GEPHE SUMMARY

Gephebase Gene
FGF5 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FGF5^#gephebase-summary-title)

GepheID
GP00002173

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

Trait
Hair length (https://www.gephebase.org/search-criteria?/and+Trait=^Hair length^#gephebase-summary-title)

Trait State in Taxon A
Syrian Hamster - WT hair

Trait State in Taxon B
Male-dominant long-haired coat (MALC) ; autosomal recessive

Ancestral State
Taxon A

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

Taxon A

Latin Name
Mesocricetus auratus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Mesocricetus auratus^#gephebase-summary-title)

Common Name
golden hamster

Synonyms
Golden hamsters; Syrian hamsters; golden hamster; Syrian golden hamster; Syrian golden hamsters; Syrian hamster; Mesocricetus auratus Waterhouse, 1839

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; Rodentia; Myomorpha; Muroidea; Cricetidae; Cricetinae; Mesocricetus

Parent
Mesocricetus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10035)

NCBI Taxonomy ID
10036 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10036)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Mesocricetus auratus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Mesocricetus auratus^#gephebase-summary-title)

Common Name
golden hamster

Synonyms
Golden hamsters; Syrian hamsters; golden hamster; Syrian golden hamster; Syrian golden hamsters; Syrian hamster; Mesocricetus auratus Waterhouse, 1839

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; Rodentia; Myomorpha; Muroidea; Cricetidae; Cricetinae; Mesocricetus

Parent
Mesocricetus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10035)

NCBI Taxonomy ID
10036 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10036)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Fgf5

Synonyms
go; Fgf-5; HBGF-5; angora

String
10090.ENSMUSP00000031280 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000031280)

Sequence Similarities
Belongs to the heparin-binding growth factors family.

GO - Molecular Function
GO:0008083 : growth factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008083)
GO:0005104 : fibroblast growth factor receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005104)

GO - Biological Process
GO:0008283 : cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008283)

UniProtKB Mus musculus
P15656 (http://www.uniprot.org/uniprot/P15656)

GenebankID or UniProtKB
ABB87177 (https://www.ncbi.nlm.nih.gov/nuccore/ABB87177)

GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:0051781 : positive regulation of cell division
(https://www.ebi.ac.uk/QuickGO/term/GO:0051781)
GO:0008543 : fibroblast growth factor receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0008543)
GO:0010001 : glial cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0010001)
GO:0023019 : signal transduction involved in regulation of gene expression
(https://www.ebi.ac.uk/QuickGO/term/GO:0023019)

GO - Cellular Component

GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#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

c.546delG p.Arg184GlyfsX6

Experimental Evidence

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

Main Reference

A 1-bp deletion in Fgf5 causes male-dominant long hair in the Syrian hamster. (2015) (https://pubmed.ncbi.nlm.nih.gov/26481120)

Authors

Yoshizawa Y; Wada K; Shimoi G; Shiomi G; Kameyama Y; Wakabayashi Y; Fukuta K; Hashizume R

Abstract

Hair length in mammals is generally regulated by the hair cycle, and its disruption leads to abnormal hair morphogenesis in several species. FGF5, one of the hair cycle regulators, has a role in inducing catagen, and that mutation causes abnormal hair length in both sexes in humans, mice, dogs, and cats. Male-dominant long-haired coat (MALC) is an inbred strain of Syrian hamster exhibiting spontaneous long hair in males. After castration, MALC exhibited significantly shorter hair than the control individuals, but testosterone administration to castrated MALC showed reversion to the original phenotype. Moreover, flutamide administration led to MALC phenotype repression. Histological analysis revealed that hair follicle regression was shown in the wild-type 4 weeks after depilation, but that of MALC remained in the anagen phase. We detected a c.546delG of Fgf5 in MALC (Fgf5malc) that might lead to truncation resulting from a frame shift in FGF5 (p.Arg184GlyfsX6). Additionally, homozygous Fgf5malc was only detected in long-haired (Slc:SyrianÃ—MALC)F2 and (J-2-NnÃ—MALC)F2 progenies, and all homozygous wild and heterozygous Fgf5malc individuals showed normal hair length. Thus, Fgf5malc leads to male-dominant long hair via a prolonged anagen phase which is affected by testosterone in hamsters. To our knowledge, this report is the first to present the sexual dimorphism of hair length caused by the Fgf5 mutation.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualDimorphism https://omia.org/OMIA000439/10036/