

GEPHE SUMMARY

	Gene	Gephebase Gene	GephelD
flavonoid 3'-hydroxylase (F3'H) (https://www.gephebase.org/search-criteria?/and+Gene		GP00000321	
Gephebase=^flavonoid 3'-hydroxylase (F3'H)^#gephebase-summary-title)			Main curator
	Status	Martin	
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait			
Category="Morphology">#gephebase-summary-title)			
	Trait		
Coloration (seed; pods) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration			
(seed; pods)^#gephebase-summary-title)			
	Trait State in Taxon A		
Glycine max - "tawny pubescence" pods			
	Trait State in Taxon B		
Glycine max - "gray pubescence" pods			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic			
Status="Domesticated">#gephebase-summary-title)			
Taxon A			
	Latin Name		
Glycine max			
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Glycine			
max^#gephebase-summary-title)			
	Common Name		
soybean			
	Synonyms		
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye			
	Rank		
species			
	Lineage		
cellular organisms; Eukaryota; Viridiplantae; Streptophytina; Embryophytina;			
Tracheophyta; Euphyllophyta; Spermatophytina; Magnoliophytina; Mesangiospermae;			
eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae;			
Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettoid clade;			
Phaseoleae; Glycine; Soja			
	Parent		
Soja () - (Rank: subgenus)			
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)			
	NCBI Taxonomy ID		
3847			
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)			
	is Taxon A an Infraspecies?		
Yes			
	Taxon A Description		
Glycine max - "tawny pubescence" pods			
Taxon B			
	Latin Name		
Glycine max			
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Glycine			
max^#gephebase-summary-title)			
	Common Name		
soybean			
	Synonyms		
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye			
	Rank		
species			
	Lineage		
cellular organisms; Eukaryota; Viridiplantae; Streptophytina; Embryophytina;			
Tracheophyta; Euphyllophyta; Spermatophytina; Magnoliophytina; Mesangiospermae;			
eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae;			
Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettoid clade;			
Phaseoleae; Glycine; Soja			
	Parent		
Soja () - (Rank: subgenus)			
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)			
	NCBI Taxonomy ID		
3847			
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)			
	is Taxon B an Infraspecies?		
Yes			
	Taxon B Description		
Glycine max - "gray pubescence" pods			

GENOTYPIC CHANGE

	Generic Gene Name		
CYP75B1			UniProtKB Arabidopsis thaliana
	Synonyms		Q9SD85 (http://www.uniprot.org/uniprot/Q9SD85)
CYP75B1; CYTOCHROME P450 75B1; D501; F13G24.190; F13G24_190; F3'H;			GenebankID or UniProtKB
FLAVONOID 3'-HYDROXYLASE; TRANSPARENT TESTA 7; TT7; At5g07990			NP_001237015 (https://www.ncbi.nlm.nih.gov/nuccore/NP_001237015)
	String		
3702.AT5G07990.1			
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G07990.1)			
	Sequence Similarities		
Belongs to the cytochrome P450 family.			
	GO - Molecular Function		
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)			
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)			
GO:0016709 : oxidoreductase activity, acting on paired donors, with incorporation or			

reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen (<https://www.ebi.ac.uk/QuickGO/term/GO:0016709>)

GO - Biological Process

GO:0009733 : response to auxin (<https://www.ebi.ac.uk/QuickGO/term/GO:0009733>)

GO:0009813 : flavonoid biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009813>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)

GO:0005789 : endoplasmic reticulum membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

1bp deletion resulting in frameshift

Experimental Evidence

Linkage Mapping ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping))

Main Reference

A single-base deletion in soybean flavonoid 3'-hydroxylase gene is associated with gray pubescence color. (2002) (<https://pubmed.ncbi.nlm.nih.gov/12175012>)

Authors

Toda K; Yang D; Yamanaka N; Watanabe S; Harada K; Takahashi R

Abstract

The T locus of soybean (*Glycine max* (L.) Merr.) controls pubescence and seed coat color and is presumed to encode flavonoid 3'-hydroxylase (F3'H). The dominant T and the recessive t allele of the locus produce brown and gray pubescence, respectively. PCR primers were constructed based on the sequence of a soybean EST clone homologous to the F3'H gene. A putative full-length cDNA, sf3'h1 was isolated by 3' and 5' RACE. Sequence analysis revealed that sf3'h1 consists of 1690 nucleotides encoding 513 amino acids. It had 68% and 66% homology with corresponding F3'H protein sequences of petunia and *Arabidopsis*, respectively. A conserved amino acid sequence of F3'H proteins, GGEK, was found in the deduced polypeptide. Sequence analysis of the gene from a pair of near-isogenic lines for T, To7B (TT, brown) and To7G (tt, gray) revealed that they differed by a single C deletion in the coding region of To7G. The deletion changed the subsequent reading frame resulting in a truncated polypeptide lacking the GGEK consensus sequence and the heme-binding domain. Genomic Southern analysis probed by sf3'h1 revealed restriction fragment length polymorphisms between cultivars with different pubescence color. Further, sf3'h1 was mapped at the same position with T locus on LG3(c2). PCR-RFLP analysis was performed to detect the single-base deletion. To7B and three cultivars with brown pubescence exhibited shorter fragments, while To7G and three cultivars with gray pubescence had longer fragments due to the single-base deletion. The PCR-RFLP marker co-segregated with genotypes at the T locus in a F2 population segregating for the T locus. The above results strongly suggest that sJ3'h1 represents the T gene of soybean responsible for pubescence color and that the single-base deletion may be responsible for gray pubescence color.

Additional References

Cloning of the pleiotropic T locus in soybean and two recessive alleles that differentially affect structure and expression of the encoded flavonoid 3' hydroxylase. (2003) (<https://pubmed.ncbi.nlm.nih.gov/12586717>)

RELATED GEPHE

Related Genes

4 (Flavonoid 3'-hydroxylase (F3'H), flavonoid 3';5'-hydroxylase (F3'5'H), PH4/GmMYB-G20-1, R/glyma09g36983) ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+TaxonID=^3847^/and+Trait=Coloration/and+groupHaplotypes=true))

Related Haplotypes

4 ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^flavonoid+3'-hydroxylase+(F3'H)^/and+Taxon+ID=^3847^/or+Gene+Gephebase=^flavonoid+3'-hydroxylase+(F3'H)^/and+Taxon+ID=^3847^))

EXTERNAL LINKS

COMMENTS