GEPHE SUMMARY

Gephebase Gene

coatomer protein complex subunit alpha (COPA) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^coatomer protein complex subunit alpha (COPA)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001329

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^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

Holstein dairy cattle-wild type

Trait State in Taxon B

Holstein dairy cattle-Dominant Red

Ancestral State

Taxon A

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bos taurus^#gephebase-summary-title)

Common Name

cattle

Synonyms

Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Tauurus

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent

Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)

NCBI Taxonomy ID

9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Holstein dairy cattle-wild type

Taxon B

Latin Name

Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bos taurus^#gephebase-summary-title)

Common Name

cattle

Synonyms

Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Tauurus

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent

Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)

NCBI Taxonomy ID

9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Holstein dairy cattle-Dominant Red

GENOTYPIC CHANGE

Generic Gene Name

COPA

Synonyms

AILJK; HEP-COP; alpha-COP

String

9606.ENSP00000357048 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000357048)

Sequence Similarities

-

GO - Molecular Function

GO:0005198 : structural molecule activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005198)
GO:0005179 : hormone activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005179)

UniProtKB Homo sapiens

P53621 (http://www.uniprot.org/uniprot/P53621)

GenebankID or UniProtKB

()

GO - Biological Process

GO:0006886 : intracellular protein transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006886)
GO:0006888 : ER to Golgi vesicle-mediated transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006888)
GO:0006891 : intra-Golgi vesicle-mediated transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006891)
GO:0030157 : pancreatic juice secretion (https://www.ebi.ac.uk/QuickGO/term/GO:0030157)
GO:0006890 : retrograde vesicle-mediated transport, Golgi to ER (https://www.ebi.ac.uk/QuickGO/term/GO:0006890)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0000139 : Golgi membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0000139)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0070062 : extracellular exosome (https://www.ebi.ac.uk/QuickGO/term/GO:0070062)
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)
GO:0005789 : endoplasmic reticulum membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005789)
GO:0030133 : transport vesicle (https://www.ebi.ac.uk/QuickGO/term/GO:0030133)
GO:0030126 : COPI vesicle coat (https://www.ebi.ac.uk/QuickGO/term/GO:0030126)

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

c.C>T p.Arg160Cys

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Arg	Cys	160

Main Reference

Dominant Red Coat Color in Holstein Cattle Is Associated with a Missense Mutation in the Coatomer Protein Complex, Subunit Alpha (COPA) Gene. (2015) (https://pubmed.ncbi.nlm.nih.gov/26042826)

Authors

Dorshorst B; Henegar C; Liao X; SÃ¤llman AlmÃ©n M; Rubin CJ; Ito S; Wakamatsu K; Stothard P; Van Doormaal B; Plastow G; Barsh GS; Andersson L

Abstract

Coat color in Holstein dairy cattle is primarily controlled by the melanocortin 1 receptor (MC1R) gene, a central determinant of black (eumelanin) vs. red/brown pheomelanin synthesis across animal species. The major MC1R alleles in Holsteins are Dominant Black (MC1RD) and Recessive Red (MC1Re). A novel form of dominant red coat color was first observed in an animal born in 1980. The mutation underlying this phenotype was named Dominant Red and is epistatic to the constitutively activated MC1RD. Here we show that a missense mutation in the coatomer protein complex, subunit alpha (COPA), a gene with previously no known role in pigmentation synthesis, is completely associated with Dominant Red in Holstein dairy cattle. The mutation results in an arginine to cysteine substitution at an amino acid residue completely conserved across eukaryotes. Despite this high level of conservation we show that both heterozygotes and homozygotes are healthy and viable. Analysis of hair pigment composition shows that the Dominant Red phenotype is similar to the MC1R Recessive Red phenotype, although less effective at reducing eumelanin synthesis. RNA-seq data similarly show that Dominant Red animals achieve predominantly pheomelanin synthesis by downregulating genes normally required for eumelanin synthesis. COPA is a component of the coat protein I seven subunit complex that is involved with retrograde and cis-Golgi intracellular coated vesicle transport of both protein and RNA cargo. This suggests that Dominant Red may be caused by aberrant MC1R protein or mRNA trafficking within the highly compartmentalized melanocyte, mimicking the effect of the Recessive Red loss of function MC1R allele.

Additional References

RELATED GEPHE

Related Genes

11 (Agouti, Kit (type III receptor protein-tyrosine kinase), Kit ligand, MC1R, Melanophilin (MLPH), Microphtalmia-associated transcription factor, PMEL17, SLC45A2=MATP, Twist2, tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9913^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Epistasis - Probably hypomorphic as homozygous are viable and healthy - https://omia.org/OMIA001529/9913/