

GEPHE SUMMARY

| | | | |
|--|----------------|------------|--------------|
| MC1R (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^MC1R^#gephebase-summary-title) | Gephebase Gene | GP00001355 | GepheID |
| Published | Entry Status | Prigent | 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 | | |
| Arctic skua ; nonmelanic (pale) | Trait State in Taxon A | | |
| Arctic skua ; melanic (intermediate and dark) | Trait State in Taxon B | | |
| Unknown | Ancestral State | | |
| Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title) | Taxonomic Status | | |

| Taxon A | | Taxon B | |
|--|---|--|---|
| | Latin Name | | Latin Name |
| Stercorarius parasiticus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Stercorarius+parasiticus^#gephebase-summary-title) | Stercorarius parasiticus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Stercorarius+parasiticus^#gephebase-summary-title) | Stercorarius parasiticus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Stercorarius+parasiticus^#gephebase-summary-title) | Stercorarius parasiticus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Stercorarius+parasiticus^#gephebase-summary-title) |
| - | Common Name | - | Common Name |
| - | Synonyms | - | 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; Charadriiformes; Stercorariidae; Stercorarius | 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 | Lineage |
| 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 Intraspecies? | No | is Taxon B an Intraspecies? |

GENOTYPIC CHANGE

| | | | |
|---|-------------------------|--|-------------------------|
| Mcr1 | Generic Gene Name | Q01727 (http://www.uniprot.org/uniprot/Q01727) | UniProtKB Mus musculus |
| e; Tob; Mcr1; 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](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](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](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](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

Related Genes

No matches found.

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](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=))

EXTERNAL LINKS

COMMENTS

@SeveralCandidateMutations @BalancingSelection - Heterozygous are intermediate (melanic)