

GEPHE SUMMARY

	Gephebase Gene	GephelD
MC1R (#gephebase-summary-title)	GP00001355	Main curator
Published	Entry Status	Prigent

PHENOTYPIC CHANGE

	Trait Category
Morphology (#gephebase-summary-title)	Trait
Coloration (feathers) (#gephebase-summary-title)	Trait State in Taxon A
Arctic skua ; nonmelanic (pale)	Trait State in Taxon B
Arctic skua ; melanic (intermediate and dark)	Ancestral State
Unknown	Taxonomic Status
Intraspecific (#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Stercorarius parasiticus (#gephebase-summary-title))		Stercorarius parasiticus (#gephebase-summary-title))	
-	Common Name	-	Common Name
-	Synonyms	-	Synonyms
-	Rank	-	Rank
species	Lineage	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; Charadriiformes; Stercorariidae; Stercorarius		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; Charadriiformes; Stercorariidae; Stercorarius	
Stercorarius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 54057)	Parent	Stercorarius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 54057)	Parent
54059 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 54059)	NCBI Taxonomy ID	54059 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 54059)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Mctr1	Generic Gene Name	UniProtKB Mus musculus
e; Tob; Mctr1; Mshra; Msh-r	Synonyms	GenebankID or UniProtKB
10090.ENSMUSP00000095929 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000095929)	String	
Belongs to the G-protein coupled receptor 1 family.	Sequence Similarities	
GO:0004977 : melanocortin receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004977)	GO - Molecular Function	
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:0042562 : hormone binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0042562>)
GO - Biological Process

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: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: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:0070914 : UV-damage excision repair
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070914>)

GO:2000253 : positive regulation of feeding behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000253>)

GO:0060259 : regulation of feeding behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060259>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

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

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

Melanic and nonmelanic haplotypes in the Arctic skua are defined by three amino acid changes: nonmelanic: His8-Glu12-Arg230; melanic: Arg8-Lys12-His230. The effect of each single amino acid change has not been tested

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

Molecular population genetics of the melanic plumage polymorphism in Arctic skuas (*Stercorarius parasiticus*): evidence for divergent selection on plumage colour. (2013)

(<https://pubmed.ncbi.nlm.nih.gov/23980902>)

Authors

Janssen K; Mundy NI

Abstract

The Arctic skua (*Stercorarius parasiticus*) is a classic example of an avian plumage polymorphism, with variation in melanin-based ventral plumage coloration defining pale, intermediate and dark morphs in adults of both sexes. However, despite several decades of field research, there is an incomplete understanding of how the polymorphism in ventral plumage colour is maintained and the selective forces involved. Here, we investigate selection on a locus (MC1R) that is strongly associated with plumage colour variation in Arctic skuas using patterns of nucleotide variation and comparison to neutral loci (nuclear introns and mtDNA). We find that three linked nonsynonymous mutations in MC1R, including the single mutation described previously, are associated with plumage colour in the Arctic skua. The position of nonsynonymous mutations on a MC1R haplotype network implies that divergent selection drove the initial evolution of the colour morphs. Comparisons of F(ST)s of MC1R vs. nuclear introns among five skua populations differing in proportion of dark morphs along an approximate north-south cline reveal a signature of divergent selection on MC1R. In contrast, we find limited evidence for balancing selection on MC1R within populations, although the power is low. Our results provide strong evidence for both past and ongoing selection on MC1R, and, by implication, plumage colour in Arctic skuas. The results suggest that a fruitful avenue for future ecological studies will be analysis of selection on morphs in colonies at the extremes along the morph ratio cline.

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Additional References

RELATED GEPHE

No matches found.

Related Genes

1 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^MC1R^/and+Taxon ID=^54059^/or+Gene Gephebase=^MC1R^/and+Taxon ID=^54059^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

@SeveralCandidateMutations @BalancingSelection - Heterozygous are intermediate (melanic)