GEPHE SUMMARY

Gephebase Gene

FAD2B (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FAD2B^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002073

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

Oil composition (oleate levels) (https://www.gephebase.org/search-criteria?/and+Trait=^Oil composition (oleate levels)^#gephebase-summary-title)

Trait State in Taxon A

Arachis hypogaea (Peanut) normal oleate level

Trait State in Taxon B

Arachis hypogaea (Peanut) high oleate level

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

peanut

Synonyms

peanut; goober; ground-nut; Arachis hypogaea L.; Arachis hypogea

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; dalbergioids sensu lato; Dalbergieae; Pterocarpus clade; Arachis

Parent

Arachis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3817)

NCBI Taxonomy ID

3818 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3818)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

peanut

Synonyms

peanut; goober; ground-nut; Arachis hypogaea L.; Arachis hypogea

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; dalbergioids sensu lato; Dalbergieae; Pterocarpus clade; Arachis

Parent

Arachis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3817)

NCBI Taxonomy ID

3818 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3818)

is Taxon B an Infraspecies?

Yes

Taxon B Description

chemically induced mutant Mycogen-Flavo

GENOTYPIC CHANGE

Generic Gene Name

FAD2B

Synonyms

FAD; FAD2

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0050184 : phosphatidylcholine desaturase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0050184)

GO - Biological Process

GO:0006629 : lipid metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006629)

GO - Cellular Component

UniProtKB Arachis hypogaea

Q9LKK6 (http://www.uniprot.org/uniprot/Q9LKK6)

GenebankID or UniProtKB

()

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Insertion Size

100-999 bp

Molecular Details of the Mutation

insertion of 205-bp miniature inverted-repeat transposable element (MITE) called ahMITE1 at position 665 near the center of the coding region in the case of MF; which causes a frameshift

Experimental Evidence

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

Main Reference

High-oleate peanut mutants result from a MITE insertion into the FAD2 gene. (2004) (https://pubmed.ncbi.nlm.nih.gov/14968307)

Authors

Patel M; Jung S; Moore K; Powell G; Ainsworth C; Abbott A

Abstract

A high-oleate trait in the cultivated peanut (Arachis hypogaea L.) was reported to rely on the allelic composition of the two homeologous, microsomal oleoyl-PC desaturase genes (ahFAD2A or ahFAD2B). The enzyme activity of either ahFAD2A or ahFAD2B is sufficient for a normal oleate phenotype, and a significant reduction in the levels of ahFAD2B and a mutation in ahFAD2A were reported to be responsible for the high-oleate phenotype in one chemically induced mutant (M2-225) and one derived from a naturally occurring (8-2122) mutant. Here, we report an insertion of the same miniature inverted-repeat transposable element (MITE) in the ahFAD2B gene in another chemically induced mutant (Mycogen-Flavo) and the previously characterized M2-225 mutant. In both cases, this MITE insertion in ahFAD2B causes a frameshift, resulting in a putatively truncated protein sequence in both mutants. The insertion of this MITE in ahFAD2B, in addition to the point mutation in ahFAD2A, appears to be the cause of the high-oleate phenotype in Mycogen-Flavo and M2-225 mutants. Utilizing sequences of the MITE, we developed a DNA marker strategy to differentiate the two insertion-containing mutants from the normal oleate peanut variety (AT-108) and the naturally occurring, high-oleate mutant 8-2122. Reverse transcript-PCR/differential digestion results reveal the expression of both ahFAD2A and ahFAD2B genes in Mycogen-Flavo mutant. This result is in contrast to the observation that ahFAD2B transcripts are greatly reduced in the M2-225 mutant having the MITE insertion further 3′ in ahFAD2B gene.

Additional References

RELATED GEPHE

Related Genes

1 (FAD2A) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3818^/and+Trait=Oil composition/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^FAD2B^/and+Taxon ID=^3818^/or+Gene Gephebase=^FAD2B^/and+Taxon ID=^3818^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@TE - The null mutation in FAD2A is also necessary for the high oleate level phenotype.