Canine Genetic Health Certificate™

Call Name:	Millie	**Laboratory #:**	375067
Registered Name:	Kidd You Knot What's One More	**Registration #:**	-
Breed:	Miniature American Shepherd	**Certificate Date:**	June 12, 2023
Sex:	Female		
DOB:	June 2022		

This canine's DNA showed the following genotype(s):

Disease	Gene	Genotype	Interpretation
Collie Eye Anomaly	*NHEJ1*	WT/WT	Normal (Clear)
Degenerative Myelopathy	*SOD1*	WT/WT	Normal (Clear)
Dermatomyositis	*PAN2*, *MAP3K7CL*, *DRB1*	Aabbcc	Unknown Risk
Hereditary Cataracts (Australian Shepherd Type)	*HSF4*	WT/WT	Normal (Clear)
Hyperuricosuria	*SLC2A9*	WT/WT	Normal (Clear)
Intestinal Cobalamin Malabsorption (Australian Shepherd Type)	*AMN*	WT/WT	Normal (Clear)
Intestinal Cobalamin Malabsorption (Border Collie Type)	*CUBN*	WT/WT	Normal (Clear)
Multidrug Resistance 1	*ABCB1*	WT/WT	Normal (Clear)
Multifocal Retinopathy 1	*BEST1*	WT/WT	Normal (Clear)
Progressive Retinal Atrophy, Progressive Rod-Cone Degeneration	*PRCD*	WT/WT	Normal (Clear)

WT, wild type (normal); M, mutant; Y, Y chromosome (male)

Blake C Ballif, PhD
Laboratory & Scientific Director

Christina J Ramirez, PhD, DVM, DACVP
Medical Director

Paw Print Genetics® performed the testing on the dog listed on this certificate. See the Laboratory Report for interpretation and recommendations based on these findings. The genes/diseases reported here were selected by the client. Normal results do not exclude inherited mutations not tested in these or other genes that may cause medical problems or may be passed on to offspring. The results included in this report relate only to the items tested using the sample provided. These tests were developed and their performance determined by Paw Print Genetics. This laboratory has established and verified the test(s)' accuracy and precision with >99.9% sensitivity and specificity. The presence of mosaicism may not be detected by this test. Non-paternity may lead to unexpected results. This is not a breed identification test. Because all tests performed are DNA-based, rare genomic variations may interfere with the performance of some tests producing false results. If you think these results are in error, please contact the laboratory immediately for further evaluation. In the event of a valid dispute of results claim, Paw Print Genetics will do its best to resolve such a claim to the customer's satisfaction. If no resolution is possible after investigation by Paw Print Genetics with the cooperation of the customer, the extent of the customer's sole remedy is a refund of the fee paid. In no event shall Paw Print Genetics be liable for indirect, consequential or incidental damages of any kind. Any claim must be asserted within 60 days of the report of the test results. Genetic counseling is available at Paw Print Genetics.

KIDD U KNOT WHATS ONE MORE

DN72435305

F BLUE MERLE MINIATURE AMERICAN SHEPHERD

Born Jun 20 2022

Sire: DN65132601
Dam: DN64117101

Registry	Test Date	Report Date	Age(m)	Conclusion	OFA Number
*EYES **	*Mar 25 2023*	*Apr 9 2024*	*9*	*NORMAL*	*MAS-EYE2226/9F-NOPI*

* Eye Certification is valid for one year from the date of the exam.

Animal Disease Diagnostic Laboratory

Purdue University, 406 S. University Street, West Lafayette, IN 47907-2065
Phone: (765)494-7440 Fax (765)494-9181 Email: addl@purdue.edu
Web: http://www.addl.purdue.edu

ADDL Case #: A24-18221 **Other ID:** **Date Received:** 3/18/2024

Submitter	Premises	Owner
PURDUE CANINE GENETICS LAB 625 HARRISON STREET WEST LAFAYETTE, IN 47907	DOG INFO CH KIDD U KNOT WHATS ONE MORE FDC 06/20/2022 DN72435305 / AKC	MARLO WIN TINA WINSTON PO BOX 187 PHILPOT, KY 42366

Vet Phone:
Vet Fax:
Premise ID: DOG INFO
Tests Requested in: CanineG

Species: Canine
Breed: Miniature American Shepherd

Sex: Female
Age: 1.5 Years

Test	Ordered	Status	Completed
Neuroaxonal Dystrophy	3/18/2024	Complete	3/19/2024
Non-HSF4 Hereditary Cataracts	3/18/2024	Complete	3/19/2024

Owner Report

3/28/2024 9:30:37 AM

Canine Genetics by Dr. Rebecca Wilkes, Section Head

The following tests were performed using **PCR**.

