

GEPHE SUMMARY

	Gephebase Gene	GephelD
flavonoid 3'-hydroxylase (F3'H) (https://www.gephebase.org/search-criteria?/and+Gene	GP00000318	
Gephebase=^flavonoid 3'-hydroxylase (F3'H)^#gephebase-summary-title)		Main curator
	Entry Status	Martin
Published		

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	Taxon B
Glycine max		Glycine max
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Glycine		(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Glycine
max^#gephebase-summary-title)		max^#gephebase-summary-title)
	Common Name	
soybean		soybean
	Synonyms	
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye		soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye
	Rank	
species		species
	Lineage	
cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophytina; Tracheophytina; Euphyllophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettoid clade; Phaseoleae; Glycine; Soja		cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophytina; Tracheophytina; 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)		Soja () - (Rank: subgenus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)
	NCBI Taxonomy ID	
3847		3847
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)
	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
No		No

GENOTYPIC CHANGE

CYP75B1	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	GenebankID or UniProtKB
CYP75B1; CYTOCHROME P450 75B1; D501; F13G24.190; F13G24_190; F3'H; 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

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Cis-regulatory%22#gephebase-summary-title>)

Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22Insertion%22#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=%22Candidate+Gene%22#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

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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/glyma09g369983) (<https://www.gephebase.org/search-criteria?/or+TaxonID=%223847%22/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

4 ([https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%22flavonoid+3'-hydroxylase+\(F3'H\)%22/and+Taxon+ID=%223847%22/or+Gene+Gephebase=%22flavonoid+3'-hydroxylase+\(F3'H\)%22/and+Taxon+ID=%223847%22#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%22flavonoid+3'-hydroxylase+(F3'H)%22/and+Taxon+ID=%223847%22/or+Gene+Gephebase=%22flavonoid+3'-hydroxylase+(F3'H)%22/and+Taxon+ID=%223847%22#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

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