

GEPHE SUMMARY

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

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=Physiology#gephebase-summary-title)</p> <p>Oil composition (oleate levels) (https://www.gephebase.org/search-criteria?/and+Trait=Oil+composition+oleate+levels#gephebase-summary-title)</p> <p>Arachis hypogaea (Peanut) normal oleate level</p> <p>Arachis hypogaea (Peanut) high oleate level</p> <p>Taxon A</p> <p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Domesticated#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Arachis hypogaea (Peanut) normal oleate level</p> <p>Arachis hypogaea (Peanut) high oleate level</p>	<p>Taxon A</p> <p>Taxon B</p>
<p>Arachis hypogaea (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Arachis+hypogaea#gephebase-summary-title)</p> <p>peanut</p> <p>peanut; goober; ground-nut; Arachis hypogaea L.; Arachis hypogaea</p> <p>species</p> <p>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</p> <p>Arachis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3817)</p> <p>3818 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3818)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p>	<p>Arachis hypogaea (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Arachis+hypogaea#gephebase-summary-title)</p> <p>peanut</p> <p>peanut; goober; ground-nut; Arachis hypogaea L.; Arachis hypogaea</p> <p>species</p> <p>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</p> <p>Arachis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3817)</p> <p>3818 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3818)</p> <p>is Taxon B an Intraspecies?</p> <p>No</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p>

GENOTYPIC CHANGE

<p>FAD2A</p> <p>-</p> <p>-</p> <p>-</p> <p>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)</p> <p>GO:0006629 : lipid metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006629)</p> <p>GO:0016021 : integral component of membrane</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p> <p>GO - Biological Process</p> <p>GO - Cellular Component</p>	<p>E2GJC1 (http://www.uniprot.org/uniprot/E2GJC1)</p> <p>()</p> <p>UniProtKB Arachis hypogaea var. hirsuta</p> <p>GenebankID or UniProtKB</p>
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(<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](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](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](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](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](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.