

GEPHE SUMMARY

<p>MC1R (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~MC1R^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001350</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)</p>		<p>Trait Category</p>		
<p>Coloration (coat) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+coat^#gephebase-summary-title)</p>		<p>Trait</p>		
<p>Reindeer ; wild type light ventral color</p>		<p>Trait State in Taxon A</p>		
<p>Reindeer ; dark ventral color</p>		<p>Trait State in Taxon B</p>		
<p>Taxon A</p>		<p>Ancestral State</p>		
<p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated^#gephebase-summary-title)</p>		<p>Taxonomic Status</p>		
<p>Taxon A</p>	<p>Latin Name</p>	<p>Taxon B</p>	<p>Latin Name</p>	
<p>Rangifer tarandus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Rangifer+tarandus^#gephebase-summary-title)</p>	<p>Rangifer tarandus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Rangifer+tarandus^#gephebase-summary-title)</p>	<p>Rangifer tarandus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Rangifer+tarandus^#gephebase-summary-title)</p>	<p>Rangifer tarandus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Rangifer+tarandus^#gephebase-summary-title)</p>	
<p>reindeer</p>	<p>Common Name</p>	<p>reindeer</p>	<p>Common Name</p>	
<p>reindeer; caribou; Rangifer tarandus Linnaeus</p>	<p>Synonyms</p>	<p>reindeer; caribou; Rangifer tarandus Linnaeus</p>	<p>Synonyms</p>	
<p>species</p>	<p>Rank</p>	<p>species</p>	<p>Rank</p>	
<p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Odocoileinae; Rangifer</p>		<p>Lineage</p>	<p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Odocoileinae; Rangifer</p>	
<p>Rangifer () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9869)</p>		<p>Parent</p>	<p>Rangifer () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9869)</p>	
<p>9870 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9870)</p>	<p>NCBI Taxonomy ID</p>	<p>9870 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9870)</p>	<p>NCBI Taxonomy ID</p>	
<p>No</p>	<p>is Taxon A an Intraspecies?</p>	<p>No</p>	<p>is Taxon B an Intraspecies?</p>	

GENOTYPIC CHANGE

<p>Mcr1</p>	<p>Generic Gene Name</p>	<p>Q01727 (http://www.uniprot.org/uniprot/Q01727)</p>	<p>UniProtKB Mus musculus</p>
<p>e; Tob; Mcr1; Mshra; Msh-r</p>	<p>Synonyms</p>	<p>0</p>	<p>GenebankID or UniProtKB</p>
<p>10090.ENSMUSP00000095929 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000095929)</p>	<p>String</p>		
<p>Belongs to the G-protein coupled receptor 1 family.</p>	<p>Sequence Similarities</p>		
<p>GO:0004977 : melanocortin receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004977)</p> <p>GO:0004980 : melanocyte-stimulating hormone receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004980)</p> <p>GO:0031625 : ubiquitin protein ligase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031625)</p> <p>GO:0042562 : hormone binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042562)</p>	<p>GO - Molecular Function</p>		

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>)

Mutation #1

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=`No`#gephebase-summary-title>)

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

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

Nonsynonymous

c.218T>C p.Met73Thr and c.839T>G p.Phe280Cys

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

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Met	Thr	73

Main Reference

Two missense mutations in melanocortin 1 receptor (MC1R) are strongly associated with dark ventral coat color in reindeer (*Rangifer tarandus*). (2014)
(<https://pubmed.ncbi.nlm.nih.gov/25039753>)

Authors

VÃ¶ge DI; Nieminen M; Anderson DG; RÃed KH

Abstract

The protein-coding region of melanocortin 1 receptor (MC1R) was sequenced to identify potential variation affecting coat color in reindeer (*Rangifer tarandus*). A TÃC sequence variation at nucleotide position 218 (c.218T>C) causing an amino acid (aa) change from methionine to threonine at aa position 73 (p.Met73Thr) was identified. In addition, a TÃG sequence variation was found at nucleotide position 839 (c.839T>G), causing phenylalanine to be exchanged by cysteine at aa position 280 (p.Phe280Cys). The two sequence variants (c.218C and c.839G) were found to be closely associated with a darker belly coat compared with animals not having any of these two variants. The aa acid change p.Met73Thr affects the same position as p.Met73Lys previously reported to give constitutive activation of MC1R in black sheep (*Ovis aries*), whereas p.Phe280Cys is identical to one of two variants previously reported to be associated with dark coat color in Arctic fox (*Alopex lagopus*), supporting that the two variants found in reindeer are functional. The complete absence of Thr73 and Cys280 among the 51 wild reindeer analyzed provides some evidence that these variants are more common in the domestic herds.

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Additional References

Mutation #2

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=`No`#gephebase-summary-title>)

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

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

Presumptive Null

Molecular Type

Aberration Type

Nonsynonymous

Molecular Details of the Mutation

c.218T>C p.Met73Thr and c.839T>G p.Phe280Cys

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	Phe	Cys	280

Main Reference

Two missense mutations in melanocortin 1 receptor (MC1R) are strongly associated with dark ventral coat color in reindeer (*Rangifer tarandus*). (2014) (<https://pubmed.ncbi.nlm.nih.gov/25039753>)

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Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

p.Phe280Cys is also known in Arctic fox (*Alopex lagopus*) ; p.Met73 is also mutated in black sheep (*Ovis aries*)