

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait)	Trait Category	
Category="Morphology"#gephebase-summary-title)		
Coloration (flowers) (<a "="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait=")	Trait	
(flowers)"#gephebase-summary-title)		
Glycine max - purple	Trait State in Taxon A	
Glycine max - pink	Trait State in Taxon B	
Taxon A	Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic)	Taxonomic Status	
Status="Domesticated"#gephebase-summary-title)		

Taxon A	Latin Name	Taxon B	Latin Name
Glycine max (<a "="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=")	Glycine max (<a "="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=")	Glycine max (<a "="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=")	Glycine max (<a "="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=")
soybean	Common Name	soybean	Common Name
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	Synonyms	soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	Synonyms
species	Rank	species	Rank
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	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	Lineage
Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)	Parent	Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)	Parent
3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)	NCBI Taxonomy ID	3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

CYP75B1	Generic Gene Name	Q9SD85 (http://www.uniprot.org/uniprot/Q9SD85)	UniProtKB Arabidopsis thaliana
CYP75B1; CYTOCHROME P450 75B1; D501; F13G24.190; F13G24_190; F3'H; FLAVONOID 3'-HYDROXYLASE; TRANSPARENT TESTA 7; TT7; At5g07990	Synonyms	NP_001237015 (https://www.ncbi.nlm.nih.gov/nuccore/NP_001237015)	GenebankID or UniProtKB
3702.AT5G07990.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G07990.1)	String		
Belongs to the cytochrome P450 family.	Sequence Similarities		
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)	GO - Molecular Function		
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=~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

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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/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](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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