

GEPHE SUMMARY

	Gephebase Gene		GepheID
MC1R (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MC1R^#gephebase-summary-title)		GP00000598	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~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		
Vulpes vulpes ; red		Trait State in Taxon B	
Vulpes vulpes ; Alaska Silver ; and Chocolate foxes			
	Ancestral State		
Data not curated		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated^#gephebase-summary-title)			

Taxon A		Taxon B	
	Latin Name		Latin Name
Vulpes vulpes (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Vulpesvulpes^#gephebase-summary-title)		Vulpes vulpes (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Vulpesvulpes^#gephebase-summary-title)	
	Common Name		Common Name
red fox		red fox	
	Synonyms		Synonyms
Canis vulpes; red fox; silver fox		Canis vulpes; red fox; silver fox	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Vulpes		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Vulpes	
	Parent		Parent
Vulpes () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9625)		Vulpes () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9625)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
9627 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9627)		9627 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9627)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
MC1R		Q01726 (http://www.uniprot.org/uniprot/Q01726)	
	Synonyms		GenebankID or UniProtKB
CMM5; MSH-R; SHEP2; MSHR		AHY21737 (https://www.ncbi.nlm.nih.gov/nuccore/AHY21737)	
	String		
9606.ENSPP00000451605 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000451605)			
	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)			
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)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
C125R; constitutively active receptor	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)	Experimental Evidence

	Taxon A	Taxon B	Position
Codon	TGT	CGT	373
Amino-acid	Cys	Arg	125

A non-epistatic interaction of agouti and extension in the fox, <i>Vulpes vulpes</i> . (1997) (https://pubmed.ncbi.nlm.nih.gov/9054949)	Main Reference
VÃ¥ge DI; Lu D; Klungland H; Lien S; Adalsteinsson S; Cone RD	Authors
	Abstract

Agouti and extension are two genes that control the production of yellow-red (phaeomelanin) and brown-black (eumelanin) pigments in the mammalian coat. Extension encodes the melanocyte-stimulating hormone receptor (MC1R) while agouti encodes a peptide antagonist of the receptor. In the mouse, extension is epistatic to agouti, hence dominant mutants of the MC1R encoding constitutively active receptors are not inhibited by the agouti antagonist, and animals with dominant alleles of both loci remain darkly pigmented. In the fox the proposed extension locus is not epistatic to the agouti locus. We have cloned and characterized the MC1R and the agouti gene in coat colour variants of the fox (*Vulpes vulpes*). A constitutively activating C125R mutation in the MC1R was found specifically in darkly pigmented animals carrying the Alaska Silver allele (EA). A deletion in the first coding exon of the agouti gene was found associated with the proposed recessive allele of agouti in the darkly pigmented Standard Silver fox (aa). Thus, as in the mouse, dark pigmentation can be caused by a constitutively active MC1R, or homozygous recessive status at the agouti locus. Our results, demonstrating the presence of dominant extension alleles in foxes with significant red coat colouration, suggest the ability of the fox agouti protein to counteract the signalling activity of a constitutively active fox MC1R.

Genetic variations of the coding region of the melanocortin receptor 1 (MC1R) gene in the fox. (2016) (https://pubmed.ncbi.nlm.nih.gov/27072328)	Additional References
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RELATED GEPHE

2 (Agouti, Kit (type III receptor protein-tyrosine kinase)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9627^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
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EXTERNAL LINKS

COMMENTS

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