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His traits

Explore the genetics behind Leo's appearance and size.



Coat Color

A number of genes are known to affect coat color in dogs. They all interact and in some cases other, often unknown, genetic effects may also influence color and pattern.

We cannot yet test for some color patterns, for example, spotting and ticking.

Collapse all

E Locus (MC1R)

No dark hairs anywhere (ee)



The E Locus determines if and where a dog can produce dark (black or brown) hair. Dogs with two copies of the recessive **e** variant do not produce dark hairs and will express a red pigment called pheomelanin over their entire body. The shade of red, which can range from a deep copper to white, depends on other

genetic factors, including the Intensity loci. In addition to determining if a dog can develop dark hairs, the E Locus can give a dog a black "mask" or "widow's peak" unless the dog has overriding coat color genetic factors.

Dogs with one or two copies of the **E^m** variant may have a melanistic mask (dark facial hair as commonly seen in the German Shepherd Dog and Pug). In the absence of **E^m**, dogs with the **E^g** variant can have a "grizzle" phenotype (darker color on the head and top with a melanistic "widow's peak" and a lighter underside, commonly seen in the Afghan Hound and Borzoi and also referred to as "domino"). In the absence of both **E^m** and **E** variants, dogs with the **E^a** or **E^h** variants can express the grizzle phenotype. Additionally, a dog with any combination of two of the **E^g**, **E^a**, or **E^h** variants (example: **E^gE^a**) is also expected to express the grizzle phenotype.

Subloci

MC1R_E

Genetic result

ee

Subloci

MC1R_EA

Genetic result

Not Available

Subloci

MC1R_EG

Genetic result

(Not Eg)(Not Eg)

Subloci

MC1R_EM

Genetic result

(Not Em)(Not Em)

Subloci

MC1R_EH

Genetic result

Not Available

Subloci

MC1R_e2

Genetic result

Not Available

Subloci

MC1R_e3

Genetic result

Not Available

Citations

[Anderson et al 2020](#)

[Dreger and Schmutz 2010](#)

[Schmutz et al 2003](#)

[Honkanen et al 2024](#)

[Durig N et al 2018](#)

More Information

<http://www.doggenetics.co.uk/masks.html>

K Locus (CBD103)

Not expressed ($K^B k^y$)



Gene

Canine Beta-Defensin 103 (CBD103)

Genetic result

$K^B k^y$

The K Locus K^B allele “overrides” the A Locus, meaning that it prevents the A Locus genotype from affecting coat color. For this reason, the K^B allele is referred to as the “dominant black” allele. As a result, dogs with at least one K^B allele will usually have solid black or brown coats (or red/cream coats if they are **ee** at the E Locus) regardless of their genotype at the A Locus, although several other genes could impact the dog’s coat and cause other patterns, such as white spotting. Dogs with the $k^y k^y$ genotype will show a coat color pattern based on the genotype they have at the A Locus. Dogs who test as $K^B k^y$ may be brindle rather than black or brown.

Citations

[Candille et al 2007](#)

More Information

<http://www.doggenetics.co.uk/black.htm>

Intensity Loci

Linkage Test

Any pigmented hair likely apricot or red (Intense Red Pigmentation)



Areas of a dog's coat where dark (black or brown) pigment is not expressed either contain red/yellow pigment, or no pigment at all. Five locations across

five chromosomes explain approximately 70% of red pigmentation "intensity" variation across all dogs. Dogs with a result of **Intense Red Pigmentation** will likely have deep red hair like an Irish Setter or "apricot" hair like some Poodles, dogs with a result of **Intermediate Red Pigmentation** will likely have tan or yellow hair like a Soft-Coated Wheaten Terrier, and dogs with **Dilute Red Pigmentation** will likely have cream or white hair like a Samoyed. Because the mutations we test may not directly cause differences in red pigmentation intensity, we consider this to be a linkage test.

What is a linkage test? >

Subloci

Intensity_red_pigment_chr18

Genetic result

Red/Cream

Subloci

Intensity_red_pigment_chr2

Genetic result

Red/Red

Subloci

Intensity_red_pigment_chr21

Genetic result

Red/Cream

Subloci

Intensity_red_pigment_KITLG

Genetic result

Red/Red

Subloci

Intensity_red_pigment_MFSD12

Genetic result

Red/Red
[Slavney et al 2021](#)

[Weich et al 2020](#)

[Hedan et al 2019](#)

A Locus (ASIP)

Not expressed ($a^y a^t$)

Gene

Agouti Signalling Protein (ASIP)

Genetic result

$a^y a^t$

The A Locus controls switching between black and red pigment in hair cells, but it will only be expressed in dogs that are not **ee** at the E Locus and are **$k^y k^y$** at the K Locus. Sable (also called "Fawn") dogs have a mostly or entirely red coat with some interspersed black hairs. Agouti (also called "Wolf Sable") dogs have red hairs with black tips, mostly on their head and back. Black and tan dogs are mostly black or brown with lighter patches on their cheeks, eyebrows, chest, and legs. Recessive black dogs have solid-colored black or brown coats.

