## 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
GP00000318

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

Trait State in Taxon A
Glycine max - purple

Trait State in Taxon B
Glycine max - pink

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?
No

### 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?
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
NP_001237015 (https://www.ncbi.nlm.nih.gov/nuccore/NP_001237015)

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

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

Transposon insertion in intron 2

Experimental Evidence

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

Main Reference

The wp mutation of Glycine max carries a gene-fragment-rich transposon of the CACTA superfamily. (2005) (https://pubmed.ncbi.nlm.nih.gov/16141454)

Authors

Zabala G; Vodkin LO

Abstract

We used soybean (Glycine max) cDNA microarrays to identify candidate genes for a stable mutation at the Wp locus in soybean, which changed a purple-flowered phenotype to pink, and found that flavanone 3-hydroxylase cDNAs were overexpressed in purple flower buds relative to the pink. Restriction fragment length polymorphism analysis and RNA gel blots of purple and pink flower isolines, as well as the presence of a 5.7-kb transposon insertion in the wp mutant allele, have unequivocally shown that flavanone 3-hydroxylase gene 1 is the Wp locus. Moreover, the 5.7-kb insertion in wp represents a novel transposable element (termed Tgm-Express1) with inverted repeats closely related to those of other Tgms (transposable-like elements, G. max) but distinct in several characteristics, including the lack of subterminal inverted repeats. More significantly, Tgm-Express1 contains four truncated cellular genes from the soybean genome, resembling the Pack-MULEs (Mutator-like transposable elements) found in maize (Zea mays), rice (Oryza sativa), and Arabidopsis thaliana and the Helitrons of maize. The presence of the Tgm-Express1 element causing the wp mutation, as well as a second Tgm-Express2 element elsewhere in the soybean genome, extends the ability to acquire and transport host DNA segments to the CACTA family of elements, which includes both Tgm and the prototypical maize Spm/En.

Additional References

## 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

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