

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)	GP00000324	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
lochroma cyaneum; blue	Trait State in Taxon B
lochroma cyaneum; gesnerioides	Ancestral State
Data not curated	Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Interspecific">#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
lochroma cyaneum (#gephebase-summary-title)		lochroma cyaneum (#gephebase-summary-title)	
-	Common Name	-	Common Name
lochroma cyaneum (Lindl.) M.L.Green	Synonyms	lochroma cyaneum (Lindl.) M.L.Green	Synonyms
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoidae; Physaleae; lochroma		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoidae; Physaleae; lochroma	
lochroma () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=304104)	Parent	lochroma () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=304104)	Parent
362357 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=362357)	NCBI Taxonomy ID	362357 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=362357)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

CYP75A2	Generic Gene Name	UniProtKB Solanum melongena
CYP75; CYPEG1	Synonyms	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: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 - Molecular Function	
GO:0009718 : anthocyanin-containing compound biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009718)	GO - Biological Process	

Yes (#gephebase-summary-title)	Presumptive Null
Gene Loss (#gephebase-summary-title)	Molecular Type
Complex Change (#gephebase-summary-title)	Aberration Type
Large deletion	Molecular Details of the Mutation
Linkage Mapping (#gephebase-summary-title)	Experimental Evidence
Gene loss and parallel evolution contribute to species difference in flower color. (2011) (https://pubmed.ncbi.nlm.nih.gov/21551271)	Main Reference
Smith SD; Rausher MD	Authors
Although the importance of regulatory and functional sequence evolution in generating species differences has been studied to some extent, much less is known about the role of other types of genomic changes, such as fluctuation in gene copy number. Here, we apply analyses of gene function and expression of anthocyanin pigment pathway genes, as well as cosegregation analyses in backcross populations, to examine the genetic changes involved in the shift from blue to red flowers in Andean <i>lochroma</i> (Solanaceae). We demonstrate that deletion of a gene coding for an anthocyanin pathway enzyme was necessary for the transition to red floral pigmentation. The downregulation of a second pathway gene was also necessary for the novel flower color, and this regulatory pattern parallels the genetic change in the two other red-flowered species in the sister family Convolvulaceae in which flower color change has been examined genetically. Finally, we document a shift in enzymatic function at a third locus, but the importance of this change in the transition to red flowers depends on the exact order with which the three changes occurred. This study shows that gene inactivation or loss can be involved in the origin of phenotypic differences between species, thereby restricting the possibility of reversion to the ancestral state. It also demonstrates that parallel evolution of red flowers in three different species occurs via a common developmental/regulatory change but by mutations in different genes.	Abstract
	Additional References

RELATED GEPHE

1 (dihydroflavonol reductase (DFR)) (#gephebase-summary-title)	Related Genes
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS