

GEPHE SUMMARY

Gephebase Gene
Agouti (ASIP)

Entry Status
Published

GepheID
GP00002061

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Coloration (coat)

Trait State in Taxon A
winter-white

Trait State in Taxon B
winter-gray

Ancestral State
Taxon A

Taxonomic Status
Intraspecific

Taxon A

Latin Name
Lepus timidus

Common Name
Mountain hare

Synonyms
Lepus tanaiticus; Mountain hare; Lepus timidus Linnaeus, 1758

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; Euarchontoglires; Glires; Lagomorpha; Leporidae; Lepus

Parent
Lepus (hares) - (Rank: genus)

NCBI Taxonomy ID
62621

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Lepus timidus

Common Name
Mountain hare

Synonyms
Lepus tanaiticus; Mountain hare; Lepus timidus Linnaeus, 1758

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; Euarchontoglires; Glires; Lagomorpha; Leporidae; Lepus

Parent
Lepus (hares) - (Rank: genus)

NCBI Taxonomy ID
62621

is Taxon B an Intraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Asip

Synonyms
As; ASP; A γ ; ASIP; a

String
10090.ENSMUSP00000029123

Sequence Similarities
-

GO - Molecular Function
GO:0031779 : melanocortin receptor binding
GO:0031781 : type 3 melanocortin receptor binding
GO:0031782 : type 4 melanocortin receptor binding

GO - Biological Process
GO:0008343 : adult feeding behavior
GO:0006091 : generation of precursor metabolites and energy
GO:0071514 : genetic imprinting
GO:0009755 : hormone-mediated signaling pathway
GO:0042438 : melanin biosynthetic process
GO:0032438 : melanosome organization

UniProtKB Mus musculus
Q03288

GenebankID or UniProtKB

GO:0032402 : melanosome transport
GO:0043473 : pigmentation
GO:0048023 : positive regulation of melanin biosynthetic process
GO:0040030 : regulation of molecular function, epigenetic

GO - Cellular Component
GO:0005576 : extracellular region
GO:0005623 : cell

Presumptive Null
No

Molecular Type
Cis-regulatory

Aberration Type
Unknown

Molecular Details of the Mutation
exact mutation(s) unknown

Experimental Evidence
Association Mapping

Main Reference
Introgression drives repeated evolution of winter coat color polymorphism in hares. (2019)

Authors
Giska I; Farello L; Pimenta J; Seixas FA; Ferreira MS; Marques JP; Miranda I; Letty J; Jenny H; Hackländer K; Magnussen E; Melo-Ferreira J

Abstract
Changing from summer-brown to winter-white pelage or plumage is a crucial adaptation to seasonal snow in more than 20 mammal and bird species. Many of these species maintain nonwhite winter morphs, locally adapted to less snowy conditions, which may have evolved independently. Mountain hares (*Lepus timidus*) from Fennoscandia were introduced into the Faroe Islands in 1855. While they were initially winter-white, within $\hat{\approx}1/465$ y all Faroese hares became winter-gray, a morph that occurs in the source population at low frequency. The documented population history makes this a valuable model for understanding the genetic basis and evolution of the seasonal trait polymorphism. Through whole-genome scans of differentiation and single-nucleotide polymorphism (SNP) genotyping, we associated winter coat color polymorphism to the genomic region of the pigmentation gene *Agouti*, previously linked to introgression-driven winter coat color variation in the snowshoe hare (*Lepus americanus*). Lower *Agouti* expression in the skin of winter-gray individuals during the autumn molt suggests that regulatory changes may underlie the color polymorphism. Variation in the associated genomic region shows signatures of a selective sweep in the Faroese population, suggesting that positive selection drove the fixation of the variant after the introduction. Whole-genome analyses of several hare species revealed that the winter-gray variant originated through introgression from a noncolor changing species, in keeping with the history of ancient hybridization between the species. Our findings show the recurrent role of introgression in generating winter coat color variation by repeatedly recruiting the regulatory region of *Agouti* to modulate seasonal coat color change.

[Additional References](#)

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No matches found.
[Related Haplotypes](#)
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COMMENTS

@Introgression of the winter-gray allele from Iberian hares (*Lepus granatensis*)