

GEPHE SUMMARY

flavonoid 3':5'-hydroxylase (F3'5'H) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~flavonoid+3':5'-hydroxylase+(F3'5'H)^#gephebase-summary-title)	Gephebase Gene	GP00000327	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)	Trait Category		
Coloration (flowers) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+(flowers)^#gephebase-summary-title)	Trait		
Pisum sativum- line JI15	Trait State in Taxon A		
Pisum sativum - b type line JI73 and others	Trait State in Taxon B		
Taxon A	Ancestral State		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated^#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Pisum sativum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Pisum+sativum^#gephebase-summary-title)	Latin Name	Pisum sativum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Pisum+sativum^#gephebase-summary-title)	Latin Name
pea	Common Name	pea	Common Name
pea; garden pea; peas; Pisum sativum L.	Synonyms	pea; garden pea; peas; Pisum sativum L.	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; Hologalegina; IRL clade; Fabaeae; Pisum	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; Hologalegina; IRL clade; Fabaeae; Pisum	Lineage
Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3887)	Parent	Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3887)	Parent
3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3888)	NCBI Taxonomy ID	3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3888)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Pisum sativum- line JI15	Taxon A Description	Pisum sativum - b type line JI73 and others	Taxon B Description

GENOTYPIC CHANGE

CYP75A2	Generic Gene Name	P37120 (http://www.uniprot.org/uniprot/P37120)	UniProtKB Solanum melongena
CYP75; CYPEG1	Synonyms	ADW66161 (https://www.ncbi.nlm.nih.gov/nuccore/ADW66161)	GenebankID or UniProtKB
-	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:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)			
GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (https://www.ebi.ac.uk/QuickGO/term/GO:0016705)			

GO - Biological Process

GO:0009718 : anthocyanin-containing compound biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009718>)

GO - Cellular Component

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Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes^#gephebase-summary-title](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](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](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Deletion^#gephebase-summary-title))

Deletion Size

10-99 bp

Molecular Details of the Mutation

23bp deletion resulting in frameshift and truncated protein

Experimental Evidence

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping^#gephebase-summary-title))

Main Reference

The B gene of pea encodes a defective flavonoid 3',5'-hydroxylase, and confers pink flower color. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22492867>)

Authors

Moreau C; Ambrose MJ; Turner L; Hill L; Ellis TH; Hofer JM

Abstract

The inheritance of flower color in pea (*Pisum sativum*) has been studied for more than a century, but many of the genes corresponding to these classical loci remain unidentified. Anthocyanins are the main flower pigments in pea. These are generated via the flavonoid biosynthetic pathway, which has been studied in detail and is well conserved among higher plants. A previous proposal that the *Clarifloroseus* (B) gene of pea controls hydroxylation at the 5' position of the B ring of flavonoid precursors of the anthocyanins suggested to us that the gene encoding flavonoid 3',5'-hydroxylase (F3'5'H), the enzyme that hydroxylates the 5' position of the B ring, was a good candidate for B. In order to test this hypothesis, we examined mutants generated by fast neutron bombardment. We found allelic pink-flowered b mutant lines that carried a variety of lesions in an F3'5'H gene, including complete gene deletions. The b mutants lacked glycosylated delphinidin and petunidin, the major pigments present in the progenitor purple-flowered wild-type pea. These results, combined with the finding that the F3'5'H gene cosegregates with b in a genetic mapping population, strongly support our hypothesis that the B gene of pea corresponds to a F3'5'H gene. The molecular characterization of genes involved in pigmentation in pea provides valuable anchor markers for comparative legume genomics and will help to identify differences in anthocyanin biosynthesis that lead to variation in pigmentation among legume species.

Additional References

RELATED GEPHE

Related Genes

1 (PsbHLH = A) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~3888^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~3888^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~flavonoid 3':5'-hydroxylase \(F3'5'H\)^/and+Taxon ID=~3888^/or+Gene Gephebase=~flavonoid 3':5'-hydroxylase \(F3'5'H\)^/and+Taxon ID=~3888^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~flavonoid+3':5'-hydroxylase+(F3'5'H)^/and+Taxon+ID=~3888^/or+Gene+Gephebase=~flavonoid+3':5'-hydroxylase+(F3'5'H)^/and+Taxon+ID=~3888^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS