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
GP00000315

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 (flowers; pubescence; seeds) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (flowers; pubescence; seeds)^#gephebase-summary-title)

Trait State in Taxon A
Glycine max

Trait State in Taxon B
Glycine soja

Ancestral State
Taxon A

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#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?
No

Taxon B

Latin Name
Glycine soja (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Glycine soja^#gephebase-summary-title)

Common Name
-

Synonyms
wild soybean; Glycine soja Siebold & Zucc.

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
3848 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3848)

is Taxon B an Infraspecies?
No

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 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)

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

GenebankID or UniProtKB
ABQ96219 (https://www.ncbi.nlm.nih.gov/nuccore/ABQ96219)

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 at +973 resulting in premature stop codon

Experimental Evidence

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

Main Reference

Allele-specific marker development and selection efficiencies for both flavonoid 3′-hydroxylase and flavonoid 3′,5′-hydroxylase genes in soybean subgenus soja. (2013)
(https://pubmed.ncbi.nlm.nih.gov/23463490)

Authors

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Abstract

Color is one of the phenotypic markers mostly used to study soybean (Glycine max L. Merr.) genetic, molecular and biochemical processes. Two P450-dependent mono-oxygenases, flavonoid 3′-hydroxylase (F3′H; EC1.14.3.21) and flavonoid 3′,5′-hydroxylase (F3′5′H, EC1.14.13.88), both catalyzing the hydroxylation of the B-ring in flavonoids, play an important role in coloration. Previous studies showed that the T locus was a gene encoding F3′H and the W1 locus co-segregated with a gene encoding F3′5′H in soybean. These two genetic loci have identified to control seed coat, flower and pubescence colors. However, the allelic distributions of both F3′H and F3′5′H genes in soybean were unknown. In this study, three novel alleles were identified (two of four alleles for GmF3′H and one of three alleles for GmF3′5′H). A set of gene-tagged markers was developed and verified based on the sequence diversity of all seven alleles. Furthermore, the markers were used to analyze soybean accessions including 170 cultivated soybeans (G. max) from a mini core collection and 102 wild soybeans (G. soja). For both F3′H and F3′5′H, the marker selection efficiencies for pubescence color and flower color were determined. The results showed that one GmF3′H allele explained 92.2 % of the variation in tawny and two gmf3′h alleles explained 63.8 % of the variation in gray pubescence colors. In addition, two GmF3′5′H alleles and one gmF3′5′h allele explained 94.0 % of the variation in purple and 75.3 % in white flowers, respectively. By the combination of the two loci, seed coat color was determined. In total, 90.9 % of accessions possessing both the gmf3′h-b and gmf3′5′h alleles had yellow seed coats. Therefore, seed coat colors are controlled by more than two loci.

Additional References

RELATED GEPHE

Related Genes

4 (flavonoid 3′;5′-hydroxylase (F3′5′H), flavonoid 3′-hydroxylase (F3′H), PH4/GmMYB-G20-1, R/glyma09g36983) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3847^/and+Trait=Coloration/or+Taxon ID=^3848^/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=^3848^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS