

GEPHE SUMMARY

MC1R (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^MC1R^#gephebase-summary-title)	Gephebase Gene	GP00000600	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)	Trait Category		
Coloration (feathers) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+feathers^#gephebase-summary-title)	Trait		
Coereba flaveola	Trait State in Taxon A		
Coereba flaveola	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)	Taxonomic Status		

Taxon A	Latin Name	Taxon B	Latin Name
Coereba flaveola (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Coereba+flaveola^#gephebase-summary-title)	Coereba flaveola	Coereba flaveola (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Coereba+flaveola^#gephebase-summary-title)	Coereba flaveola
Bananaquit	Common Name	Bananaquit	Common Name
Bananaquit; Coereba flaveola (Linnaeus, 1758)	Synonyms	Bananaquit; Coereba flaveola (Linnaeus, 1758)	Synonyms
species	Rank	species	Rank
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; Thraupidae; Coereba	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; Thraupidae; Coereba	Lineage
Coereba () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=87176)	Parent	Coereba () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=87176)	Parent
87177 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=87177)	NCBI Taxonomy ID	87177 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=87177)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

MC1R	Generic Gene Name	Q01726 (http://www.uniprot.org/uniprot/Q01726)	UniProtKB Homo sapiens
CMM5; MSH-R; SHEP2; MSHR	Synonyms	AAK50812 (https://www.ncbi.nlm.nih.gov/nuccore/AAK50812)	GenebankID or UniProtKB
9606.ENSP00000451605 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000451605)	String		
Belongs to the G-protein coupled receptor 1 family.	Sequence Similarities		
GO:0008528 : G protein-coupled peptide receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008528)	GO - Molecular Function		
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>)

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

E92K

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence+Candidate Gene^#gephebase-summary-title>)

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

Main Reference

The molecular basis of an avian plumage polymorphism in the wild: a melanocortin-1-receptor point mutation is perfectly associated with the melanic plumage morph of the bananaquit, *Coereba flaveola*. (2001) (<https://pubmed.ncbi.nlm.nih.gov/11369199>)

Authors

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Abstract

Evolution depends on natural selection acting on phenotypic variation, but the genes responsible for phenotypic variation in natural populations of vertebrates are rarely known. The molecular genetic basis for plumage color variation has not been described in any wild bird. Bananaquits (*Coereba flaveola*) are small passerine birds that occur as two main plumage variants, a widespread yellow morph with dark back and yellow breast and a virtually all black melanic morph. A candidate gene for this color difference is the melanocortin-1 receptor (MC1R), a key regulator of melanin synthesis in feather melanocytes.

We sequenced the MC1R gene from four Caribbean populations of the bananaquit; two populations of the yellow morph and two populations containing both the yellow morph and the melanic morph. A point mutation resulting in the replacement of glutamate with lysine was present in at least one allele of the MC1R gene in all melanic birds and was absent in all yellow morph birds. This substitution probably causes the color variation, as the same substitution is responsible for melanism in domestic chickens and mice. The evolutionary relationships among the MC1R haplotypes show that the melanic alleles on Grenada and St. Vincent had a single origin. The low prevalence of nonsynonymous substitutions among yellow haplotypes suggests that they have been under stabilizing selection, whereas strong selective constraint on melanic haplotypes is absent.

We conclude that a mutation in the MC1R is responsible for the plumage polymorphism in a wild bird population and that the melanic MC1R alleles in Grenada and St. Vincent bananaquit populations have a single evolutionary origin from a yellow allele.

Additional References

RELATED GEPHE

No matches found.

[Related Genes](#)

No matches found.

[Related Haplotypes](#)

EXTERNAL LINKS

COMMENTS

T960C in 3'UTR is in perfect association with the coding mutations and the color, suggesting that no recombination between these positions within the MC1R gene has occurred since the melanic haplotype originated - this mutation may also be causal