

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)	GP00000325	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	
Phlox drummondi - Light-colored flowers	Trait State in Taxon B	
Phlox drummondi - Dark-colored flowers	Ancestral State	
Data not curated	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific">#gephebase-summary-title)		
Taxon A		Taxon B
	Latin Name	Latin Name
Phlox drummondii (#gephebase-summary-title)	Phlox drummondii (#gephebase-summary-title)	
-	Common Name	Common Name
	Synonyms	Synonyms
Phlox drummondii Hook.; Phlox drummondi	Phlox drummondii Hook.; Phlox drummondi	
species	Rank	Rank
	Lineage	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; Ericales; Polemoniaceae; Phlox		
	Parent	Parent
Phlox (phloxes) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=40749)	Phlox (phloxes) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=40749)	
103529 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=103529)	103529 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=103529)	NCBI Taxonomy ID is Taxon B an Infraspecies?
No		No

GENOTYPIC CHANGE

CYP75A2	Generic Gene Name	UniProtKB Solanum melongena
CYP75; CYPEG1	Synonyms	GenebankID or UniProtKB
-	String	AFD05068 (https://www.ncbi.nlm.nih.gov/nuccore/AFD05068)
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)	GO - Biological Process	
GO:0009718 : anthocyanin-containing compound biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009718)		
	GO - Cellular Component	

Unknown (#gephebase-summary-title)	Presumptive Null
Cis-regulatory (#gephebase-summary-title)	Molecular Type
Unknown (#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Linkage Mapping (#gephebase-summary-title)	Experimental Evidence
Identification of two genes causing reinforcement in the Texas wildflower <i>Phlox drummondii</i> . (2011) (https://pubmed.ncbi.nlm.nih.gov/21217687)	Main Reference
Hopkins R; Rausher MD	Authors
Species formation generates biological diversity and occurs when traits evolve that prevent gene flow between populations. Discerning the number and distribution of genes underlying these traits and, in a few cases, identifying the genes involved, has greatly enhanced our understanding over the past 15 years of species formation (reviewed by Noor and Feder and Wolf et al.). However, this work has almost exclusively focused on traits that restrict gene flow between populations that have evolved as a by-product of genetic divergence between geographically isolated populations. By contrast, little is known about the characteristics of genes associated with reinforcement, the process by which natural selection directly favours restricted gene flow during the formation of species. Here we identify changes in two genes that appear to cause a flower colour change in <i>Phlox drummondii</i> , which previous work has shown contributes to reinforcement. Both changes involve cis-regulatory mutations to genes in the anthocyanin biosynthetic pathway (ABP). Because one change is recessive whereas the other is dominant, hybrid offspring produce an intermediate flower colour that is visited less by pollinators, and is presumably maladaptive. Thus genetic change selected to increase prezygotic isolation also appears to result in increased postzygotic isolation.	Abstract
	Additional References

RELATED GEPHE

1 (R2R3-Myb) (#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS