GEPHE SUMMARY

Gephebase Gene
T-box transcription factor (TBX3) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^T-box transcription factor (TBX3)^#gephebase-summary-title)

GepheID
GP00001461

Entry Status
Published

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
Dun horse characterized by diluted pigment with dark primitive markings - radially asymmetric deposition of pigment in hair

Trait State in Taxon B
Non-dun horse intensely pigmented associated with markings - circumferential distribution of melanocytes and pigment granules in hair

Ancestral State
Taxon A

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

Taxon A

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

Common Name
horse

Synonyms
Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus 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; Perissodactyla; Equidae; Equus; Equus

Parent
Equus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 35510)

NCBI Taxonomy ID
9796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9796)

is Taxon A an Infraspecies?
Yes

Taxon A Description
-

Taxon B

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

Common Name
horse

Synonyms
Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus 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; Perissodactyla; Equidae; Equus; Equus

Parent
Equus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 35510)

NCBI Taxonomy ID
9796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9796)

is Taxon B an Infraspecies?
Yes

Taxon B Description
-

GENOTYPIC CHANGE

Generic Gene Name
TBX3

Synonyms
UMS; XHL; TBX3-ISO

String
9606.ENSP00000257566 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000257566)

Sequence Similarities
-

GO - Molecular Function
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)

UniProtKB Homo sapiens
O15119 (http://www.uniprot.org/uniprot/O15119)

GenebankID or UniProtKB
KT896509 (https://www.ncbi.nlm.nih.gov/nuccore/KT896509)

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:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001078)
GO:0001102 : RNA polymerase II activating transcription factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0001102)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process (https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
GO:0006357 : regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0006357)
GO:0001501 : skeletal system development (https://www.ebi.ac.uk/QuickGO/term/GO:0001501)
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0045892 : negative regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0045892)
GO:0045893 : positive regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0045893)
GO:0060021 : roof of mouth development (https://www.ebi.ac.uk/QuickGO/term/GO:0060021)
GO:0008284 : positive regulation of cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:0001701 : in utero embryonic development (https://www.ebi.ac.uk/QuickGO/term/GO:0001701)
GO:0009887 : animal organ morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0009887)
GO:0001947 : heart looping (https://www.ebi.ac.uk/QuickGO/term/GO:0001947)
GO:0030539 : male genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0030539)
GO:0090398 : cellular senescence (https://www.ebi.ac.uk/QuickGO/term/GO:0090398)
GO:0045787 : positive regulation of cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0045787)
GO:0060412 : ventricular septum morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0060412)
GO:0019827 : stem cell population maintenance (https://www.ebi.ac.uk/QuickGO/term/GO:0019827)
GO:0035116 : embryonic hindlimb morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0035116)
GO:2000648 : positive regulation of stem cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:2000648)
GO:0035136 : forelimb morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0035136)
GO:0030879 : mammary gland development (https://www.ebi.ac.uk/QuickGO/term/GO:0030879)
GO:0045662 : negative regulation of myoblast differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0045662)
GO:0035115 : embryonic forelimb morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0035115)
GO:0048332 : mesoderm morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048332)
GO:0008595 : anterior/posterior axis specification, embryo (https://www.ebi.ac.uk/QuickGO/term/GO:0008595)
GO:0003167 : atrioventricular bundle cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0003167)
GO:0001568 : blood vessel development (https://www.ebi.ac.uk/QuickGO/term/GO:0001568)
GO:0060444 : branching involved in mammary gland duct morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0060444)
GO:0060923 : cardiac muscle cell fate commitment (https://www.ebi.ac.uk/QuickGO/term/GO:0060923)
GO:0007569 : cell aging (https://www.ebi.ac.uk/QuickGO/term/GO:0007569)
GO:0042733 : embryonic digit morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0042733)
GO:0030540 : female genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0030540)
GO:0046884 : follicle-stimulating hormone secretion (https://www.ebi.ac.uk/QuickGO/term/GO:0046884)
GO:0021761 : limbic system development (https://www.ebi.ac.uk/QuickGO/term/GO:0021761)
GO:0032275 : luteinizing hormone secretion (https://www.ebi.ac.uk/QuickGO/term/GO:0032275)
GO:0060596 : mammary placode formation (https://www.ebi.ac.uk/QuickGO/term/GO:0060596)

GO:0030857 : negative regulation of epithelial cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030857)
GO:0003151 : outflow tract morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0003151)
GO:0060931 : sinoatrial node cell development (https://www.ebi.ac.uk/QuickGO/term/GO:0060931)
GO:0010159 : specification of animal organ position (https://www.ebi.ac.uk/QuickGO/term/GO:0010159)

GO - Cellular Component

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

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

Molecular Details of the Mutation

G>T predicted to affect binding of the CCAT box-binding transcription factors NF-Y and NF-I ; Differs from the wild-type allele by a SNP downstream of the wild-type TBX3 sequence (located 1067bp downstream of the start of the larger nd2 deletion described in the nd2 entry) with allele nd1 = T compared with the wild-type D allele = G); an ancient variant

Experimental Evidence

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

Main Reference

Regulatory mutations in TBX3 disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. (2016) (https://pubmed.ncbi.nlm.nih.gov/26691985)

Authors

Imsland F; McGowan K; Rubin CJ; Henegar C; SundstrÃ¶m E; Berglund J; Schwochow D; Gustafson U; Imsland P; Lindblad-Toh K; Lindgren G; Mikko S; Millon L; Wade C; Schubert M; Orlando L; Penedo MC; Barsh GS; Andersson L

Abstract

Dun is a wild-type coat color in horses characterized by pigment dilution with a striking pattern of dark areas termed primitive markings. Here we show that pigment dilution in Dun horses is due to radially asymmetric deposition of pigment in the growing hair caused by localized expression of the T-box 3 (TBX3) transcription factor in hair follicles, which in turn determines the distribution of hair follicle melanocytes. Most domestic horses are non-dun, a more intensely pigmented phenotype caused by regulatory mutations impairing TBX3 expression in the hair follicle, resulting in a more circumferential distribution of melanocytes and pigment granules in individual hairs. We identified two different alleles (non-dun1 and non-dun2) causing non-dun color. non-dun2 is a recently derived allele, whereas the Dun and non-dun1 alleles are found in ancient horse DNA, demonstrating that this polymorphism predates horse domestication. These findings uncover a new developmental role for T-box genes and new aspects of hair follicle biology and pigmentation.

Additional References

RELATED GEPHE

Related Genes

13 (Agouti, Endothelin receptor B, Kit (type III receptor protein-tyrosine kinase), MC1R, MFSD12, Microphtalmia-associated transcription factor, Pax3, PMEL17, SLC24A, SLC36A1, SLC45A2=MATP, syntaxin-17, TRPM1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9796^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^T-box transcription factor (TBX3)^/and+Taxon ID=^9796^/or+Gene Gephebase=^T-box transcription factor (TBX3)^/and+Taxon ID=^9796^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@AllelicSeries ; Dun is dominant over non-dun. This allele was already present in horse before domestication ; https://omia.org/OMIA001972/9796/