

GEPHE SUMMARY

	Gephebase Gene	GephelD
LIGHT AREAS1 (LAR1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^LIGHT AREAS1 (LAR1)^#gephebase-summary-title)	GP00000543	Main curator
	Entry Status	Courtier
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
Mimulus lewisii - bumblebee-pollinated - Light-Area allele (dominant)	Trait State in Taxon B
Mimulus cardinalis - hummingbird-pollinated	Ancestral State
Data not curated	Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Interspecific">#gephebase-summary-title)	

Taxon A		Taxon B	
	Latin Name		Latin Name
Erythranthe lewisi		Erythranthe lewisi	
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Erythranthe lewisi>#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Erythranthe lewisi>#gephebase-summary-title)	
-	Common Name	-	Common Name
	Synonyms		Synonyms
Mimulus lewisi; Erythranthe lewisi (Pursh) G.L.Nesom & N.S.Fraga; Mimulus lewisi Pursh		Mimulus lewisi; Erythranthe lewisi (Pursh) G.L.Nesom & N.S.Fraga; Mimulus lewisi Pursh	
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Lamiales; Phrymaceae; Erythranthe		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Lamiales; Phrymaceae; Erythranthe	
	Parent		Parent
Erythranthe () - (Rank: genus)		Erythranthe () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1502711)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1502711)	
69919	NCBI Taxonomy ID	69919	NCBI Taxonomy ID
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69919)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69919)	
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

LAR1	Generic Gene Name	UniProtKB Erythranthe lewisi
-	Synonyms	GenebankID or UniProtKB
-	String	ALP48587 (https://www.ncbi.nlm.nih.gov/nuccore/ALP48587)
-	Sequence Similarities	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	GO - Molecular Function	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	GO - Biological Process	
	GO - Cellular Component	
No (#gephebase-summary-title)		Presumptive Null
Cis-regulatory (#gephebase-summary-title)		Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%5EUnknown%23gephebase-summary-title>)

Molecular Details of the Mutation

unknown

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%5ELinkage+Mapping%23gephebase-summary-title>)

Main Reference

Competition between anthocyanin and flavonol biosynthesis produces spatial pattern variation of floral pigments between *Mimulus* species. (2016) (<https://pubmed.ncbi.nlm.nih.gov/26884205>)

Authors

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Abstract

Flower color patterns have long served as a model for developmental genetics because pigment phenotypes are visually striking, yet generally not required for plant viability, facilitating the genetic analysis of color and pattern mutants. The evolution of novel flower colors and patterns has played a key role in the adaptive radiation of flowering plants via their specialized interactions with different pollinator guilds (e.g., bees, butterflies, birds), motivating the search for allelic differences affecting flower color pattern in closely related plant species with different pollinators. We have identified LIGHT AREAS1 (LAR1), encoding an R2R3-MYB transcription factor, as the causal gene underlying the spatial pattern variation of floral anthocyanin pigmentation between two sister species of monkeyflower: the bumblebee-pollinated *Mimulus lewisii* and the hummingbird-pollinated *Mimulus cardinalis*. We demonstrated that LAR1 positively regulates FLAVONOL SYNTHASE (FLS), essentially eliminating anthocyanin biosynthesis in the white region (i.e., light areas) around the corolla throat of *M. lewisii* flowers by diverting dihydroflavonol into flavonol biosynthesis from the anthocyanin pigment pathway. FLS is preferentially expressed in the light areas of the *M. lewisii* flower, thus prepatternning the corolla. LAR1 expression in *M. cardinalis* flowers is much lower than in *M. lewisii*, explaining the unpatterned phenotype and recessive inheritance of the *M. cardinalis* allele. Furthermore, our gene-expression analysis and genetic mapping results suggest that cis-regulatory change at the LAR1 gene played a critical role in the evolution of different pigmentation patterns between the two species.

Additional References

RELATED GEPHE

Related Genes

2 (Dihydroflavonol 4 reductase (MIDfr), ROSE INTENSITY1 (ROI)) (<https://www.gephebase.org/search-criteria?/or+TaxonID=%5E69919%23and+Trait=Coloration%23and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

RNAi results suggest role of regulatory change