GEPHE SUMMARY

Gephebase Gene

DEFICIENS (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^DEFICIENS^#gephebase-summary-title)

GepheID

GP00002100

Entry Status

Published

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait

Fruit shape (https://www.gephebase.org/search-criteria?/and+Trait=^Fruit shape^#gephebase-summary-title)

Trait State in Taxon A

Elaeis guineensis; round fruit

Trait State in Taxon B

Elaeis guineensis; mantled fruit - homeotic floral phenotype - staminodes of pistillate flowers and stamens of staminate flowers develop as pseudocarpels often resulting in sterile parthenocarpic flowers with abortive fruit and very low oil yields

Ancestral State

Taxon A

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Elaeis guineensis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Elaeis guineensis^#gephebase-summary-title)

Common Name

African oil palm

Synonyms

African oil palm; Elaeis guineensis Jacq.; Elaeis guineensis var. tenera (Oil palm); Elaeis guinensi; Elaeis guinensis; Elaeis gunieensis; Eleais guineensis

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Arecales; Arecaceae; Arecoideae; Cocoseae; Elaeidinae; Elaeis

Parent

Elaeis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51952)

NCBI Taxonomy ID

51953 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51953)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Elaeis guineensis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Elaeis guineensis^#gephebase-summary-title)

Common Name

African oil palm

Synonyms

African oil palm; Elaeis guineensis Jacq.; Elaeis guineensis var. tenera (Oil palm); Elaeis guinensi; Elaeis guinensis; Elaeis gunieensis; Eleais guineensis

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Arecales; Arecaceae; Arecoideae; Cocoseae; Elaeidinae; Elaeis

Parent

Elaeis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51952)

NCBI Taxonomy ID

51953 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51953)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

AP3

Synonyms

APETALA 3; ATAP3; FLORAL HOMEOTIC PROTEIN APETALA 3; At3g54340; T12E18_30

String

3702.AT3G54340.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT3G54340.1)

Sequence Similarities

-

GO - Molecular Function

GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)
GO:0003700 : DNA-binding transcription factor activity

UniProtKB Arabidopsis thaliana

P35632 (http://www.uniprot.org/uniprot/P35632)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000977)
GO:0043565 : sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0008134 : transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0008134)
GO:0044212 : transcription regulatory region DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0044212)

GO - Biological Process

GO:0007275 : multicellular organism development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007275)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0010093 : specification of floral organ identity
(https://www.ebi.ac.uk/QuickGO/term/GO:0010093)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

Epigenetic Change (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Epigenetic Change^#gephebase-summary-title)

Molecular Details of the Mutation

hypomethylation of the 3.2 kb oil palm Karma transposable element located within an intron of the DEFICIENS gene - this results in unmasking of a cryptic splice acceptor site and a premature termination signal and causes the mantled fruit phenotype- epigenetic derepression of a TE associated with a deleterious phenotype

Experimental Evidence

Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)

Main Reference

Loss of Karma transposon methylation underlies theÂ mantled somaclonal variant of oil palm. (2015) (https://pubmed.ncbi.nlm.nih.gov/26352475)

Authors

Ong-Abdullah M; Ordway JM; Jiang N; Ooi SE; Kok SY; Sarpan N; Azimi N; Hashim AT; Ishak Z; Rosli SK; Malike FA; Bakar NA; Marjuni M; Abdullah N; Yaakub Z; Amiruddin MD; Nookiah R; Singh R; Low ET; Chan KL; Azizi N; Smith SW; Bacher B; Budiman MA; Van Brunt A; Wischmeyer C; Beil M; Hogan M; Lakey N; Lim CC; Arulandoo X; Wong CK; Choo CN; Wong WC; Kwan YY; Alwee SS; Sambanthamurthi R; Martienssen RA

Abstract

Somaclonal variation arises in plants and animals when differentiated somatic cells are induced into a pluripotent state, but the resulting clones differ from each other and from their parents. In agriculture, somaclonal variation has hindered the micropropagation of elite hybrids and genetically modified crops, but the mechanism responsible remains unknown. The oil palm fruit 'mantled' abnormality is a somaclonal variant arising from tissue culture that drastically reduces yield, and has largely halted efforts to clone elite hybrids for oil production. Widely regarded as an epigenetic phenomenon, 'mantling' has defied explanation, but here we identify the MANTLED locus using epigenome-wide association studies of the African oil palm Elaeis guineensis. DNA hypomethylation of a LINE retrotransposon related to rice Karma, in the intron of the homeotic gene DEFICIENS, is common to all mantled clones and is associated with alternative splicing and premature termination. Dense methylation near the Karma splice site (termed the Good Karma epiallele) predicts normal fruit set, whereas hypomethylation (the Bad Karma epiallele) predicts homeotic transformation, parthenocarpy and marked loss of yield. Loss of Karma methylation and of small RNA in tissue culture contributes to the origin of mantled, while restoration in spontaneous revertants accounts for non-Mendelian inheritance. The ability to predict and cull mantling at the plantlet stage will facilitate the introduction of higher performing clones and optimize environmentally sensitive land resources.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE DEFICIENS is the oil palm ortholog of the B class MADS box transcription factor genes Antirrhinum majus DEFICIENS (DEF) and Arabidopsis APETALA3 (AP3)