

GEPHE SUMMARY

| | | | |
|--|----------------|------------|--------------|
| PMEL17 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~PMEL17~#gephebase-summary-title) | Gephebase Gene | GP00002072 | GepheID |
| Published | Entry Status | II | Main curator |

PHENOTYPIC CHANGE

| | | | |
|--|-----------------------------|--|-----------------------------|
| Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title) | Trait Category | | |
| Coloration (coat) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+coat~#gephebase-summary-title) | Trait | | |
| Shetland Sheepdog of wild-type color - nonmerle | Trait State in Taxon A | | |
| Shetland Sheepdog of merle color - patches of diluted pigment - autosomal and incompletely dominant | Trait State in Taxon B | | |
| | Ancestral State | | |
| Taxon A | | Taxon B | |
| Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated~#gephebase-summary-title) | Taxonomic Status | | |
| | Latin Name | | Latin Name |
| Canis lupus familiaris (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Canis+lupus+familiaris~#gephebase-summary-title) | | Canis lupus familiaris (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Canis+lupus+familiaris~#gephebase-summary-title) | |
| dog | Common Name | dog | Common Name |
| Canis canis; Canis domesticus; Canis familiaris; dog; dogs; Canis familiaris Linnaeus, 1758; Canis lupus familiaris Linnaeus, 1758 | Synonyms | Canis canis; Canis domesticus; Canis familiaris; dog; dogs; Canis familiaris Linnaeus, 1758; Canis lupus familiaris Linnaeus, 1758 | Synonyms |
| subspecies | Rank | subspecies | Rank |
| cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Canis; Canis lupus | 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; Caniformia; Canidae; Canis; Canis lupus | Lineage |
| Canis lupus (gray wolf) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9612) | Parent | Canis lupus (gray wolf) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9612) | Parent |
| 9615 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9615) | NCBI Taxonomy ID | 9615 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9615) | NCBI Taxonomy ID |
| Yes | is Taxon A an Intraspecies? | Yes | is Taxon B an Intraspecies? |
| Shetland Sheepdog | Taxon A Description | Shetland Sheepdog | Taxon B Description |

GENOTYPIC CHANGE

| | | | |
|--|-------------------------|--|-------------------------|
| Pmel | Generic Gene Name | Q60696 (http://www.uniprot.org/uniprot/Q60696) | UniProtKB Mus musculus |
| D10H12S53E; Pmel17; Si; Silv | Synonyms | 0 | GenebankID or UniProtKB |
| 10090.ENSMUSP00000051869 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000051869) | String | | |
| Belongs to the PMEL/NMB family. | Sequence Similarities | | |
| GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802) | GO - Molecular Function | | |
| | GO - Biological Process | | |

GO:0042438 : melanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042438>)
GO:0032438 : melanosome organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032438>)
GO:0048023 : positive regulation of melanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048023>)

GO - Cellular Component

GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0005783 : endoplasmic reticulum
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005783>)
GO:0005789 : endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)
GO:0042470 : melanosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0042470>)
GO:0032585 : multivesicular body membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032585>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title](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](https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Cis-regulatory~#gephebase-summary-title))

Aberration Type

Insertion ([https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Insertion~#gephebase-summary-title))

Insertion Size

100-999 bp

Molecular Details of the Mutation

due to a short interspersed element (SINE) insertion at the intron 10/exon 11 boundary. The SINE segregates with the merle phenotype in multiple breeds (Collie, Border Collie, Australian Shepherd, Cardigan Welsh Corgi, Dachshund, and Great Dane) and is absent from dogs representing breeds that do not have merle patterning. All examined harlequin Great Danes harbored the insertion in either a heterozygous or homozygous state.

Experimental Evidence

Association Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping~#gephebase-summary-title))

Main Reference

Retrotransposon insertion in SILV is responsible for merle patterning of the domestic dog. (2006) (<https://pubmed.ncbi.nlm.nih.gov/16407134>)

Authors

Clark LA; Wahl JM; Rees CA; Murphy KE

Abstract

Merle is a pattern of coloring observed in the coat of the domestic dog and is characterized by patches of diluted pigment. This trait is inherited in an autosomal, incompletely dominant fashion. Dogs heterozygous or homozygous for the merle locus exhibit a wide range of auditory and ophthalmologic abnormalities, which are similar to those observed for the human auditory-pigmentation disorder Waardenburg syndrome. Mutations in at least five genes have been identified as causative for Waardenburg syndrome; however, the genetic bases for all cases have not been determined. Linkage disequilibrium was identified for a microsatellite marker with the merle phenotype in the Shetland Sheepdog. The marker is located in a region of CFA10 that exhibits conservation of synteny with HSA12q13. This region of the human genome contains SILV, a gene important in mammalian pigmentation. Therefore, this gene was evaluated as a candidate for merle patterning. A short interspersed element insertion at the boundary of intron 10/exon 11 was found, and this insertion segregates with the merle phenotype in multiple breeds. Another finding was deletions within the oligo(dA)-rich tail of the short interspersed element. Such deletions permit normal pigmentation. These data show that SILV is responsible for merle patterning and is associated with impaired function of the auditory and ophthalmologic systems. Although the mutant phenotype of SILV in the human is unknown, these results make it an intriguing candidate gene for human auditory-pigmentation disorders.

Additional References

RELATED GEPHE

Related Genes

12 (Agouti (ASIP), GPR22, MFSD12, SLC45A2=MATP, FGF3; FGF4; FGF19; ORAOV1, Kit, MC1R, Melanophilin (MLPH), Microphthalmia-associated transcription factor, PSMB7, tyrosinase-related protein 1 (TYRP1), beta-defensin 103 (CBD103)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~9615~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~9615~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

5 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~PMEL17~/and+Taxon ID=~9615~/or+Gene Gephebase=~PMEL17~/and+Taxon ID=~9615~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~PMEL17~/and+Taxon+ID=~9615~/or+Gene+Gephebase=~PMEL17~/and+Taxon+ID=~9615~#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@HeterozygoteAdvantage @Splicing @TE - PMEL17 is also known as SILV and gp100 - Dogs heterozygous or homozygous for the merle locus exhibit a wide range of auditory and ophthalmologic abnormalities. Dogs homozygous for merle (MM) are known as double merles and are predominantly white - reversion rate (excision of the TE and reversion to the nonmerle color, which is then stable through the next progeny) in the germ line is quite high: 3&acaron;4%. @Pleiotropy with deleterious effect similar to the human auditory&acaron;pigmentation disorder Waardenburg syndrome @HeterozygoteAdvantage @AllelicSeries <https://omia.org/OMIA000211/9615/>

