GEPHE SUMMARY

Gephebase Gene

HES7 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^HES7^#gephebase-summary-title)

GepheID

GP00002190

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

Organ size (tail; short) (https://www.gephebase.org/search-criteria?/and+Trait=^Organ size (tail; short)^#gephebase-summary-title)

Trait State in Taxon A

WT cat

Trait State in Taxon B

Short tail - Chinese short-tailed feral cat ; and Japanese Bobtail cat

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

domestic cat

Synonyms

Felis domesticus; Felis silvestris catus; domestic cat; cat; cats; Felis catus Linnaeus, 1758; Korat cats L.

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; Carnivora; Feliformia; Felidae; Felinae; Felis

Parent

Felis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9682)

NCBI Taxonomy ID

9685 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9685)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

domestic cat

Synonyms

Felis domesticus; Felis silvestris catus; domestic cat; cat; cats; Felis catus Linnaeus, 1758; Korat cats L.

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; Carnivora; Feliformia; Felidae; Felinae; Felis

Parent

Felis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9682)

NCBI Taxonomy ID

9685 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9685)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

HES7

Synonyms

SCDO4; bHLHb37; BHLHB37

String

9606.ENSP00000446205 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000446205)

Sequence Similarities

-

GO - Molecular Function

GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)
GO:0008134 : transcription factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008134)

UniProtKB Homo sapiens

Q9BYE0 (http://www.uniprot.org/uniprot/Q9BYE0)

GenebankID or UniProtKB

()

GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)
GO:0001227 : DNA-binding transcription repressor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001227)

GO - Biological Process

GO:0050767 : regulation of neurogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0050767)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0001501 : skeletal system development (https://www.ebi.ac.uk/QuickGO/term/GO:0001501)
GO:0009952 : anterior/posterior pattern specification (https://www.ebi.ac.uk/QuickGO/term/GO:0009952)
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0007219 : Notch signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007219)
GO:0001756 : somitogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0001756)
GO:0007498 : mesoderm development (https://www.ebi.ac.uk/QuickGO/term/GO:0007498)
GO:0036342 : post-anal tail morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0036342)
GO:0048511 : rhythmic process (https://www.ebi.ac.uk/QuickGO/term/GO:0048511)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0000790 : nuclear chromatin (https://www.ebi.ac.uk/QuickGO/term/GO:0000790)

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

g.2819475A>G c.5A>G p.V2A

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Val	Ala	2

Main Reference

Whole genome sequencing in cats, identifies new models for blindness in AIPL1 and somite segmentation in HES7. (2016) (https://pubmed.ncbi.nlm.nih.gov/27030474)

Authors

Lyons LA; Creighton EK; Alhaddad H; Beale HC; Grahn RA; Rah H; Maggs DJ; Helps CR; Gandolfi B

Abstract

The reduced cost and improved efficiency of whole genome sequencing (WGS) is drastically improving the development of cats as biomedical models. Persian cats are models for Leber's congenital amaurosis (LCA), the most severe and earliest onset form of visual impairment in humans. Cats with innocuous breed-defining traits, such as a bobbed tail, can also be models for somite segmentation and vertebral column development.

The first WGS in cats was conducted on a trio segregating for LCA and the bobbed tail abnormality. Variants were identified using FreeBayes and effects predicted using SnpEff. Variants within a known haplotype block for cat LCA and specific candidate genes for both phenotypes were prioritized by the predicted variant effect on the proteins and concordant segregation within the trio. The efficiency of WGS of a single trio of domestic cats was evaluated.

A stop gain was identified at position c.577C > T in cat AIPL1, a predicted p.Arg193*. A c.5A > G variant causing a p.V2A was identified in HES7. The variants segregated concordantly in a Persian - Japanese bobtail pedigree. Over 1700 cats from 40 different breeds and populations were genotyped for the AIPL1 variant, defining an allelic frequency in only Persian -related breeds of 1.15%. A sub-set of cats was genotyped for the HES7 variant, supporting the variant as private to the Japanese bobtail breed. Approximately 18 million SNPs were identified for application in cat research. The cat AIPL1 variant would have been considered a high priority variant for evaluation, regardless of a priori knowledge from previous genetic studies.

This study represents the first effort of the 99 Lives Cat Genome Sequencing Initiative to identify disease--causing variants in the domestic cat using WGS. The current cat reference assembly is efficient for gene and variant identification. However, as the feline variant database improves, development of cats as biomedical models for human disease will be more efficient, providing an alternative, large animal model for drug and gene therapy trials. Undiagnosed human patients with early-onset blindness should be screened for this AIPL1 variant. The HES7 variant should further calibrate the somite segmentation clock.

Additional References

Whole Genome Sequencing Identifies a Missense Mutation in HES7 Associated with Short Tails in Asian Domestic Cats. (2016) (https://pubmed.ncbi.nlm.nih.gov/27560986)

RELATED GEPHE

Related Genes

1 (TBXT) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9685^/and+Trait=Organ size/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

https://omia.org/OMIA001987/9685/