Subloci

ASIP_at

Genetic result

AtAt

Subloci

ASIP_{aw}

Genetic result

Aw(Not Aw)

Subloci

ASIP_{ay}

Genetic result

Ay(Not Ay)

Citations

[Dreger and Schmutz 2011](#)

[Berryere et al 2005](#)

More Information

<http://www.doggenetics.co.uk/tan.html>

D Locus (MLPH)

Not expressed (DD)



Gene

Melanophilin (MLPH)

Genetic result

DD

The D locus result that we report is determined by three different genetic variants that can work together to cause diluted pigmentation. These are the common **d** allele, also known as "**d1**", and the less common alleles known as "**d2**" and "**d3**". Dogs with two **d** alleles, regardless of which variant, will have all black pigment lightened ("diluted") to gray, or brown pigment lightened to

lighter brown in their hair, skin, and sometimes eyes. There are many breed-specific names for these dilute colors, such as "blue", "charcoal", "fawn", "silver", and "Isabella". Note that in certain breeds, dilute dogs have a higher incidence of Color Dilution Alopecia. Dogs with one **d** allele will not be dilute, but can pass the **d** allele on to their puppies.

Subloci

MLPH_D1

Genetic result

DD

Subloci

MLPH_D2

Genetic result

DD

Subloci

MLPH_D3

Genetic result

Not Available

Citations

[Drogemuller et al 2007](#)

[Bauer et al 2018](#)

[Van Buren et al 2020](#)

More Information

<http://www.doggenetics.co.uk/dilutes.html>

Cocoa (HPS3)

No co alleles, not expressed (NN)



Gene

HPS3

Genetic result

NN

Dogs with the **coco** genotype will produce dark brown pigment instead of black in both their hair and skin. Dogs with the **Nco** genotype will produce black pigment, but can pass the **co** allele on to their puppies. Dogs that have the **coco** genotype as well as the **bb** genotype at the B locus are generally a lighter brown than dogs that have the **Bb** or **BB** genotypes at the B locus.

Citations

[Kiener et al 2020](#)

More Information

<http://www.doggenetics.co.uk/liver.html#cocoa>

B Locus (TYRP1)

Likely black colored nose/feet (BB)



Gene

Tyrosinase Related Protein 1 (TYRP1)

Genetic result

BB

Dogs with two copies of the **b** allele produce brown pigment instead of black in both their hair and skin. Dogs with one copy of the **b** allele will produce black pigment, but can pass the **b** allele on to their puppies. E Locus **ee** dogs that carry two **b** alleles will have red or cream coats, but have brown noses, eye rims, and footpads (sometimes referred to as "Dudley Nose" in Labrador Retrievers). "Liver" or "chocolate" is the preferred color term for brown in most breeds; in the Doberman Pinscher it is referred to as "red".

Subloci

TYRP1_bc

Genetic result

BB

Subloci

TYRP1_bd

Genetic result

BB

Subloci

TYRP1_bn

Genetic result

Not Available

Subloci

TYRP1_bs

Genetic result

BB

Citations

[Schmutz et al 2002](#)

[Hrckova Turnova et al 2017](#)

[Jancuskova et al 2018](#)

More Information

Saddle Tan (RALY)

Not expressed (NI)



Gene

RALY

Genetic result

NI

The "Saddle Tan" pattern causes the black hairs to recede into a "saddle" shape on the back, leaving a tan face, legs, and belly, as a dog ages. The Saddle Tan pattern is characteristic of breeds like the Corgi, Beagle, and German Shepherd. Dogs that have the **ll** genotype at this locus are more likely to be mostly black with tan points on the eyebrows, muzzle, and legs as commonly seen in the Doberman Pinscher and the Rottweiler. This gene modifies the A Locus **a^t** allele, so dogs that do not express **a^t** are not influenced by this gene.

Citations

[Dreger et al 2013](#)

S Locus (MITF)

Likely to have little to no white in coat (SS)



Likely to have little to no white in coat (SS)

Gene

MITF

Genetic result

SS

The S Locus determines white spotting and pigment distribution. MITF controls where pigment is produced, and an insertion in the MITF gene causes a loss of pigment in the coat and skin, resulting in white hair and/or pink skin. Dogs with two copies of this variant will likely have breed-dependent white patterning, with a nearly white, parti, or piebald coat. Dogs with one copy of this variant will have more limited white spotting and may be considered flash, parti or piebald. This MITF variant does not explain all white spotting patterns in dogs and other variants are currently being researched. Some dogs may have small amounts of white on the paws, chest, face, or tail regardless of their S Locus genotype.

Citations

[Karlsson et al 2007](#)

More Information

<http://www.doggenetics.co.uk/white.htm>

M Locus (PMEL)

No merle alleles (mm)



Gene

PMEL

Genetic result

mm

Merle coat patterning is common to several dog breeds including the Australian Shepherd, Catahoula Leopard Dog, and Shetland Sheepdog, among many others. Merle arises from an unstable SINE insertion (which we term the "M*" allele) that disrupts activity of the pigmentary gene PMEL, leading to mottled or patchy coat color. Dogs with an **M*m** result are likely to be phenotypically merle or could be "non-expressing" merle, meaning that the merle pattern is very subtle or not at all evident in their coat. Dogs with an **M*M*** result are likely to be phenotypically merle or double merle. Dogs with an **mm** result have no merle alleles and are unlikely to have a merle coat pattern.

Note that Embark does not currently distinguish between the recently described cryptic, atypical, atypical+, classic, and harlequin merle alleles. Our merle test only detects the presence, but not the length of the SINE insertion. We do not recommend making breeding decisions on this result alone. Please pursue further testing for allelic distinction prior to breeding decisions.

Citations

[Clark et al 2006](#)

More Information

<http://www.doggenetics.co.uk/merle.html>

PMEL (1000000000)

Linkage Test



Likely no impact on coat pattern (rr)

Gene

USH2A

Genetic result

rr

The R Locus regulates the presence or absence of the roan coat color pattern. Partial duplication of the USH2A gene is strongly associated with this coat pattern. Dogs with at least one **R** allele will likely have roaning on otherwise uniformly unpigmented white areas. Roan appears in white areas controlled by the S Locus but not in other white or cream areas created by other loci, such as the E Locus with **ee** along with Dilute Red Pigmentation by I Locus (for example, in Samoyeds). Mechanisms for controlling the extent of roaning are currently unknown, and roaning can appear in a uniform or non-uniform pattern. Further, non-uniform roaning may appear as ticked, and not obviously roan. The roan pattern can appear with or without ticking.

What is a linkage test? >

Citations

[Brancalion et al 2021](#)

[Kawakami et al 2021](#)

More Information

<http://www.doggenetics.co.uk/ticking.html>

H Locus (Harlequin)

No harlequin alleles (hh)



Gene
PSMB

Genetic result
hh

This pattern is recognized in Great Danes and causes dogs to have a white coat with patches of darker pigment. A dog with an **Hh** result will be harlequin if they are also **M*m** or **M*M*** at the M Locus and are not **ee** at the E locus. Dogs with a result of **hh** will not be harlequin. This trait is thought to be homozygous

Other Coat Traits

Furnishings, shedding, and curls are all genetic. Several genes are at work here, and they all interact. In fact, the combination of these genes explains the coat traits of 90 percent of AKC registered dog breeds.

[Expand all](#)

Furnishings (RSPO2)

Linkage Test



Likely furnished (mustache, beard, and/or eyebrows) (FF)

Coat Length (FGF5)

Likely long coat (LhLh)



Shedding (MC5R)

Likely light shedding (CC)



Coat Texture (KRT71)

Likely wavy coat (CC)



Hairlessness (FOXI3)

Very unlikely to be hairless (NN)

Linkage Test



Hairlessness (SGK3)

Very unlikely to be hairless (NN)



Oculocutaneous Albinism Type 2 (SLC45A2)

Likely not albino (NN)

Linkage Test



Other Body Features

We are discovering the genetic basis for an increasing number of other body features, including hind dew claws and the shape of your dog's head. Take our surveys to help us make new discoveries.

Expand all

Muzzle Length (BMP3)

Likely medium or long muzzle (CC)



Tail Length (T)

Likely normal-length tail (CC)



Hind Dewclaws (LMBR1)

Unlikely to have hind dew claws (CC)



Blue Eye Color (ALX4)

Linkage Test

Less likely to have blue eyes (NN)



Back Muscling & Bulk, Large Breed (ACSL4)

Likely normal muscling (CC)



Body Size

Body size is a complex trait that is affected by both genetic and environmental variation. Our genetic analysis includes genes that, together, explain over 85 percent of the variation in dog body size. Below are your dog's results for some of the most important size-related genes.

Expand all

Predicted Adult Weight

32 lbs



Body Size (IGF1)

Intermediate (NI)



Body Size (IGF1)

Larger (GG)



Body Size (STC2)

Larger (TT)



Body Size (GHR - E191K)

Larger (GG)



Body Size (GHR - P177L)

Larger (CC)



Performance

Physical performance traits are interesting for all dogs, especially those that want to perform in more strenuous environments. These traits also shed light on the history of dogs and what they have been bred for. For example, the high altitude mutation we test for causes similar changes in oxygen usage as a mutation found in people from the Himalayas!

Expand all

Altitude Adaptation (EPAS1)

Normal altitude tolerance (GG)



Appetite (POMC)

Normal food motivation (NN)

Linkage Test

