GEPHE SUMMARY

Gephebase Gene
PMEL17 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^PMEL17^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00002270

Main curator
Martin

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
Normal coat

Trait State in Taxon B
Numerous breeds : Harlequin or Minimal Merle with areas deleted to white; tweed

Ancestral State
Taxon A

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

Taxon A

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

Common Name
dog

Synonyms
Canis canis; Canis domesticus; Canis familiaris; dog; dogs; Canis familiaris Linnaeus, 1758; Canis lupus familiaris Linnaeus, 1758

Rank
subspecies

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

Parent
Canis lupus (gray wolf) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9612)

NCBI Taxonomy ID
9615 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9615)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
dog

Synonyms
Canis canis; Canis domesticus; Canis familiaris; dog; dogs; Canis familiaris Linnaeus, 1758; Canis lupus familiaris Linnaeus, 1758

Rank
subspecies

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

Parent
Canis lupus (gray wolf) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9612)

NCBI Taxonomy ID
9615 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9615)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Pmel

Synonyms
D10H12S53E; Pmel17; Si; Silv

String
10090.ENSMUSP00000051869 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 10090.ENSMUSP00000051869)

Sequence Similarities
Belongs to the PMEL/NMB family.

GO - Molecular Function
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)

GO - Biological Process
GO:0042438 : melanin biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0042438)
GO:0032438 : melanosome organization

UniProtKB Mus musculus
Q60696 (http://www.uniprot.org/uniprot/Q60696)

GenebankID or UniProtKB
()

(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)

Molecular Type

Cis-regulatory (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)

Insertion Size

100-999 bp

Molecular Details of the Mutation

Allele of the Merle SINE insertion : Mh (269-277bp)

Experimental Evidence

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

Main Reference

Merle phenotypes in dogs - SILV SINE insertions from Mc to Mh. (2018) (https://pubmed.ncbi.nlm.nih.gov/30235206)

Authors

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Abstract

It has been recognized that the Merle coat pattern in dogs is not only a visually interesting feature, but it also exerts an important biological role, in terms of hearing and vision impairments. In 2006, the Merle (M) locus was mapped to the SILV gene (aka PMEL) with a SINE element in it, and the inserted retroelement was proven causative to the Merle phenotype. Mapping of the M locus was a genetic breakthrough and many breeders started implementing SILV SINE testing in their breeding programs. Unfortunately, the situation turned out complicated as genotypes of Merle tested individuals did not always correspond to expected phenotypes, sometimes with undesired health consequences in the offspring. Two variants of SILV SINE, allelic to the wild type sequence, have been described so far-Mc and M. Here we report a significantly larger portfolio of existing Merle alleles (Mc, Mc+, Ma, Ma+, M, Mh) in Merle dogs, which are associated with unique coat color features and stratified health impairment risk. The refinement of allelic identification was made possible by systematic, detailed observation of Merle phenotypes in a cohort of 181 dogs from known Merle breeds, by many breeders worldwide, and the use of advanced molecular technology enabling the discrimination of individual Merle alleles with significantly higher precision than previously available. We also show that mosaicism of Merle alleles is an unexpectedly frequent phenomenon, which was identified in 30 out of 181 (16.6%) dogs in our study group. Importantly, not only major alleles, but also minor Merle alleles can be inherited by the offspring. Thus, mosaic findings cannot be neglected and must be reported to the breeder in their whole extent. Most importantly, sperm cells seem to be a significant source of germline Merle allelic variants which can be passed to the offspring on Mendelian basis and explain unusual genotype / phenotype findings in the offspring. In light of negative health consequences that may be attributed to certain Merle breeding strategies, we strongly advocate implementation of the refined Merle allele testing for all dogs of Merle breeds to help the breeders in selection of suitable mating partners and production of healthy offspring.

Additional References

Being Merle: The Molecular Genetic Background of the Canine Merle Mutation. (2020) (https://pubmed.ncbi.nlm.nih.gov/32560567)

RELATED GEPHE

Related Genes

12 (Agouti (ASIP), GPR22, MFSD12, SLC45A2=MATP, FGF3; FGF4; FGF19; ORAOV1, Kit, MC1R, Melanophilin (MLPH), Microphtalmia-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)

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)

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 high. @Pleiotropy with deleterious effect similar to the human auditoryâ€“pigmentation disorder Waardenburg syndrome @HeterozygoteAdvantage @AllelicSeries https://omia.org/OMIA000211/9615/