

## GEPHE SUMMARY

<p>Microphthalmia-associated transcription factor (<a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Microphthalmia-associated+transcription+factor">#gephebase-summary-title</a>)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>GP00000659</p> <p>Martin</p> <p>Entry Status</p>	<p>GepheID</p> <p>Main curator</p>
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## PHENOTYPIC CHANGE

<p>Morphology (<a href="https://www.gephebase.org/search-criteria?/and+Trait+Category+Morphology">#gephebase-summary-title</a>)</p> <p>Coloration (coat) (<a href="https://www.gephebase.org/search-criteria?/and+Trait+Coloration+coat">#gephebase-summary-title</a>)</p> <p>Equus caballus</p> <p>Equus caballus - "macchiato" coat</p> <p>Taxon A</p> <p>Domesticated (<a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Domesticated">#gephebase-summary-title</a>)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Equus caballus</p> <p>Equus caballus</p> <p>horse</p> <p>Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus Linnaeus, 1758</p> <p>species</p> <p>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</p> <p>Equus () - (Rank: subgenus) (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510</a>)</p> <p>9796 (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796</a>)</p> <p>No is Taxon A an Intraspecies?</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p> <p>Taxon B Description</p>	<p>Equus caballus</p> <p>Equus caballus</p> <p>horse</p> <p>Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus Linnaeus, 1758</p> <p>species</p> <p>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</p> <p>Equus () - (Rank: subgenus) (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510</a>)</p> <p>9796 (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796</a>)</p> <p>Yes is Taxon B an Intraspecies?</p> <p>Equus caballus - "macchiato" coat</p>
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## GENOTYPIC CHANGE

<p>Mitf</p> <p>Wh; bw; mi; vit; BCC2; Bhlhe32; Gsfbcc2; Vitiligo; Bw; Mi; Vit</p> <p>10090.ENSMUSP00000044938 (<a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000044938">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000044938</a>)</p> <p>Belongs to the MiT/TFE family.</p> <p>GO:0046983 : protein dimerization activity (<a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046983">https://www.ebi.ac.uk/QuickGO/term/GO:0046983</a>)</p> <p>GO:0003700 : DNA-binding transcription factor activity</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>Q08874 (<a href="http://www.uniprot.org/uniprot/Q08874">http://www.uniprot.org/uniprot/Q08874</a>)</p> <p>()</p> <p>UniProtKB Mus musculus</p> <p>GenebankID or UniProtKB</p>
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(<https://www.ebi.ac.uk/QuickGO/term/GO:0003700>)  
 GO:0043565 : sequence-specific DNA binding  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0043565>)  
 GO:0003677 : DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003677>)  
 GO:0003682 : chromatin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003682>)  
 GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0000981>)  
 GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA  
 polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)  
 GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)  
 GO:0070888 : E-box binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0070888>)  
 GO:0003705 : transcription factor activity, RNA polymerase II distal enhancer sequence-  
 specific binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003705>)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)  
 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:0006355 : regulation of transcription, DNA-templated  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)  
 GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)  
 GO:0043473 : pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0043473>)  
 GO:0000122 : negative regulation of transcription by RNA polymerase II  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)  
 GO:0045893 : positive regulation of transcription, DNA-templated  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)  
 GO:0010628 : positive regulation of gene expression  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)  
 GO:0006351 : transcription, DNA-templated  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006351>)  
 GO:0045165 : cell fate commitment (<https://www.ebi.ac.uk/QuickGO/term/GO:0045165>)  
 GO:0010468 : regulation of gene expression  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010468>)  
 GO:0030318 : melanocyte differentiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030318>)  
 GO:0043010 : camera-type eye development  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0043010>)  
 GO:0030316 : osteoclast differentiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030316>)  
 GO:0042127 : regulation of cell proliferation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0042127>)  
 GO:0046849 : bone remodeling (<https://www.ebi.ac.uk/QuickGO/term/GO:0046849>)  
 GO:0044336 : canonical Wnt signaling pathway involved in negative regulation of apoptotic  
 process (<https://www.ebi.ac.uk/QuickGO/term/GO:0044336>)  
 GO:0030336 : negative regulation of cell migration  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030336>)  
 GO:2000144 : positive regulation of DNA-templated transcription, initiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:2000144>)  
 GO:0065003 : protein-containing complex assembly  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0065003>)  
 GO:0045670 : regulation of osteoclast differentiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045670>)  
 GO:2001141 : regulation of RNA biosynthetic process  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:2001141>)  
 GO:0016055 : Wnt signaling pathway  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0016055>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)  
 GO:0032991 : protein-containing complex  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0032991>)

No ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=)) Presumptive Null  
 Coding ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=)) Molecular Type  
 SNP ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=)) Aberration Type  
 Nonsynonymous SNP Coding Change  
 c.629A>G N310S yielding defective DNA-binding Molecular Details of the Mutation  
 Candidate Gene ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=)) Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Asn	Ser	310

#### Main Reference

Mutations in MITF and PAX3 cause "splashed white" and other white spotting phenotypes in horses. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22511888>)

#### Authors

Hauswirth R; Haase B; Blatter M; Brooks SA; Burger D; DrÄqgemÄ¼ller C; Gerber V; Henke D; Janda J; Jude R; Magdesian KG; Matthews JM; Poncet PA; Svansson V; Tozaki T; Wilkinson-White L; Penedo MC; Rieder S; Leeb T

#### Abstract

During fetal development neural-crest-derived melanoblasts migrate across the entire body surface and differentiate into melanocytes, the pigment-producing cells. Alterations in this precisely regulated process can lead to white spotting patterns. White spotting patterns in horses are a complex trait with a large phenotypic variance ranging from minimal white markings up to completely white horses. The "splashed white" pattern is primarily characterized by an extremely large blaze, often accompanied by extended white markings at the distal limbs and blue eyes. Some, but not all, splashed white horses are deaf. We analyzed a Quarter Horse family segregating for the splashed white coat color. Genome-wide linkage analysis in 31 horses gave a positive LOD score of 1.6 in a region on chromosome 6 containing the PAX3 gene. However, the linkage data were not in agreement with a monogenic inheritance of a single fully penetrant mutation. We sequenced the PAX3 gene and identified a missense mutation in some, but not all, splashed white Quarter Horses. Genome-wide association analysis indicated a potential second signal near MITF. We therefore sequenced the MITF gene and found a 10 bp insertion in the melanocyte-specific promoter. The MITF promoter variant was present in some splashed white Quarter Horses from the studied family, but also in splashed white horses from other horse breeds. Finally, we identified two additional non-synonymous mutations in the MITF gene in unrelated horses with white spotting phenotypes. Thus, several independent mutations in MITF and PAX3 together with known variants in the EDNRB and KIT genes explain a large proportion of horses with the more extreme white spotting phenotypes.

#### Additional References

## RELATED GEPHE

#### Related Genes

13 (Agouti, Endothelin receptor B, Kit (type III receptor protein-tyrosine kinase), MC1R, MFSD12, Pax3, PMEL17, SLC24A, SLC36A1, SLC45A2=MATP, syntaxin-17, T-box transcription factor (TBX3), TRPM1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^9796^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

#### Related Haplotypes

5 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Microphthalmia-associated transcription factor^/and+Taxon ID=^9796^/or+Gene Gephebase=^Microphthalmia-associated transcription factor^/and+Taxon ID=^9796^#gephebase-summary-title>)

## EXTERNAL LINKS

## COMMENTS

@Parallelism @HeterozygoteAdvantage <https://omia.org/OMIA000214/9796/>