GEPHE SUMMARY

Gephebase Gene

MC1R (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MC1R^#gephebase-summary-title)

GepheID

GP00001333

Entry Status

Published

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

Coloration (coat) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (coat)^#gephebase-summary-title)

Trait State in Taxon A

Chestnut-bellied flycatcher-chesnut-bellied form of Makira island

Trait State in Taxon B

Chestnut-bellied flycatcher-melanic form of Santa Ana island

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Monarcha castaneiventris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Monarcha castaneiventris^#gephebase-summary-title)

Common Name

Makira monarch

Synonyms

Makira monarch; Monarcha castaneiventris Verreaux, J, 1858

Rank

species

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; Corvoidea; Monarchidae; Monarcha

Parent

Monarcha () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 175125)

NCBI Taxonomy ID

338458 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 338458)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Chestnut-bellied flycatcher-chesnut-bellied form of Makira island

Taxon B

Latin Name

Monarcha castaneiventris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Monarcha castaneiventris^#gephebase-summary-title)

Common Name

Makira monarch

Synonyms

Makira monarch; Monarcha castaneiventris Verreaux, J, 1858

Rank

species

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; Corvoidea; Monarchidae; Monarcha

Parent

Monarcha () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 175125)

NCBI Taxonomy ID

338458 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 338458)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Chestnut-bellied flycatcher-melanic form of Santa Ana island

GENOTYPIC CHANGE

Generic Gene Name

MC1R

Synonyms

CMM5; MSH-R; SHEP2; MSHR

String

9606.ENSP00000451605 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000451605)

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)

UniProtKB Homo sapiens

Q01726 (http://www.uniprot.org/uniprot/Q01726)

GenebankID or UniProtKB

()

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)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Asp119Asn

Experimental Evidence

Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)

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

Main Reference

Mutations in different pigmentation genes are associated with parallel melanism in island flycatchers. (2016) (https://pubmed.ncbi.nlm.nih.gov/27412275)

Authors

Uy JA; Cooper EA; Cutie S; Concannon MR; Poelstra JW; Moyle RG; Filardi CE

Abstract

The independent evolution of similar traits across multiple taxa provides some of the most compelling evidence of natural selection. Little is known, however, about the genetic basis of these convergent or parallel traits: are they mediated by identical or different mutations in the same genes, or unique mutations in different genes? Using a combination of candidate gene and reduced representation genomic sequencing approaches, we explore the genetic basis of and the evolutionary processes that mediate similar plumage colour shared by isolated populations of the Monarcha castaneiventris flycatcher of the Solomon Islands. A genome-wide association study (GWAS) that explicitly controlled for population structure revealed that mutations in known pigmentation genes are the best predictors of parallel plumage colour. That is, entirely black or melanic birds from one small island share an amino acid substitution in the melanocortin-1 receptor (MC1R), whereas similarly melanic birds from another small island over 100 km away share an amino acid substitution in a predicted binding site of agouti signalling protein (ASIP). A third larger island, which separates the two melanic populations, is inhabited by birds with chestnut bellies that lack the melanic MC1R and ASIP allelic variants. Formal FST outlier tests corroborated the results of the GWAS and suggested that strong, directional selection drives the near fixation of the MC1R and ASIP variants across islands. Our results, therefore, suggest that selection acting on different mutations with large phenotypic effects can drive the evolution of parallel melanism, despite the relatively small population size on islands.

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Additional References

RELATED GEPHE

Related Genes

1 (Agouti (ASIP)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^338458^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

2 other candidate regions were identified but without known gene