

GEPHE SUMMARY

	Gephebase Gene		GepheID
MC1R (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MC1R^#gephebase-summary-title)		GP00000610	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology^#gephebase-summary-title)		Trait	
Coloration (feathers) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration(feathers)^#gephebase-summary-title)			
	Trait State in Taxon A		
Malurus leucopterus leuconotus (blue)		Trait State in Taxon B	
Malurus leucopterus leucopterus (black)			
	Ancestral State		
Data not curated		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Malurus leucopterus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Malurusleucopterus^#gephebase-summary-title)		Malurus leucopterus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Malurusleucopterus^#gephebase-summary-title)	
	Common Name		Common Name
white-winged fairy-wren		white-winged fairy-wren	
	Synonyms		Synonyms
white-winged fairy-wren		white-winged fairy-wren	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves; Neognathae; Passeriformes; Meliphagides; Maluridae; Malurus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves; Neognathae; Passeriformes; Meliphagides; Maluridae; Malurus	
	Parent		Parent
Malurus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 55806)		Malurus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 55806)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
228326 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 228326)		228326 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 228326)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Malurus leucopterus leuconotus (blue)		Malurus leucopterus leucopterus (black)	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
MC1R		Q01726 (http://www.uniprot.org/uniprot/Q01726)	
	Synonyms		GenebankID or UniProtKB
CMM5; MSH-R; SHEP2; MSHR		ADQ27896 (https://www.ncbi.nlm.nih.gov/nuccore/ADQ27896)	
	String		
9606.ENSPP00000451605 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000451605)			
	Sequence Similarities		
Belongs to the G-protein coupled receptor 1 family.			
	GO - Molecular Function		
GO:0008528 : G protein-coupled peptide receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008528)			
GO:0004977 : melanocortin receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004977)			

GO:0004980 : melanocyte-stimulating hormone receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004980>)
GO:0031625 : ubiquitin protein ligase binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031625>)

GO - Biological Process

GO:0007275 : multicellular organism development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007275>)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0042438 : melanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042438>)
GO:0043473 : pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0043473>)
GO:0007186 : G protein-coupled receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007186>)
GO:0051897 : positive regulation of protein kinase B signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051897>)
GO:0019233 : sensory perception of pain
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019233>)
GO:0007189 : adenylate cyclase-activating G protein-coupled receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007189>)
GO:0035556 : intracellular signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035556>)
GO:0007187 : G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (<https://www.ebi.ac.uk/QuickGO/term/GO:0007187>)
GO:0032720 : negative regulation of tumor necrosis factor production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032720>)
GO:0010739 : positive regulation of protein kinase A signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010739>)
GO:0090037 : positive regulation of protein kinase C signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0090037>)
GO:0009650 : UV protection (<https://www.ebi.ac.uk/QuickGO/term/GO:0009650>)
GO:0070914 : UV-damage excision repair
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070914>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)

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=))

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=))

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

A16T caused by guanine-to-adenine (G_A) transition at site 46; and/or I38N cause by a tyrosine-to-adenine (T_A) transition at site 113; and/or V11N caused by a G_A transition at site 331; and/or Q157R caused by an A_G substitution at site 470; Val166Ileu - exact causing amino acid change(s) unknown

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=))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Concordant evolution of plumage colour, feather microstructure and a melanocortin receptor gene between mainland and island populations of a fairy-wren. (2004)
(<https://pubmed.ncbi.nlm.nih.gov/15306285>)

Authors

Doucet SM; Shawkey MD; Rathburn MK; Mays HL; Montgomerie R

Abstract

Studies of the patterns of diversification of birds on islands have contributed a great deal to the development of evolutionary theory. In white-winged fairy-wrens, *Malurus leucopterus*, mainland males develop a striking blue nuptial plumage whereas those on nearby islands develop black nuptial plumage. We explore the proximate basis for this divergence by combining microstructural feather analysis with an investigation of genetic variation at the melanocortin-1 receptor locus (MC1R). Fourier analysis revealed that the medullary keratin matrix (spongy layer) of the feather barbs of blue males was ordered at the appropriate nanoscale to produce the observed blue colour by coherent light scattering. Surprisingly, the feather barbs of black males also contained a spongy layer that could produce a similar blue colour. However, black males had more melanin in their barbs than blue males, and this melanin may effectively mask any structural colour produced by the spongy layer. Moreover, the presence of this spongy layer suggests that black island males evolved from a blue-plumaged ancestor. We also document concordant patterns of variation at the MC1R locus, as five amino acid substitutions were perfectly associated with the divergent blue and black plumage phenotypes. Thus, with the possible involvement of a melanocortin receptor locus, increased melanin density may mask the blue-producing microstructure in black island males, resulting in the divergence of plumage coloration between mainland and island white-winged fairy-wrens. Such mechanisms may also be responsible for plumage colour diversity across broader geographical and evolutionary scales.

Additional References

RELATED GEPHE

No matches found.

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS