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LABOR FÜR KLINISCHE DIAGNOSTIK GMBH & CO. KG

LABOKLIN GmbH&CoKG . Postfach 1810 .DE-97688 Bad Kissingen

Mrs.
Hanna Bolhuis
Meenteweg 13
7971 RZ Havelte
Niederlande

Report
No.: 2011-W-83353
Date of arrival: 13-11-2020
Testing started: 13-11-2020
Date of report: 21-12-2020
Testing completed:

Patient identification:	Dog Male	* 30.10.2019
	Miniature Australian Shepherd	
Owner / Animal-ID:	Bolhuis, Hanna	
Type of sample:	EDTA-Blood	
Date sample was taken:	06-11-2020	

Name:	**midwest Nebraska's red willow**
ZB-Nummer:	---
Chip-Nummer:	**990000003627203**
Tattoo-Nummer:	---

Degenerative Myelopathy - PCR

Result: Genotype N/N (exon 2)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the high-risk factor for DM in exon 2 of the SOD1-gene.

Trait of inheritance: autosomal-recessive

Please note: In the Bernese Mountain Dog breed the mutation in exon 1 of the SOD1-gene also occurs in correlation with DM.

Brachyury - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for brachyury.

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Trait of inheritance: autosomal-dominant

Neuronal Ceroid Lipofuszinosis (NCL) -PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for NCL in the CLN6-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Shepherd
Please note: nomenclature of this variant was changed from CLN8 to CLN6 at 25/04/19

Neuronale Ceroid Lipofuszinose (NCL) adult onset - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for NCL in the CLN8-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds:
Australian Shepherd

*MDR1 genetic test - PCR

Result: Genotype N/N (+/+)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for MDR in the ABCB1-gene.
Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Shepherd, Border Collie, Elo, German Shepherd, Longhaired Whippet, McNab, Old English Sheepdog, Rough/Smooth Collie, Shetland Sheepdog, Silken Windhound, Wäller, White Shepherd

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Please note: in individual cases, heterozygous dogs can show clinical signs!

The DNA-test is run according to the publication of Mealey et al. (2001) "Ivermectin sensitivity in collies is associated with a deletion mutation of the mdr1 gene." and detects the mutation MDR1 nt230 (del4).

MDR1 genetic test carried out according to DIN EN ISO/IEC 17025 in our partnerlaboratory. Liability for specification of samples (e.g. name, identity of animal) lies by the sender.

*prcd-PRA (partner lab) - PCR

Result: Genotype N/N (A)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for prcd-PRA in the PRCD-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian cattle dog, American Cocker Spaniel, American Eskimo Dog, Australian Shepherd, Australian Stumpy Tail Cattle Dog, Barbet, Bearded Collie, Bolognese, Bolonka Zwetna, Chesapeake Bay Retriever, Chihuahua, Chinese Crested, English Cocker Spaniel, English Shepherd, Entlebucher Mountain Dog, Finnish Lapphund, German Spitz, Giant Schnauzer, Golden Retriever, Jack Russell Terrier, Karelian Beardog, Kuvasz, Lagotto Romagnolo, Lapponian Herder, Labrador Retriever, Markiesje, Norwegian Elkhound, Nova Scotia Duck Tolling Retriever, Parson Russell Terrier, Portugese Water Dog, Poodle, Schipperke, Swedish Lapphound, Silky Terrier, Spanish Water Dog, Swedish Lapphund, Wäller, Yorkshire Terrier.

*Collie Eye Anomaly (CEA) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for

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CEA in the NHEJ1-gene.
Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Kelpie and Shepherd, Bearded Collie, Border Collie, Boykin Spaniel, Hokkaido, Lancashire Heeler, Longhaired Wippet, Nova Scotia Duck Tolling Retriever, Rough/Smooth Collie, Shetland Sheepdogs, Silken Windhound

Hereditary Cataract - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype–allele. It does not carry the risk factor for hereditary cataract in the HSF4–gene.

Trait of inheritance: unknown

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Shepherd, Wäller

M-locus* (alleles: Mh, M, Ma+, Ma, Mc+, Mc, m and mosaics) - PCR

Result: Genotype m/m

Interpretation: The examined animal is homozygous for the m-allele for non-merle.

The test detects the alleles Mh (harlequin merle), M (merle), Ma+ and Ma (atypic merle), Mc+ and Mc (cryptic merle) and m (non-merle).

