

GEPHE SUMMARY

Gephebase Gene

flavonoid 3',5'-hydroxylase (F3'5'H)

Entry Status

Published

GepheID

GP00000322

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Morphology

Trait

Coloration (flowers; pubescence; seeds)

Trait State in Taxon A

Glycine max

Trait State in Taxon B

Glycine soja

Ancestral State

Taxon A

Taxonomic Status

Intraspecific

Taxon A

Latin Name

Glycine max

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; Pentapetales; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Glycine; Soja

Parent

Soja () - (Rank: subgenus)

NCBI Taxonomy ID

3847

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Glycine soja

Common Name

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Synonyms

wild soybean; Glycine soja Siebold & Zucc.

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Glycine; Soja

Parent

Soja () - (Rank: subgenus)

NCBI Taxonomy ID

3848

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

CYP75A2

Synonyms

CYP75; CYPEG1

String

-

Sequence Similarities

Belongs to the cytochrome P450 family.

GO - Molecular Function

GO:0020037 : heme binding

GO:0005506 : iron ion binding

GO:0004497 : monooxygenase activity

GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen

GO - Biological Process

GO:0009718 : anthocyanin-containing compound biosynthetic process

GO - Cellular Component

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UniProtKB Solanum melongena

P37120

GenebankID or UniProtKB

ABQ96219

Presumptive Null

Yes

Molecular Type

Coding

Aberration Type

Insertion

Insertion Size

10-99 bp

Molecular Details of the Mutation

53bp insertion at +1352

Experimental Evidence

Candidate Gene

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)

Authors

Guo Y; Qiu LJ

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'-hydroxylase (F3'H), flavonoid 3'-hydroxylase (F3'H), PH4/GmMYB-G20-1, R/glyma09g36983)

Related Haplotypes

No matches found.

COMMENTS