

GEPHE SUMMARY

PsbHLH = A (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=~PsbHLH = A~#gephebase-summary-title)	Gephebase Gene	GepheID
	GP00000935	
	Entry Status	Martin
Published		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		Trait State in Taxon A
Pisum sativum - Knight’s Marrow and Knight’s Dwarf White		Trait State in Taxon B
Data not curated		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)		Pisum sativum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Pisum sativum~#gephebase-summary-title)
pea		pea
pea; garden pea; peas; Pisum sativum L.		pea; garden pea; peas; Pisum sativum L.
species		species
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; Fabeae; Pisum		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; Fabeae; Pisum
Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3887)		Pisum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3887)
3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3888)		3888 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3888)
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes
		Taxon B Description
		Pisum sativum - Knight’s Marrow and Knight’s Dwarf White

GENOTYPIC CHANGE

BHLH	Generic Gene Name	UniProtKB Pisum sativum
	Synonyms	E3SXU4 (http://www.uniprot.org/uniprot/E3SXU4)
	String	GU132941 (https://www.ncbi.nlm.nih.gov/nucore/GU132941)
Sequence Similarities		
Belongs to the bHLH protein family.		
GO - Molecular Function		
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)		
GO - Biological Process		
GO:0009813 : flavonoid biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009813)		
GO - Cellular Component		

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

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

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

SNP Coding Change

-

Molecular Details of the Mutation

Splice site mutation: a simple G to A transition in a splice donor site that leads to a mis-spliced mRNA with a premature stop codon

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))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Identification of Mendel’s white flower character. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20949001>)

Authors

Hellens RP; Moreau C; Lin-Wang K; Schwinn KE; Thomson SJ; Fiers MW; Frew TJ; Murray SR; Hofer JM; Jacobs JM; Davies KM; Allan AC; Bendahmane A; Coyne CJ; Timmerman-Vaughan GM; Ellis TH

Abstract

The genetic regulation of flower color has been widely studied, notably as a character used by Mendel and his predecessors in the study of inheritance in pea.

We used the genome sequence of model legumes, together with their known synteny to the pea genome to identify candidate genes for the A and A2 loci in pea. We then used a combination of genetic mapping, fast neutron mutant analysis, allelic diversity, transcript quantification and transient expression complementation studies to confirm the identity of the candidates.

We have identified the pea genes A and A2. A is the factor determining anthocyanin pigmentation in pea that was used by Gregor Mendel 150 years ago in his study of inheritance. The A gene encodes a bHLH transcription factor. The white flowered mutant allele most likely used by Mendel is a simple G to A transition in a splice donor site that leads to a mis-spliced mRNA with a premature stop codon, and we have identified a second rare mutant allele. The A2 gene encodes a WD40 protein that is part of an evolutionarily conserved regulatory complex.

Additional References

RELATED GEPHE

Related Genes

1 (flavonoid 3’;5’-hydroxylase (F3’5’H)) ([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

No matches found.

EXTERNAL LINKS

COMMENTS

@Splicing