

GEPHE SUMMARY

	Gephebase Gene	GephelD
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)	GP00000327	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	
Pisum sativum- line JI15	Trait State in Taxon B	
Pisum sativum - b type line JI73 and others	Ancestral State	
Taxon A	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)		
Taxon A		Taxon B
Pisum sativum	Latin Name	Latin Name
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Pisum sativum^#gephebase-summary-title)		
pea	Common Name	Common Name
pea; garden pea; peas; Pisum sativum L.	Synonyms	Synonyms
species	Rank	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilioideae; 50 kb inversion clade; NPAAA clade; Hologalegina; IRL clade; Fabeae; Pisum	Lineage	Lineage
Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3887)	Parent	Parent
3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3888)	NCBI Taxonomy ID	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Pisum sativum- line JI15	Taxon A Description	Taxon B Description
Belongs to the cytochrome P450 family.	Sequence Similarities	
	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: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)		

GENOTYPIC CHANGE

CYP75A2	Generic Gene Name	UniProtKB Solanum melongena
CYP75; CYPEG1	Synonyms	GenebankID or UniProtKB
-	String	
	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: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

-		Presumptive Null
Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=%27Yes%27#gephebase-summary-title)		Molecular Type
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Coding%27#gephebase-summary-title)		Aberration Type
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Deletion%27#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=%27Linkage Mapping%27#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 (<i>Pisum sativum</i>) 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 Clariroseus (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

1 (PsbHLH = A) (https://www.gephebase.org/search-criteria?/or+Taxon ID=%273888%27/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%27flavonoid 3';5'-hydroxylase (F3'5'H)%27/and+Taxon ID=%273888%27/or+Gene Gephebase=%27flavonoid 3';5'-hydroxylase (F3'5'H)%27/and+Taxon ID=%273888%27#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS