



Rose Rep

Certificate of Breed

OWNER'S NAME: Jay Miller

DOG'S NAME: Milo

TEST DATE: May 27th, 2022

OWNER SUPPLIED BREED: Poodle (Toy)

REGISTRATION ORGANIZATION: American Kennel Club (AKC)

REGISTRATION NUMBER: --

This certifies the authenticity of **Milo's** canine genetic background as determined following careful analysis of more than 200,000 genetic markers.

Welcome to the Embark family!

POODLE



92.6% Poodle (Small)



7.4% Poodle (Standard)



MATERNAL **B81**
HAPLOTYPE

PATERNAL **H1a.45**
HAPLOTYPE

Purebred certification is separate from genetic ancestry. Purebred status is defined by pedigrees at registration bodies. Ancestry looks at segments of shared DNA.

Adam Boyko, Ph.D.
CHIEF SCIENCE OFFICER

Ryan Boyko
CHIEF EXECUTIVE OFFICER

PATERNAL LINE



Through Milo's Y chromosome we can trace his father's ancestry back to where dogs and people first became friends. This map helps you visualize the routes that his ancestors took to your home. Their story is described below the map.

HAPLOGROUP: A1a

Some of the wolves that became the original dogs in Central Asia around 15,000 years ago came from this long and distinguished line of male dogs. After domestication, they followed their humans from Asia to Europe and then didn't stop there. They took root in Europe, eventually becoming the dogs that founded the Vizsla breed 1,000 years ago. The Vizsla is a Central European hunting dog, and all male Vizslas descend from this line. During the Age of Exploration, like their owners, these pooches went by the philosophy, "Have sail, will travel!" From the windy plains of Patagonia to the snug and homey towns of the American Midwest, the beaches of a Pacific paradise, and the broad expanse of the Australian outback, these dogs followed their masters to the outposts of empires. Whether through good fortune or superior genetics, dogs from the A1a lineage traveled the globe and took root across the world. Now you find village dogs from this line frolicking on Polynesian beaches, hanging out in villages across the

HAPLOTYPE: H1a.45

Part of the A1a haplogroup, this haplotype occurs most frequently in mixed breed dogs.

Registration: American Kennel Club
(AKC)

DNA Test Report

Test Date: May 27th, 2022

embk.me/milo4729

BREED ANCESTRY



GENETIC STATS

Predicted adult weight: **16 lbs**

Genetic age: **7 human years**

Based on the date of birth you provided

TEST DETAILS

Kit number: EM-38512260

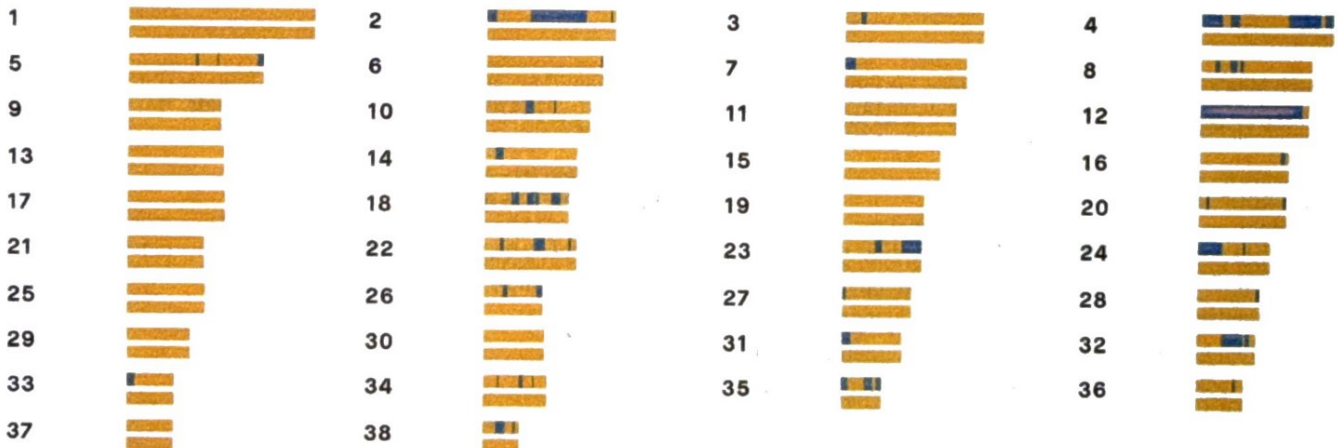
Swab number: 31211051901941

BREED ANCESTRY BY CHROMOSOME

Our advanced test identifies from where Milo inherited every part of the chromosome pairs in his genome.

Breed colors:

Poodle (Small) **Poodle (Standard)**



TRAITS: COAT COLOR (CONTINUED)

TRAIT	RESULT
<p>Intensity Loci LINKAGE</p> <p>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.</p>	<p>Any pigmented hair likely yellow or tan (Intermediate Red Pigmentation)</p>
<p>A Locus (ASIP)</p> <p>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^Yk^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.</p>	<p>Not expressed (a⁺a⁺)</p>
<p>D Locus (MLPH)</p> <p>The D locus result that we report is determined by two different genetic variants that can work together to cause diluted pigmentation. These are the common d allele, also known as "d1", and a less common allele known as "d2". 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. To view your dog's d1 and d2 test results, click the "SEE DETAILS" link in the upper right hand corner of the "Base Coat Color" section of the Traits page, and then click the "VIEW SUBLOCUS RESULTS" link at the bottom of the page.</p>	<p>Not expressed (DD)</p>

TRAITS: COAT COLOR

TRAIT

RÉSULT

E Locus (MC1R)

The E Locus determines if and where a dog can produce dark (black or brown) hair. Dogs with two copies of the recessive **e** allele do not produce dark hairs at all, and will be "red" over their entire body. The shade of red, which can range from a deep copper to yellow/gold to cream, is dependent on other genetic factors including the Intensity loci. In addition to determining if a dog can develop dark hairs at all, 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 **Em** allele usually have a melanistic mask (dark facial hair as commonly seen in the German Shepherd and Pug). Dogs with no copies of **Em** but one or two copies of the **Eg** allele usually have a melanistic "widow's peak" (dark forehead hair as commonly seen in the Afghan Hound and Borzoi, where it is called either "grizzle" or "domino").

No dark hairs anywhere (ee)

K Locus (CBD103)

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^Yk^Y** genotype will show a coat color pattern based on the genotype they have at the A Locus. Dogs who test as **K^Bk^Y** may be brindle rather than black or brown.

Not expressed (K^Bk^Y)

TRAITS: COAT COLOR (CONTINUED)

TRAIT

RESULT

Cocoa (NPS3)

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.

No co alleles, not expressed (NN)

B Locus (TYRP1)

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".

Likely black colored nose/feet (Bb)

Saddle Tan (RALY)

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.

Not expressed (ll)

S Locus (MITF)

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.

Likely solid colored, but may have small amounts of white (Ssp)

TRAITS: COAT COLOR (CONTINUED)

TRAIT

RESULT

M Locus (PMEL)

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.

No merle alleles (mm)

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.

R Locus (USH2A) LINKAGE

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.

Likely no impact on coat pattern (rr)

H Locus (Harlequin)

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 lethal; a living dog with an **HH** genotype has never been found.

No harlequin alleles (hh)

Registration:

TRAITS: OTHER COAT TRAITS

TRAIT	RESULT
<p>Furnishings (RSPO2) LINKAGE</p> <p>Dogs with one or two copies of the F allele have "furnishings": the mustache, beard, and eyebrows characteristic of breeds like the Schnauzer, Scottish Terrier, and Wire Haired Dachshund. A dog with two F alleles will not have furnishings, which is sometimes called an "improper coat" in breeds where furnishings are part of the breed standard. The mutation is a genetic insertion which we measure indirectly using a linkage test highly correlated with the insertion.</p>	<p>Likely furnished (mustache, beard, and/or eyebrows) (FF)</p>
<p>Coat Length (FGF5)</p> <p>The FGF5 gene is known to affect hair length in many different species, including cats, dogs, mice, and humans. In dogs, the T allele confers a long, silky haircoat as observed in the Yorkshire Terrier and the Long Haired Whippet. The ancestral G allele causes a shorter coat as seen in the Boxer or the American Staffordshire Terrier. In certain breeds (such as Corgi), the long haircoat is described as "fluff."</p>	<p>Likely long coat (TT)</p>
<p>Shedding (MC5R)</p> <p>Dogs with at least one copy of the ancestral C allele, like many Labradors and German Shepherd Dogs, are heavy or seasonal shedders, while those with two copies of the T allele, including many Boxers, Shih Tzus and Chihuahuas, tend to be lighter shedders. Dogs with furnished/wire-haired coats caused by RSPO2 (the furnishings gene) tend to be low shedders regardless of their genotype at this gene.</p>	<p>Likely light shedding (CT)</p>
<p>Hairlessness (FOXI3) LINKAGE</p> <p>A duplication in the FOXI3 gene causes hairlessness over most of the body as well as changes in tooth shape and number. This mutation occurs in Peruvian Inca Orchid, Xoloitzcuintli (Mexican Hairless), and Chinese Crested (other hairless breeds have different mutations). Dogs with the NDup genotype are likely to be hairless while dogs with the NN genotype are likely to have a normal coat. The DupDup genotype has never been observed, suggesting that dogs with that genotype cannot survive to birth. Please note that this is a linkage test, so it may not be as predictive as direct tests of the mutation in some lines.</p>	<p>Very unlikely to be hairless (NN)</p>
<p>Hairlessness (SGK3)</p> <p>Hairlessness in the American Hairless Terrier arises from a mutation in the SGK3 gene. Dogs with the ND genotype are likely to be hairless while dogs with the NN genotype are likely to have a normal coat.</p>	<p>Very unlikely to be hairless (NN)</p>

TRAITS: OTHER COAT TRAITS (CONTINUED)

TRAIT **RESULT**

Oculocutaneous Albinism Type 2 (SLC45A2) LINKAGE

Dogs with two copies **DD** of this deletion in the SLC45A2 gene have oculocutaneous albinism (OCA), also known as Doberman Z Factor Albinism, a recessive condition characterized by severely reduced or absent pigment in the eyes, skin, and hair. Affected dogs sometimes suffer from vision problems due to lack of eye pigment (which helps direct and absorb ambient light) and are prone to sunburn. Dogs with a single copy of the deletion **ND** will not be affected but can pass the mutation on to their offspring. This particular mutation can be traced back to a single white Doberman Pinscher born in 1976, and it has only been observed in dogs descended from this individual. Please note that this is a linkage test, so it may not be as predictive as direct tests of the mutation in some lines.

Likely not albino (NN)

Coat Texture (KRT71)

Dogs with a long coat and at least one copy of the **T** allele have a wavy or curly coat characteristic of Poodles and Bichon Frises. Dogs with two copies of the ancestral **C** allele are likely to have a straight coat, but there are other factors that can cause a curly coat, for example if they at least one **F** allele for the Furnishings (RSPO2) gene then they are likely to have a curly coat. Dogs with short coats may carry one or two copies of the **T** allele but still have straight coats.

Likely curly coat (TT)

TRAITS: OTHER BODY FEATURES

TRAIT	RESULT
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Muzzle Length (BMP3)

Dogs in medium-length muzzle (mesocephalic) breeds like Staffordshire Terriers and Labradors, and long muzzle (dolichocephalic) breeds like Whippet and Collie have one, or more commonly two, copies of the ancestral **C** allele. Dogs in many short-length muzzle (brachycephalic) breeds such as the English Bulldog, Pug, and Pekingese have two copies of the derived **A** allele. At least five different genes affect muzzle length in dogs, with BMP3 being the only one with a known causal mutation. For example, the skull shape of some breeds, including the dolichocephalic Scottish Terrier or the brachycephalic Japanese Chin, appear to be caused by other genes. Thus, dogs may have short or long muzzles due to other genetic factors that are not yet known to science.

Likely short muzzle (AA)

Tail Length (T)

Whereas most dogs have two **C** alleles and a long tail, dogs with one **G** allele are likely to have a bobtail, which is an unusually short or absent tail. This mutation causes natural bobtail in many breeds including the Pembroke Welsh Corgi, the Australian Shepherd, and the Brittany Spaniel. Dogs with **GG** genotypes have not been observed, suggesting that dogs with the **GG** genotype do not survive to birth. Please note that this mutation does not explain every natural bobtail! While certain lineages of Boston Terrier, English Bulldog, Rottweiler, Miniature Schnauzer, Cavalier King Charles Spaniel, and Parson Russell Terrier, and Dobermans are born with a natural bobtail, these breeds do not have this mutation. This suggests that other unknown genetic mutations can also lead to a natural bobtail.

Likely normal-length tail (CC)

Hind Dewclaws (LMBR1)

Common in certain breeds such as the Saint Bernard, hind dewclaws are extra, nonfunctional digits located midway between a dog's paw and hock. Dogs with at least one copy of the **T** allele have about a 50% chance of having hind dewclaws. Note that other (currently unknown to science) mutations can also cause hind dewclaws, so some **CC** or **TC** dogs will have hind dewclaws.

Unlikely to have hind dew claws (CC)

TRAITS: OTHER BODY FEATURES (CONTINUED)

TRAIT

RESULT

Blue Eye Color (ALX4) LINKAGE

Embark researchers discovered this large duplication associated with blue eyes in Arctic breeds like Siberian Husky as well as tri-colored (non-merle) Australian Shepherds. Dogs with at least one copy of the duplication (**Dup**) are more likely to have at least one blue eye. Some dogs with the duplication may have only one blue eye (complete heterochromia) or may not have blue eyes at all; nevertheless, they can still pass the duplication and the trait to their offspring. **NN** dogs do not carry this duplication, but may have blue eyes due to other factors, such as merle. Please note that this is a linkage test, so it may not be as predictive as direct tests of the mutation in some lines.

Less likely to have blue eyes (NN)

Back Muscling & Bulk, Large Breed (ACSL4)

The **T** allele is associated with heavy muscling along the back and trunk in characteristically "bulky" large-breed dogs including the Saint Bernard, Bernese Mountain Dog, Greater Swiss Mountain Dog, and Rottweiler. The "bulky" **T** allele is absent from leaner shaped large breed dogs like the Great Dane, Irish Wolfhound, and Scottish Deerhound, which are fixed for the ancestral **C** allele. Note that this mutation does not seem to affect muscling in small or even mid-sized dog breeds with notable back muscling, including the American Staffordshire Terrier, Boston Terrier, and the English Bulldog.

Likely normal muscling (CC)

TRAITS: PERFORMANCE

TRAIT

RESULT

Altitude Adaptation (EPAS1)

This mutation causes dogs to be especially tolerant of low oxygen environments (hypoxia), such as those found at high elevations. Dogs with at least one **A** allele are less susceptible to "altitude sickness." This mutation was originally identified in breeds from high altitude areas such as the Tibetan Mastiff.

Normal altitude tolerance (GG)

Appetite (POMC) LINKAGE

This mutation in the POMC gene is found primarily in Labrador and Flat Coated Retrievers. Compared to dogs with no copies of the mutation (**NN**), dogs with one (**ND**) or two (**DD**) copies of the mutation are more likely to have high food motivation, which can cause them to eat excessively, have higher body fat percentage, and be more prone to obesity. Read more about the genetics of POMC, and learn how you can contribute to research, in our blog post (<https://embarkvet.com/resources/blog/pomc-dogs/>). We measure this result using a linkage test.

Normal food motivation (NN)

TRAITS: BODY SIZE

TRAIT	RESULT
Body Size (IGF1) The I allele is associated with smaller body size.	Smaller (II)
Body Size (IGFR1) The A allele is associated with smaller body size.	Intermediate (GA)
Body Size (STC2) The A allele is associated with smaller body size.	Smaller (AA)
Body Size (GHR - E191K) The A allele is associated with smaller body size.	Larger (GG)
Body Size (GHR - P177L) The T allele is associated with smaller body size.	Larger (CC)

HEALTH REPORT

How to interpret Milo's genetic health results:

If Milo inherited any of the variants that we tested, they will be listed at the top of the Health Report section, along with a description of how to interpret this result. We also include all of the variants that we tested Milo for that we did not detect the risk variant for.

A genetic test is not a diagnosis

This genetic test does not diagnose a disease. Please talk to your vet about your dog's genetic results, or if you think that your pet may have a health condition or disease.



Milo is at increased risk for one genetic health condition.

Chondrodystrophy and Intervertebral Disc Disease, CDDY/IVDD, Type I IVDD



Breed-Relevant Genetic Conditions

6 variants not detected



Additional Genetic Conditions

212 variants not detected



CLINICAL TOOLS

These clinical genetic tools can inform clinical decisions and diagnoses. These tools do not predict increased risk for disease.

Alanine Aminotransferase Activity (GPT)

Milo's baseline ALT level is likely to be Normal

What is Alanine Aminotransferase Activity?

Alanine aminotransferase (ALT) is a clinical tool that can be used by veterinarians to better monitor liver health. This result is not associated with liver disease. ALT is one of several values veterinarians measure on routine blood work to evaluate the liver. It is a naturally occurring enzyme located in liver cells that helps break down protein. When the liver is damaged or inflamed, ALT is released into the bloodstream.

How vets diagnose this condition

Genetic testing is the only way to provide your veterinarian with this clinical tool.

How this condition is treated

Veterinarians may recommend blood work to establish a baseline ALT value for healthy dogs with one or two copies of this variant.

BREED-RELEVANT CONDITIONS TESTED



Milo did not have the variants that we tested for, that are relevant to his breed:

- ✓ Von Willebrand Disease Type I, Type I vWD (VWF)
- ✓ Progressive Retinal Atrophy, prcd (PRCD Exon 1)
- ✓ GM2 Gangliosidosis (HEXB, Poodle Variant)
- ✓ Degenerative Myelopathy, DM (SOD1A)
- ✓ Neonatal Encephalopathy with Seizures, NEWS (ATF2)
- ✓ Osteochondrodysplasia, Skeletal Dwarfism (SLC13A1, Poodle Variant)

HEALTH REPORT

Chondrodystrophy and Intervertebral Disc Disease, CDDY/IVDD, Type I IVDD (FGF4 retrogene - CFA12)

 Milo inherited one copy of the variant we tested

Milo is at increased risk for Type I IVDD

How to interpret this result

Milo has one copy of an FGF4 retrogene on chromosome 12. In some breeds such as Beagles, Cocker Spaniels, and Dachshunds (among others) this variant is found in nearly all dogs. While those breeds are known to have an elevated risk of IVDD, many dogs in those breeds never develop IVDD. For mixed breed dogs and purebreds of other breeds where this variant is not as common, risk for Type I IVDD is greater for individuals with this variant than for similar dogs.

What is Chondrodystrophy and Intervertebral Disc Disease, CDDY/IVDD, Type I IVDD?

Type I Intervertebral Disc Disease (IVDD) is a back/spine issue that refers to a health condition affecting the discs that act as cushions between vertebrae. With Type I IVDD, affected dogs can have a disc event where it ruptures or herniates towards the spinal cord. This pressure on the spinal cord causes neurologic signs which can range from a wobbly gait to impairment of movement. Chondrodystrophy (CDDY) refers to the relative proportion between a dog's legs and body, wherein the legs are shorter and the body longer. There are multiple different variants that can cause a markedly chondrodystrophic appearance as observed in Dachshunds and Corgis. However, this particular variant is the only one known to also increase the risk for IVDD.

When signs & symptoms develop in affected dogs

Signs of CDDY are recognized in puppies as it affects body shape. IVDD is usually first recognized in adult dogs, with breed specific differences in age of onset.

Signs & symptoms

Research indicates that dogs with one or two copies of this variant have a similar risk of developing IVDD. However, there are some breeds (e.g. Beagles and Cocker Spaniels, among others) where this variant has been passed down to nearly all dogs of the breed and most do not show overt clinical signs of the disorder. This suggests that there are other genetic and environmental factors (such as weight, mobility, and family history) that contribute to an individual dog's risk of developing clinical IVDD. Signs of IVDD include neck or back pain, a change in your dog's walking pattern (including dragging of the hind limbs), and paralysis. These signs can be mild to severe, and if your dog starts exhibiting these signs, you should schedule an appointment with your veterinarian for a diagnosis.

How vets diagnose this condition

For CDDY, dogs with one copy of this variant may have mild proportional differences in their leg length. Dogs with two copies of this variant will often have visually longer bodies and shorter legs. For IVDD, a neurological exam will be performed on any dog showing suspicious signs. Based on the result of this exam, radiographs to detect the presence of calcified discs or advanced imaging (MRI/CT) to detect a disc rupture may be recommended.

How this condition is treated

IVDD is treated differently based on the severity of the disease. Mild cases often respond to medical management which includes cage rest and pain management, while severe cases are often treated with surgical intervention. Both conservative and surgical treatment should be followed up with rehabilitation and physical therapy.

Registration:



ADDITIONAL CONDITIONS TESTED



Milo did not have the variants that we tested for, in the following conditions that the potential effect on dogs with Milo's breed may not yet be known.

- ✓ MDR1 Drug Sensitivity (ABCB1)
- ✓ P2Y12 Receptor Platelet Disorder (P2Y12)
- ✓ Factor IX Deficiency, Hemophilia B (F9 Exon 7, Terrier Variant)
- ✓ Factor IX Deficiency, Hemophilia B (F9 Exon 7, Rhodesian Ridgeback Variant)
- ✓ Factor VII Deficiency (F7 Exon 5)
- ✓ Factor VIII Deficiency, Hemophilia A (F8 Exon 10, Boxer Variant)
- ✓ Factor VIII Deficiency, Hemophilia A (F8 Exon 11, German Shepherd Variant 1)
- ✓ Factor VIII Deficiency, Hemophilia A (F8 Exon 1, German Shepherd Variant 2)
- ✓ Thrombopathia (RASGRP1 Exon 5, Basset Hound Variant)
- ✓ Thrombopathia (RASGRP1 Exon 8, Landseer Variant)
- ✓ Thrombopathia (RASGRP1 Exon 5, American Eskimo Dog Variant)
- ✓ Von Willebrand Disease Type III, Type III vWD (VWF Exon 4, Terrier Variant)
- ✓ Von Willebrand Disease Type III, Type III vWD (VWF Exon 7, Shetland Sheepdog Variant)
- ✓ Von Willebrand Disease Type II, Type II vWD (VWF, Pointer Variant)
- ✓ Canine Leukocyte Adhesion Deficiency Type I, CLAD I (ITGB2, Setter Variant)
- ✓ Canine Leukocyte Adhesion Deficiency Type III, CLAD III (FERMT3, German Shepherd Variant)
- ✓ Congenital Macrothrombocytopenia (TUBB1 Exon 1, Cairn and Norfolk Terrier Variant)
- ✓ Canine Elliptocytosis (SPTB Exon 30)
- ✓ Glanzmann's Thrombasthenia Type I (ITGA2B Exon 13, Great Pyrenees Variant)
- ✓ Glanzmann's Thrombasthenia Type I (ITGA2B Exon 12, Otterhound Variant)
- ✓ May-Hegglin Anomaly (MYH9)
- ✓ Prekallikrein Deficiency (KLKB1 Exon 8)
- ✓ Pyruvate Kinase Deficiency (PKLR Exon 5, Basenji Variant)

Registration: American Kennel Club



(AKC)