Animal ID	Specimen	Organism	Result
MILLIE	Cheek Swab	Neuroaxonal Dystrophy	Clear (N/N)
		Non-HSF4 Hereditary Cataracts	Clear (N/N)

Coat Color and Trait Certificate

Call Name:	Millie	**Laboratory #:**	375067
Registered Name:	Kidd You Knot What's One More	**Registration #:**	-
Breed:	Miniature American Shepherd	**Certificate Date:**	Dec. 27, 2022
Sex:	Female		
DOB:	June 2022		

This canine's DNA showed the following genotype(s):

Coat Color/Trait Test	Gene	Genotype	Interpretation
M Locus (Merle)	*PMEL*	m/M274	*See detailed interpretation

Interpretation:

M Locus Genotype: m/M^{274}

This dog carries one copy of the **m** (non-merle, wild-type) allele and one copy of the **M** (merle insertion variant) allele of the *PMEL* gene. This dog will pass on one copy of the **m** (non-merle, wild-type) allele to 50% of its offspring and one copy of the **M** (merle insertion variant) allele to 50% of its offspring. The approximate size of the M allele of this dog (+/- 1 base pair) is listed in superscript in the genotype. Merle is inherited in a dominant fashion, meaning that only one copy of an M allele is necessary for a dog to display some variation of the merle coat color/pattern, which is marked by random dilution of eumelanin (black pigment) leaving patches of normal coat color within areas of diluted pigmentation.

Specific sizes of the M allele have been associated with the potential to produce “classic” merle patterning or other M-associated coat color variations. Merle is most appropriately viewed as a spectrum of coat colors/patterns and the size of the variant M allele is associated with a coat color/pattern somewhere within that spectrum. Although some coat color/pattern variations have been associated with specific sizes of the M allele in certain breeds, referred to here as a ‘bin’, the size of the M allele does not guarantee a specific outcome. In general, dogs with M allele sizes between 200 – 246 base pairs (bp) have been associated with non-merle or minimal-merle coat colors/patterns and are often referred to as “cryptic” merle; M allele sizes between 247 – 264 bp have been associated with “atypical” or “diluted” coat colors/patterns; M allele sizes between 265 – 269 bp have been associated with the “classic” merle coat colors/patterns; and M allele sizes between 270 – 280 bp have been associated with a “tweed”, “harlequin” or “patchwork” merle coat colors/patterns. Many exceptions to the coat color/pattern associations found in the various M allele bin sizes listed here have been identified. Therefore, care should be taken when correlating M allele sizes with anticipated coat color/pattern outcomes. These bin sizes should not be interpreted as having discrete boundaries but should be viewed as a range within which specific coat colors and patterns are likely. Variations in genetic background between breeds and in individual dogs within a breed may result in the identification of different coat colors/patterns not typically found in a given bin, especially when the size of an M allele is at the border between bins. Furthermore, due to the complex nature of the merle insertion variant and the limitations of currently available molecular technologies, precise sizing of the merle insertion variant is challenging. However, the sizing of the merle insertion variant in our laboratory has been validated to be accurate to within +/- 1 bp which, nevertheless, makes correlations between genotype and coat color/pattern of dogs close to the boundaries of a specific bin potentially problematic. In addition, the M allele bins defined here are only relevant to test results generated by Paw Print Genetics. The variable nature of the M gene variant and subtle differences in methodologies used by each laboratory precludes strict interlaboratory genotype comparisons. Therefore, in some cases, it may be prudent to test related dogs in a single laboratory if comparisons across related dogs or dogs within a breed are desired.

The inherent instability of the M insertion variant makes it susceptible to further mutation events that can result in “mosaicism” whereby more than one version (allele) of the M insertion variant of a potentially different size is found in various cells throughout a dog’s body. Indeed, mosaicism is likely what gives a merle dog its variable coat color/pattern with some cells having a copy of one M variant allele that results in altered pigmentation while other cells may have a different sized insertion resulting in an alternate form of the M variant allele that may express the coat color or pattern differently. It has also been documented that, due to the inherent instability of the M insertion variant, changes to the M insertion variant size can occur during the replication of each M allele, which may result in subtle changes in M allele size from cell to cell (mosaicism) and even from one generation to the next if present in egg or sperm cells (germ cells or gonads). However, current evidence suggests that lengthening of the M insertion variant is less likely to occur than shortening, although either event is theoretically possible. Thus, this “mosaicism” may result in different alleles of the M insertion variant being present in different cell lines or tissue types in the same dog. Importantly, if the mosaicism occurs in the germ cells (sperm or eggs) of a dog, the different alleles of the M insertion variant may be passed on to offspring. Furthermore, this mosaicism may be found in only a small percentage of cells and may not be present in the cells from which a given sample is obtained from a dog for genetic testing, making it difficult to always reliably detect mosaicism. Thus, all levels of mosaicism may not be detected by this test. If identified, mosaic M alleles at ~5% or greater of the total M alleles detected will be reported in the final genotype with the approximate percentage of each M allele identified in brackets.

Dogs that are identified as having a mosaic genotype may pass on each of their mosaic M alleles if they are also present in the germ cells of the dog. Germline mosaicism can only be confirmed by testing samples obtained from sperm or eggs. Dogs that inherit two copies of the M insertion variant are at an increased risk of being mostly white with hearing and/or vision deficits. To avoid producing “double merle” (M/M) puppies, dogs with a copy of M (particularly those with M alleles near the size which is likely to produce the classic merle coat color/pattern) should only be bred to dogs that do not have a copy of the M allele. Dogs related to this dog have an increased chance of carrying an M allele. Testing for the M allele is indicated for related dogs.

Paw Print Genetics® has genetic counseling available to you at no additional charge to answer any questions about these test results, their implications and potential outcomes in breeding this dog.

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