

GEPHE SUMMARY

FAD2A (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=%FAD2A%#gephebase-summary-title)	Gephebase Gene	GP00002075	GepheID
	Entry Status	Courtier	Main curator
Published			

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		Taxon B
Arachis hypogaea (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Arachis+hypogaea%#gephebase-summary-title)	Arachis hypogaea (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Arachis+hypogaea%#gephebase-summary-title)		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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3817)	Parent		Parent
3818 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3818)	NCBI Taxonomy ID		NCBI Taxonomy ID
No	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?

GENOTYPIC CHANGE

FAD2A	Generic Gene Name	UniProtKB Arachis hypogaea var. hirsuta
-	Synonyms	E2GJC1 (http://www.uniprot.org/uniprot/E2GJC1)
-	String	GenebankID or UniProtKB
-	Sequence Similarities	0
GO:0016717 : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (https://www.ebi.ac.uk/QuickGO/term/GO:0016717)	GO - Molecular Function	
GO:0006629 : lipid metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006629)	GO - Biological Process	
GO:0016021 : integral component of membrane	GO - Cellular Component	

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

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%SNP%#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

D150N in a residue that is absolutely conserved among other desaturases

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	GAY	AAY	-
Amino-acid	Asp	Asn	150

Main Reference

The high oleate trait in the cultivated peanut [*Arachis hypogaea* L]. II. Molecular basis and genetics of the trait. (2000) (<https://pubmed.ncbi.nlm.nih.gov/10905348>)

Authors

Jung S; Powell G; Moore K; Abbott A

Abstract

A peanut variety with high oleate content has previously been described. When this high oleate variety was used in breeding crosses, the F2 segregation ratio of high oleate to normal oleate progeny was 3:1 or 15:1 depending on the normal oleate varieties used in the crosses. These data suggested that the high oleate trait is controlled by two recessive genes, and some peanut varieties differ from the high oleate variety by mutations in one gene, while others differ by mutations in two genes. The objective of this study was to understand the molecular nature of the high oleate trait and the various segregation patterns. In the previous paper in this issue, we reported that the level of transcripts expressed by one (ahFAD2B) of two homoeologous genes for oleoyl-PC desaturases in cultivated peanut is significantly reduced in high oleate varieties. In this report, we examined gene expression by RT-PCR/restriction digestion in a cross that shows a one-gene segregation pattern for the high oleate trait. Our data showed that the severely reduced level of ahFAD2B transcript correlates absolutely with the high oleate phenotype in this cross, suggesting that the single gene difference is correlated with the ahFAD2B transcript level. When we tested the enzyme activity of the proteins encoded by ahFAD2A and ahFAD2B by expression of the cloned sequences in yeast, only the ahFAD2B gene product showed significant oleoyl-PC desaturase activity. These data, combined with the observation that ahFAD2A shows a change (D150N) in a residue that is absolutely conserved among other desaturases, raised the possibility that the ahFAD2A in these normal and high oleate lines is a mutant allele. In support of this hypothesis, we found that another ahFAD2A allele in a normal oleate peanut line does not have the D150N change. This peanut line displays a two-gene-segregation pattern for the high oleate trait. In conclusion, our results suggest that a mutation in ahFAD2A and a significant reduction in levels of the ahFAD2B transcript together cause the high oleate phenotype in peanut varieties, and that one expressed gene encoding a functional enzyme appears to be sufficient for the normal oleate phenotype.

Additional References

RELATED GEPHE

Related Genes

1 (FAD2B) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%3818%/and+Trait=Oil+composition/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

The null mutation in FAD2B is also necessary for the high oleate level phenotype.