

GEPHE SUMMARY

	Gephebase Gene		GepheID
dihydroflavonol reductase (DFR) (https://www.gephebase.org/search-criteria?/and+Gene)		GP00000224	
Gephebase="dihydroflavonol reductase (DFR)"#gephebase-summary-title)			Main curator
Published	Entry Status	Martin	

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)			
(flowers)"#gephebase-summary-title)	Trait State in Taxon A		
lochroma calycinum - blue morphs			
	Trait State in Taxon B		
lochroma calycinum - white morph			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic)			
Status="Intraspecific"#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
lochroma calycinum		lochroma calycinum	
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="lochroma calycinum"#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="lochroma calycinum"#gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
lochroma calycinum Benth.		lochroma calycinum Benth.	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Physaleae; lochroma		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Physaleae; lochroma	
	Parent		Parent
lochroma () - (Rank: genus)		lochroma () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=304104)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=304104)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
362353		362353	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=362353)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=362353)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
DFRA		P51102 (http://www.uniprot.org/uniprot/P51102)	
	Synonyms		GenebankID or UniProtKB
dihydroflavonol 4-reductase; DIHYDROFLAVONOL 4-REDUCTASE; DIHYDROKAEMPFEROL 4-REDUCTASE; M318; MJB21.18; MJB21_18; TT3; DFR; At5g42800		()	
	String		
3702.AT5G42800.1			
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G42800.1)			
	Sequence Similarities		
Belongs to the NAD(P)-dependent epimerase/dehydratase family. Dihydroflavonol-4-reductase subfamily.			
	GO - Molecular Function		
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)			
GO:0050662 : coenzyme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050662)			
GO:0016616 : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (https://www.ebi.ac.uk/QuickGO/term/GO:0016616)			

GO:0045552 : dihydrokaempferol 4-reductase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045552>)
GO:0047890 : flavanone 4-reductase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0047890>)

GO - Biological Process

GO:0009718 : anthocyanin-containing compound biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009718>)

GO - Cellular Component

GO:0042406 : extrinsic component of endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042406>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~No^#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

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

Deletion Size

10-99 bp

Molecular Details of the Mutation

33bp (11 a.a) deletion In coding sequence

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Candidate+Gene^#gephebase-summary-title))

Main Reference

Genetic basis for a rare floral mutant in an Andean species of Solanaceae. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25667079>)

Authors

Coburn RA; Griffin RH; Smith SD

Abstract

White forms of typically pigmented flowers are one of the most common polymorphisms in flowering plants. Although the range of genetic changes that give rise to white phenotypes is well known from model systems, few studies have identified causative mutations in natural populations.

Here we combine genetic studies, in vitro enzyme assays, and biochemical analyses to identify the mechanism underlying the loss of anthocyanin pigment production in the naturally occurring white-flowered morph of *Lochroma calycinum* (Solanaceae).

Comparison of anthocyanin gene sequences revealed a putative loss-of-function mutation, an 11 amino-acid deletion in dihydroflavonol 4-reductase (DFR), in the white morph. Functional assays of Dfr alleles from blue and white morphs demonstrated that this deletion results in a loss of enzymatic activity, indicating that the deletion could be solely responsible for the lack of pigment production. Consistent with this hypothesis, quantitative PCR showed no significant differences in expression of anthocyanin genes between the morphs. Also, thin layer chromatography confirmed that the white morph continues to accumulate compounds upstream of the DFR enzyme.

Collectively, these experiments indicate that the structural mutation at Dfr underlies the rare white flower morph of *L. calycinum*. This study is one of only a few examples where a flower color polymorphism is due to a loss-of-function mutation in the coding region of an anthocyanin enzyme. The rarity of such mutations in nature suggests that negative consequences prevent fixation across populations.

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Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS