

GEPHE SUMMARY

	Gephebase Gene		GepheID
Dihydroflavonol 4 reductase (MIDfr) (<a +dihydroflavonol+4+reductase+(midfr)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Dihydroflavonol+4+reductase+(MIDfr)+"#gephebase-summary-title)		GP00001457	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)			
	Trait		
Coloration (flower) (<a +coloration+(flower)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Coloration+(flower)+"#gephebase-summary-title)			
	Trait State in Taxon A		
Common pink flower from population in south central Oregon portion of the Modoc Plateau			
	Trait State in Taxon B		
Rare white flower from population near Crater Lake in the Oregon Cascades			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Erythranthe lewisii (<a +erythranthe+lewisii+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Erythranthe+lewisii+"#gephebase-summary-title)		Erythranthe lewisii (<a +erythranthe+lewisii+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Erythranthe+lewisii+"#gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
Mimulus lewisii; Erythranthe lewisii (Pursh) G.L.Nesom & N.S.Fraga; Mimulus lewisii Pursh		Mimulus lewisii; Erythranthe lewisii (Pursh) G.L.Nesom & N.S.Fraga; Mimulus lewisii Pursh	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; asterids; lamiids; Lamiales; Phrymaceae; Erythranthe		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; asterids; lamiids; Lamiales; Phrymaceae; Erythranthe	
	Parent		Parent
Erythranthe () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1502711)		Erythranthe () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1502711)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
69919 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69919)		69919 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69919)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Common pink flower from population in south central Oregon portion of the Modoc Plateau		Rare white flower from population near Crater Lake in the Oregon Cascades	

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		KJ011136 (https://www.ncbi.nlm.nih.gov/nuccore/KJ011136)	
	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

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

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

Insertion Size

1-9 bp

Molecular Details of the Mutation

A 2 nt (TG) insertion at position 265 causing a frameshift and a greatly truncated protein of 106 aa only about one-fourth of its functional length

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

The genetic basis of a rare flower color polymorphism in *Mimulus lewisii* provides insight into the repeatability of evolution. (2013) (<https://pubmed.ncbi.nlm.nih.gov/24312531>)

Authors

Wu CA; Streisfeld MA; Nutter LI; Cross KA

Abstract

A long-standing question in evolutionary biology asks whether the genetic changes contributing to phenotypic evolution are predictable. Here, we identify a genetic change associated with segregating variation in flower color within a population of *Mimulus lewisii*. To determine whether these types of changes are predictable, we combined this information with data from other species to investigate whether the spectrum of mutations affecting flower color transitions differs based on the evolutionary time-scale since divergence. We used classic genetic techniques, along with gene expression and population genetic approaches, to identify the putative, loss-of-function mutation that generates rare, white flowers instead of the common, pink color in *M. lewisii*. We found that a frameshift mutation in an anthocyanin pathway gene is responsible for the white-flowered polymorphism found in this population of *M. lewisii*. Comparison of our results with data from other species reveals a broader spectrum of flower color mutations segregating within populations relative to those that fix between populations. These results suggest that the genetic basis of fixed differences in flower color may be predictable, but that for segregating variation is not.

Additional References

RELATED GEPHE

Related Genes

2 (LIGHT AREAS1 (LAR1), ROSE INTENSITY1 (ROI1)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~69919~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+TaxonID=~69919~#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS