

GEPHE SUMMARY

MC1R (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MC1R^#gephebase-summary-title)	Gephebase Gene	GP00000590	GepheID
	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	
Oryctolagus cuniculus		Trait State in Taxon B	
Oryctolagus cuniculus ; Japanese, Rhinelander and Dutch tricolour rabbits		Ancestral State	
Taxon A		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated^#gephebase-summary-title)			
Taxon A		Taxon B	
Oryctolagus cuniculus		Oryctolagus cuniculus	
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Oryctolagus cuniculus^#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Oryctolagus cuniculus^#gephebase-summary-title)	
Common Name		Common Name	
rabbit		rabbit	
Synonyms		Synonyms	
Lepus cuniculus; rabbit; European rabbit; Japanese white rabbit; domestic rabbit; rabbits		Lepus cuniculus; rabbit; European rabbit; Japanese white rabbit; domestic rabbit; rabbits	
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; Euarchontoglires; Glires; Lagomorpha; Leporidae; Oryctolagus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae; Oryctolagus	
Parent		Parent	
Oryctolagus () - (Rank: genus)		Oryctolagus () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9984)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9984)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
9986		9986	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9986)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9986)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

MC1R	Generic Gene Name	UniProtKB Homo sapiens
	Synonyms	Q01726 (http://www.uniprot.org/uniprot/Q01726)
	String	GenebankID or UniProtKB
CMM5; MSH-R; SHEP2; MSHR		CBJ17605 (https://www.ncbi.nlm.nih.gov/nuccore/CBJ17605)
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)

	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
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Deletion^#gephebase-summary-title)	
	Deletion Size
1-9 bp	
	Molecular Details of the Mutation
6bp in frame deletion c.[124G>A;125_130del6] + L44 T (homozygous state in Japanese, Rhinelander and Dutch tricolour rabbits)	
	Experimental Evidence
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene^#gephebase-summary-title)	
	Main Reference
A composite six bp in-frame deletion in the melanocortin 1 receptor (MC1R) gene is associated with the Japanese brindling coat colour in rabbits (Oryctolagus cuniculus). (2010) (https://pubmed.ncbi.nlm.nih.gov/20594318)	
	Authors
Fontanesi L; Scotti E; Colombo M; Beretti F; Forestier L; Dall'Olio S; Deretz S; Russo V; Allain D; Oulmouden A	

Abstract
In the domestic rabbit (*Oryctolagus cuniculus*), classical genetic studies have identified five alleles at the Extension locus: ED (dominant black), ES (steel, weaker version of ED), E (wild type, normal extension of black), eJ (Japanese brindling, mosaic distribution of black and yellow) and e (non-extension of black, yellow/red with white belly). Sequencing almost the complete coding sequence (CDS) of the rabbit MC1R gene, we recently identified two in-frame deletions associated with dominant black (c.280_285del6; alleles ED or ES) and recessive red (c.304_333del30; allele e) coat colours. It remained to characterize the eJ allele whose phenotypic effect is similar to the Orange and Sex-linked yellow loci of cat and Syrian hamster.

We sequenced the whole CDS in 25 rabbits of different coat colours including 10 Japanese and 10 Rhinelander (tricolour) rabbits and identified another 6 bp-in frame deletion flanked by a G > A transition in 5' (c.[124G>A;125_130del6]) that was present in all animals with Japanese brindling coat colour and pattern. These mutations eliminate two amino acids in the first transmembrane domain and, in addition, cause an amino acid substitution at position 44 of the wild type sequence. Genotyping 371 rabbits of 31 breeds with different coat colour this allele (eJ) was present in homozygous state in Japanese, Rhinelander and Dutch tricolour rabbits only (except one albino rabbit). Rabbits with eJ/eJ genotype were non fixed at the non-agouti mutation we previously identified in the ASIP gene. Segregation in F1 and F2 families confirmed the order of dominance already determined by classical genetic experiments with a possible dose effect evident comparing eJ/eJ and eJ/e animals. MC1R mRNA was expressed in black hair skin regions only.

The c.[124A;125_130del6] allele may be responsible for a MC1R variant determining eumelanin production in the black areas. However, the mechanism determining the presence of both red and black hairs in the same animal seems more complex. Expression analyses of the c.[124A;125_130del6] allele suggest that MC1R transcription may be regulated epigenetically in rabbits with the Japanese brindling phenotype. Further studies are needed to clarify this issue.

Additional References

RELATED GEPHE

	Related Genes
4 (Agouti (ASIP), Melanophilin (MLPH), tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~9986^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	
	Related Haplotypes
2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~MC1R^/and+Taxon ID=~9986^/or+Gene Gephebase=~MC1R^/and+Taxon ID=~9986^#gephebase-summary-	

title)

EXTERNAL LINKS

COMMENTS