GEPHE SUMMARY

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

Entry Status
Published

GepheID
GP00002289

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

Trait State in Taxon B
Short Tail

Ancestral State
Taxon A

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

Taxon A

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

Common Name
sheep

Synonyms
Ovis ammon aries; Ovis orientalis aries; Ovis ovis; sheep; domestic sheep; lambs; wild sheep; Ovis aries 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; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis

Parent
Ovis () - (Rank: genus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9935)

NCBI Taxonomy ID
9940
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9940)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Barag sheep

Taxon B

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

Common Name
sheep

Synonyms
Ovis ammon aries; Ovis orientalis aries; Ovis ovis; sheep; domestic sheep; lambs; wild sheep; Ovis aries 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; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis

Parent
Ovis () - (Rank: genus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9935)

NCBI Taxonomy ID
9940
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9940)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Hulunbuir sheep; Kazalh and other breeds

GENOTYPIC CHANGE

Generic Gene Name
Tbxt

Synonyms
Lr; T1; Bra; Low; Tl2; Tl3; cou; Tbxt; me75; D17Mit170; T

String
10090.ENSMUSP00000074236
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 10090.ENSMUSP00000074236)

Sequence Similarities
-

GO - Molecular Function
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001228)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)

UniProtKB Mus musculus
P20293 (http://www.uniprot.org/uniprot/P20293)

GenebankID or UniProtKB
()

GO:0043565 : sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific
(https://www.ebi.ac.uk/QuickGO/term/GO:0000981)
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000978)
GO:0001085 : RNA polymerase II transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001085)
GO:0001102 : RNA polymerase II activating transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001102)

GO - Biological Process

GO:0009653 : anatomical structure morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0009653)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0006357 : regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0006357)
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:0001843 : neural tube closure (https://www.ebi.ac.uk/QuickGO/term/GO:0001843)
GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:0001756 : somitogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0001756)
GO:0060395 : SMAD protein signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0060395)
GO:0061371 : determination of heart left/right asymmetry
(https://www.ebi.ac.uk/QuickGO/term/GO:0061371)
GO:0001707 : mesoderm formation (https://www.ebi.ac.uk/QuickGO/term/GO:0001707)
GO:0030903 : notochord development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030903)
GO:0001708 : cell fate specification (https://www.ebi.ac.uk/QuickGO/term/GO:0001708)
GO:0007498 : mesoderm development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007498)
GO:0043433 : negative regulation of DNA-binding transcription factor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0043433)
GO:0023019 : signal transduction involved in regulation of gene expression
(https://www.ebi.ac.uk/QuickGO/term/GO:0023019)
GO:0036342 : post-anal tail morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0036342)
GO:0060349 : bone morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0060349)
GO:0071300 : cellular response to retinoic acid
(https://www.ebi.ac.uk/QuickGO/term/GO:0071300)
GO:0001570 : vasculogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0001570)
GO:0022414 : reproductive process (https://www.ebi.ac.uk/QuickGO/term/GO:0022414)
GO:0048706 : embryonic skeletal system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048706)
GO:0055007 : cardiac muscle cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0055007)
GO:0003007 : heart morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0003007)
GO:0007509 : mesoderm migration involved in gastrulation
(https://www.ebi.ac.uk/QuickGO/term/GO:0007509)
GO:0001839 : neural plate morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0001839)
GO:0014028 : notochord formation (https://www.ebi.ac.uk/QuickGO/term/GO:0014028)
GO:0007341 : penetration of zona pellucida
(https://www.ebi.ac.uk/QuickGO/term/GO:0007341)
GO:0003257 : positive regulation of transcription from RNA polymerase II promoter
involved in myocardial precursor cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0003257)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005654 : nucleoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005654)
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)
GO:0000785 : chromatin (https://www.ebi.ac.uk/QuickGO/term/GO:0000785)

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.G334T p.G112W

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	Gly	Trp	112

Main Reference

Whole Genome Sequencing of Hulunbuir Short-Tailed Sheep for Identifying Candidate Genes Related to the Short-Tail Phenotype. (2018) (https://pubmed.ncbi.nlm.nih.gov/29208649)

Authors

Zhi D; Da L; Liu M; Cheng C; Zhang Y; Wang X; Li X; Tian Z; Yang Y; He T; Long X; Wei W; Cao G

Abstract

The Hulunbuir short-tailed sheep (Ovis aries) is a breed native to China, in which the short-tail phenotype is the result of artificial and natural selection favoring a specific set of genetic mutations. Here, we analyzed the genetic differences between short-tail and normal-tail phenotypes at the genomic level. Selection signals were identified in genome-wide sequences. From 16 sheep, we identified 72,101,346 single nucleotide polymorphisms. Selection signals were detected based on the fixation index and heterozygosity. Seven genomic regions under putative selection were identified, and these regions contained nine genes. Among these genes, T was the strongest candidate as T is related to vertebral development. In T, a nonsynonymous mutation at c.G334T resulted in p.G112W substitution. We inferred that the c.G334T mutation in T leads to functional changes in Brachyury-encoded by this gene-resulting in the short-tail phenotype. Our findings provide a valuable insight into the development of the short-tail phenotype in sheep and other short-tailed animals.

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Additional References

Two linked TBXT (brachyury) gene polymorphisms are associated with the tailless phenotype in fat-rumped sheep. (2019) (https://pubmed.ncbi.nlm.nih.gov/31475743)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Parallelism @HeterozygoteAdvantage