

GEPHE SUMMARY

bHLH2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=%bHLH2%#gephebase-summary-title)	Gephebase Gene	GP00002085	GepheID
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

Trait Category			
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=%Morphology%#gephebase-summary-title)	Trait		
Coloration (flower; seed) (https://www.gephebase.org/search-criteria?/and+Trait=%Coloration+(flower;+seed)%#gephebase-summary-title)	Trait State in Taxon A		
fully purple flowers and dark-brown seeds	Trait State in Taxon B		
pale reddish flowers with fine red spots or sectors and ivory seeds with tiny dark brown spots	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	Latin Name
Ipomoea purpurea (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Ipomoea+purpurea%#gephebase-summary-title)		Ipomoea purpurea (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Ipomoea+purpurea%#gephebase-summary-title)	
common morning-glory	Common Name	common morning-glory	Common Name
Convolvulus purpureus; Pharbitis purpurea; common morning-glory; Convolvulus purpureus L., 1762; Ipomoea purpurea (L.) Roth, 1787; Pharbitis purpurea (L.) Voigt, 1845; Pharbitis purpurea	Synonyms	Convolvulus purpureus; Pharbitis purpurea; common morning-glory; Convolvulus purpureus L., 1762; Ipomoea purpurea (L.) Roth, 1787; Pharbitis purpurea (L.) Voigt, 1845; Pharbitis purpurea	Synonyms
Rank		Rank	
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea		cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea	
Parent		Parent	
Ipomoea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4119)	NCBI Taxonomy ID	Ipomoea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4119)	NCBI Taxonomy ID
4121 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4121)		4121 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4121)	
No	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
		ivsâ€m2 line PR43	Taxon B Description

GENOTYPIC CHANGE

BHLH2	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	GenebankID or UniProtKB
AtEGL3; ATMYC-2; EGL1; ENHANCER OF GLABRA 3; F24D7.16; F24D7_16; EGL3; EN30; MYC146; At1g63650	0	
3702.AT1G63650.3 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G63650.3)	String	
-	Sequence Similarities	
GO:0046983 : protein dimerization activity	GO - Molecular Function	

(https://www.ebi.ac.uk/QuickGO/term/GO:0046983)	
GO:0003700 : DNA-binding transcription factor activity	
(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	
	GO - Biological Process
GO:0007275 : multicellular organism development	
(https://www.ebi.ac.uk/QuickGO/term/GO:0007275)	
GO:0006355 : regulation of transcription, DNA-templated	
(https://www.ebi.ac.uk/QuickGO/term/GO:0006355)	
GO:0009867 : jasmonic acid mediated signaling pathway	
(https://www.ebi.ac.uk/QuickGO/term/GO:0009867)	
GO:0009957 : epidermal cell fate specification	
(https://www.ebi.ac.uk/QuickGO/term/GO:0009957)	
GO:0010026 : trichome differentiation	
(https://www.ebi.ac.uk/QuickGO/term/GO:0010026)	
	GO - Cellular Component
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	
	Presumptive Null
Yes (https://www.gephbase.org/search-criteria?/and+Presumptive Null=%27Yes%27#gephbase-summary-title)	
	Molecular Type
Coding (https://www.gephbase.org/search-criteria?/and+Molecular Type=%27Coding%27#gephbase-summary-title)	
	Aberration Type
Insertion (https://www.gephbase.org/search-criteria?/and+Aberration Type=%27Insertion%27#gephbase-summary-title)	
	Insertion Size
1-10 kb	
	Molecular Details of the Mutation
only one copy of Tip100 in exon 7 and no apparent footprint of Tip100 in intron 2	
	Experimental Evidence
Candidate Gene (https://www.gephbase.org/search-criteria?/and+Experimental Evidence=%27Candidate Gene%27#gephbase-summary-title)	
	Main Reference
A bHLH regulatory gene in the common morning glory, <i>Ipomoea purpurea</i> , controls anthocyanin biosynthesis in flowers, proanthocyanidin and phytomelanin pigmentation in seeds, and seed trichome formation. (2007) (https://pubmed.ncbi.nlm.nih.gov/17270013)	
	Authors
Park KI; Ishikawa N; Morita Y; Choi JD; Hoshino A; Iida S	
	Abstract
The transcriptional regulators for anthocyanin pigmentation include proteins containing R2R3-MYB domains, bHLH domains and conserved WD40 repeats, and their interactions determine the set of genes to be expressed. Spontaneous ivory seed (ivs) mutants of <i>Ipomoea purpurea</i> displaying pale pigmented flowers and ivory seeds are caused by insertions of DNA transposons into the bHLH2 gene that encodes a bHLH transcriptional regulator. A partial reduction in the expression of all structural genes encoding enzymes for anthocyanin biosynthesis was observed in the young flower buds of these ivs mutants. The DFR-B and ANS transcripts were completely abolished in the ivs seed coats, whereas the early biosynthetic genes for flavonol biosynthesis remained active. The production and accumulation of both proanthocyanidin and phytomelanin pigments in the ivory seed coats were drastically reduced. Moreover, the unbranched trichomes in the ivory seeds were smaller in size and fewer in number than those in the wild-type dark-brown seeds, and the surface of the epidermis without trichomes in the dark-brown seeds looked rougher, due to the protruding tangential walls, than that in the ivory seeds. Although the <i>I. purpurea</i> bHLH2 gene is the most closely related to the petunia AN1 gene, whose mutation is known to confer white flowers and to be deficient in acidification of their vacuoles, the vacuolar alkalization in the epidermal flower limbs of <i>I. purpurea</i> ivs mutants appears to occur normally. These results are discussed with regard to the function of bHLH transcriptional regulators controlling flower and seed pigmentation as well as other epidermal traits.	
	Additional References

RELATED GEPHE

	Related Genes
3 (Chalcone synthase D (CHS-D), flavonoid 3'-hydroxylase (F3'H), MYB1) (https://www.gephbase.org/search-criteria?/or+TaxonID=%274121%27/and+Trait=Coloration/and+groupHaplotypes=true#gephbase-summary-title)	
	Related Haplotypes

EXTERNAL LINKS

COMMENTS

@TE - The *I. purpurea* bHLH2 gene is the most closely related to the petunia AN1 gene. ivs \rightarrow m2 seems to be a precursor of ivs \rightarrow m1. Flower variegation in the ivs \rightarrow m2 mutant is due to the somatic excision of Tip100 from bHLH2 exon 7.

