

## GEPHE SUMMARY

FAD2B ( <a href="https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=%FAD2B%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=%FAD2B%#gephebase-summary-title</a> )	Gephebase Gene	GP00002073	GepheID
	Entry Status	Courtier	Main curator
Published			

## PHENOTYPIC CHANGE

Trait Category			
Physiology ( <a href="https://www.gephebase.org/search-criteria/?and+Trait+Category=%Physiology%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait+Category=%Physiology%#gephebase-summary-title</a> )	Trait		
Oil composition (oleate levels) ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=%Oil+composition+(oleate+levels)%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait=%Oil+composition+(oleate+levels)%#gephebase-summary-title</a> )	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 ( <a href="https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=%Domesticated%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=%Domesticated%#gephebase-summary-title</a> )			
Taxon A	Latin Name		Taxon B
Arachis hypogaea ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Arachis+hypogaea%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Arachis+hypogaea%#gephebase-summary-title</a> )	Arachis hypogaea ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Arachis+hypogaea%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Arachis+hypogaea%#gephebase-summary-title</a> )		Latin Name
peanut	Common Name		Common Name
peanut; goober; ground-nut; Arachis hypogaea L.; Arachis hypogaea	Synonyms		Synonyms
species	Rank		Rank
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	Lineage		Lineage
Arachis () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3817">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3817</a> )	Parent		Parent
3818 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3818">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3818</a> )	NCBI Taxonomy ID		NCBI Taxonomy ID
No	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
	Yes		Yes
			Taxon B Description
			chemically induced mutant Mycogen-Flavo

## GENOTYPIC CHANGE

FAD2B	Generic Gene Name	UniProtKB Arachis hypogaea
FAD; FAD2	Synonyms	GenebankID or UniProtKB
-	String	
-	Sequence Similarities	
GO:0050184 : phosphatidylcholine desaturase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0050184">https://www.ebi.ac.uk/QuickGO/term/GO:0050184</a> )	GO - Molecular Function	
GO:0006629 : lipid metabolic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0006629">https://www.ebi.ac.uk/QuickGO/term/GO:0006629</a> )	GO - Biological Process	
	GO - Cellular Component	

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.