GEPHE SUMMARY

Gephebase Gene
flavonoid 3′-hydroxylase (F3′H) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^flavonoid 3′-hydroxylase (F3′H)^#gephebase-summary-title)

GepheID
GP00000321

Entry Status
Published

Main curator
Martin

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; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid 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; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid 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

Synonyms
CYP75B1; CYTOCHROME P450 75B1; D501; F13G24.190; F13G24_190; F3′H; FLAVONOID 3′-HYDROXYLASE; TRANSPARENT TESTA 7; TT7; At5g07990

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

UniProtKB Arabidopsis thaliana
Q9SD85 (http://www.uniprot.org/uniprot/Q9SD85)

GenebankID or UniProtKB
NP_001237015 (https://www.ncbi.nlm.nih.gov/nuccore/NP_001237015)

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 (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

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

1bp deletion resulting in frameshift

Experimental Evidence

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

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) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3847^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

4 (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^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS