

GEPHE SUMMARY

Gephebase Gene
FAD2A

Entry Status
Published

GepheID
GP00002075

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Oil composition (oleate levels)

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

Taxon A

Latin Name
Arachis hypogaea

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)

NCBI Taxonomy ID
3818

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Arachis hypogaea

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)

NCBI Taxonomy ID
3818

is Taxon B an Intraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
FAD2A

Synonyms
-

String
-

Sequence Similarities
-

GO - Molecular Function
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

GO - Biological Process
GO:0006629 : lipid metabolic process

GO - Cellular Component
GO:0016021 : integral component of membrane

Presumptive Null
Yes

UniProtKB Arachis hypogaea var. hirsuta
E2GJC1

GenebankID or UniProtKB

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

D150N in a residue that is absolutely conserved among other desaturases

Experimental Evidence

Candidate Gene

	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)

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)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

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