mutation corresponding to nucleotide 71 of exon 1 of the SHELL gene as shown in SEQ ID NO:18, indicates the presence of a *pisifera* allele; or

(v) nucleotide 110 of exon 1 of the SHELL gene, wherein a T to A mutation corresponding to nucleotide 110 of exon 1 of the SHELL gene as shown in SEQ ID NO: 20, indicates the presence of a *pisifera* allele; or

(vi) nucleotide 122 of exon 1 of the SHELL gene, wherein a C to A mutation corresponding to nucleotide 122 of exon 1 of the SHELL gene as shown in SEQ ID NO:14, indicates the presence of a *pisifera* allele; or

(vii) nucleotides 23-37 of exon 1 of the SHELL gene, wherein a 15 base pair deletion mutation corresponding to nucleotides 23-37 of exon 1 of the SHELL gene and causing an in frame deletion of five amino acids at positions 8 to 12 of the translated open reading frame of exon 1 as shown in SEQ ID NO: 17, indicates the presence of a *pisifera* allele; or

(viii) nucleotide 34 of exon 1 of the SHELL gene, wherein a G to C mutation corresponding to nucleotide 34 of exon 1 of the SHELL gene as shown in SEQ ID NO: 16, indicates the presence of a *pisifera* allele; or

(ix) nucleotide 114 of exon 1 of the SHELL gene, wherein a T to C mutation corresponding to nucleotide 114 of exon 1 of the SHELL gene as shown in SEQ ID NO: 21, indicates the presence of a *pisifera* allele,

wherein the genotype of the polymorphic marker indicates the presence, absence, or number of *pisifera* or *dura* alleles.

~~2. The method of claim 1, wherein:~~

~~(i) an A to C mutation of nucleotide 67 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele; or~~

~~(ii) an A to T mutation of nucleotide 69 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele; or~~

~~(iii) a C to G mutation of nucleotide 70 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele; or~~

~~(iv) a G to A mutation of nucleotide 71 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele; or~~

~~(v) a T to A mutation of nucleotide 110 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele; or~~

~~(vi) a C to A mutation of nucleotide 122 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele; or~~

~~(vii) a 15 base pair deletion mutation corresponding to nucleotides 23-37 of exon 1 of the SHELL gene, which causes an in frame deletion of five amino acids at positions 8 to 12 in the translated open reading frame of exon 1, indicates the presence of a *pisifera* allele; or~~

~~(viii) a G to C mutation of nucleotide 34 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele; or~~

~~(ix) a T to C mutation of nucleotide 114 of exon 1 of the SHELL gene indicates the presence of a *pisifera* allele.~~

~~3~~2. The method of claim ~~2~~1, further comprising predicting the shell phenotype of the *E. guineensis* palm plants or seeds based on the presence, absence, or number of *pisifera* or *dura* alleles.

~~4~~3. The method of any one of claims ~~2~~ 1 ~~or~~ or23, wherein the presence of the *pisifera* allele is determined by detecting SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO:16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, or SEQ ID NO:21.

~~5~~4. The method of any one of claims 1 to ~~4~~3, further comprising segregating the palm plants or seeds into groups based on the genotype of the polymorphic markers,

wherein at least one group only contains one of (i) plants or seeds predicted to have a *tenera* shell phenotype, (ii) plants or seeds predicted to have the *dura* shell phenotype, or (iii) plants or seeds predicted to have the *pisifera* shell phenotype,

wherein the presence of one predicted *pisifera* allele and one predicted *dura* allele predicts the *tenera* shell phenotype,

wherein the *pisifera* shell phenotype comprises homozygosity of the mutant allele at the nucleotide, or

wherein the *dura* shell phenotype comprises homozygosity of the wild-type allele at the nucleotide.

~~6~~5. The method of any one of claims 1 to ~~5~~4, wherein the palm plants or seeds are generated from (i) an attempted cross between a plant having the *dura* shell phenotype and a plant having the *pisifera* shell phenotype, (ii) selfing of a *tenera* palm, (iii) a cross between two plants having the *tenera* shell phenotype, (iv) a cross between *dura* and *tenera* palms, or (v) a cross between *tenera* and *pisifera* palms.

~~7~~6. The method of any one of claims 1 to ~~6~~5, wherein the palm plants are less than 5 years old.

~~8~~7. The method of any one of claims 1 to ~~7~~6, wherein the palm plants or seeds are discarded if the palm plants or seeds do not have a genotype predictive of the *tenera* shell phenotype.

~~9~~8. The method of any one of claims 1 to ~~8~~7, further comprising selecting the palm plants or seeds for cultivation if the plam plants or seeds have a genotype predictive of the *tenera* shell phenotype.

~~10~~9. The method of any one of claims 1 to ~~9~~8, further comprising selecting the palm plants or seeds for cultivation if the palm plants or seeds have a genotype predictive of the *dura* shell phenotype.

~~11~~10. The method of any one of claims 1 to ~~10~~9, further comprising selecting the palm plants or seeds for cultivation if the palm plants or seeds have a genotype predictive of the *pisifera* shell phenotype.

~~12~~11. The method of any one of claims 1 to ~~11~~10, wherein the detecting the genotype of the polymorphic marker comprises sequencing.

~~13~~12. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 122 of exon 1 of the SHELL gene.

~~14~~13. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 34 of exon 1 of the SHELL gene.

~~15~~14. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 67 of exon 1 of the SHELL gene.

~~16~~15. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 69 of exon 1 of the SHELL gene.

~~17~~16. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 70 of exon 1 of the SHELL gene.

~~18~~17. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 71 of exon 1 of the SHELL gene.

~~19~~18. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 110 of exon 1 of the SHELL gene.

~~20~~19. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotide 122 of exon 1 of the SHELL gene.

~~21~~20. The method of any one of claims 1 to ~~12~~11, wherein the polymorphic marker is nucleotides 23-37 of exon 1 of the SHELL gene.

~~22~~21. The method of any one of claims 1 to ~~21~~20, wherein the method reduces non-*tenera* contaminant plants or seeds.