

	Gephebase Gene	GepheID
LIGHT AREAS1 (LAR1) (https://www.gephebase.org/search-criteria?/and+Gene	GP00000543	
Gephebase="*LIGHT AREAS1 (LAR1)*#gephebase-summary-title)		Main curator
	Entry Status	Courtier
Published		

	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^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+TaxonomicStatus=^Interspecific^#gephebase-summary-title)	

	Generic Gene Name	UniProtKB Erythranthe lewisii
LAR1		
	A0A0S2T0F2 (http://www.uniprot.org/uniprot/A0A0S2T0F2)	
	Synonyms	GenebankID or UniProtKB
-	ALP48587 (https://www.ncbi.nlm.nih.gov/nuccore/ALP48587)	
	String	
-		
	Sequence Similarities	
-		
	GO - Molecular Function	
	GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	
	GO - Biological Process	
-		
	GO - Cellular Component	
	GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	
		Presumptive Null
	No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=%No%#gephebase-summary-title)	
		Molecular Type
	Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=%Cis-regulatory%#gephebase-summary-title)	

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown~#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	Experimental Evidence
Competition between anthocyanin and flavonol biosynthesis produces spatial pattern variation of floral pigments between <i>Mimulus</i> species. (2016) (https://pubmed.ncbi.nlm.nih.gov/26884205)	Main Reference
Yuan YW; Rebocho AB; Sagawa JM; Stanley LE; Bradshaw HD	Authors
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 <i>Mimulus lewisii</i> and the hummingbird-pollinated <i>Mimulus cardinalis</i> . 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 <i>M. lewisii</i> flowers by diverting dihydroflavonol into flavonol biosynthesis from the anthocyanin pigment pathway. FLS is preferentially expressed in the light areas of the <i>M. lewisii</i> flower, thus prepatterning the corolla. LAR1 expression in <i>M. cardinalis</i> flowers is much lower than in <i>M. lewisii</i> , explaining the unpatterned phenotype and recessive inheritance of the <i>M. cardinalis</i> 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.	Abstract
	Additional References

RELATED GEPHE

2 (Dihydroflavonol 4 reductase (MDFr), ROSE INTENSITY1 (RO1)) (https://www.gephebase.org/search-criteria?/or+TaxonID=~69919~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

RNAi results suggest role of regulatory change