Allelic series: Mh, M, Ma+, Ma, Mc+, Mc > m

Premium SNP DNA-profile (ISAG 2020)

001_012:	AG_AA_AG_AA_AG_AG_AG_AG_AG_CC_AA_AG
013-024:	GG_AG_GG_AG_AG_AG_AG_AG_GG_GG_AA_AG
025-036:	AG_.._AG_AA_AA_AA_GG_GG_GG_AG_AA_AG
037-048:	AG_AA_CC_AA_AG_AG_AG_GG_AA_AC_AG_AA
049-060:	GG_AC_AA_AA_AG_AA_AA_AA_AG_AG_AG_AC
061-072:	AC_CC_GG_AG_AA_AG_GG_AA_AG_AG_AC_AA

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073-084:	GG CC AA GG CC AG AA GG AA AG GG AA
085-096:	AG AG GG GG AA AA CC GG AA AG AA AA
097-108:	GG AA AG GG GG AC AA AC GG AA AG AG
109-120:	AG GG AC AG AG AG GG AG GG AA AG AG
121-132:	AA AG AG AA AG AG AG GG AA AG AG AG
133-144:	GG AG AA AG GG GG AA AG GG GG AA AG
145-156:	AA AG GG GG AG AG GG CC AG GG AG AA
157-168:	AA AG GG AC AA GG CC AG AA AA AA GG
169-180:	AG AG AC AG AG AG AA GG AG AA AA AA
181-192:	GG GG GG GG AC AG AG AA AG AG AG AG
193-204:	AG GG GG GG AA AA AG AG AA AG AG AA
205-216:	AG GG GG AA AG AC AG AA AA AA AG GG
217-228:	GG AA AA AA GG CC GG GG GG AG CC AA
229-230:	AA AC
sex:	X/Y

Informationen zum Premium SNP DNA-Profil

Das Premium SNP DNA-Profil ist der genetische Fingerabdruck Ihres Tiere und erlaubt seine eindeutige Identifizierung. Es bleibt das ganze Leben lang gleich und kann nicht manipuliert werden. Jedes bei uns erstellte DNA-Profil wird in unserer DNA-Datenbank gespeichert und steht Ihnen so dauerhaft zur Verfuegung. Das DNA-Profil beinhaltet keine Informationen zu Merkmalen oder zu Krankheiten Ihres Tieres.
Das Premium SNP DNA-Profil begutachtet alle von der ISAG empfohlenen SN aus dem Kernpanel (1) und dem Zusatzpanel (2) (nummeriert von 001-230). Die folgende Tabelle zeigt die entsprechende international geltende ISAG Nomenklatur (Cfam_Chromosom:Position) der untersuchten SNPs.

Information on the Premium SNP DNA Profile

The Premium SNP DNA Profile is your animal's genetic fingerprint and uinquely identifies it. It remains the same throughout the animal's life and cannot be manipulated.
Every one of the DNA profiles created in our laboratory is saved in our DNA database and is available to you permanently.
The DNA profile does not contain any information on traits or diseases of your pet. The Premium SNP DNA Profile evaluates all of the SNPs recommended by the ISAG from (1) the core panel and (2) the auxiliary panel (numbers 001-230).
The following table lists the corresponding internationally valid ISAG nomenclature (Cfa_Chromosom:Position) of the examined SNPs.

Sampling:

Steubenstraße 4 • 97688 Bad Kissingen • Tel.: 09 71/ 7 20 20 • Fax: 09 71/ 6 85 46 • Geschäftsführender Gesellschafter: LABOKLIN Verwaltungs-GmbH • RG. Schweinfurt HRA 3631
Bankverbindung: Sparkasse Bad Kissingen (BLZ 793 510 10) Kto.-Nr. 311 596 19, IBAN: DE09 793 510 1000 311 596 19, SWIFT/BIC: BYLADEM1KIS
BCEE Luxembourg Kto.-Nr.1507/3600-5, IBAN: LU95 0019 1507 3600 5000, SWIFT/BIC: BCEELULL
e-Mail: info@laboklin.com • USt.ID DE206897824

sample ID: 2011-W-83353

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The following impartial person (veterinarian, breed warden, or similar) signed the form for the sampling and identity check of the animal:

S.M. Coenraats

The current result is only valid for the sample submitted to our laboratory. The sender is responsible for the correct information regarding the sample material.The laboratory can not be made liable. Furthermore, any obligation for compensation is limited to the value of the tests performed.

There is a possibility that other mutations may have caused the disease/phenotype. The analysis was performed according to the latest knowledge and technology.

The laboratory is accredited for the performed tests according to DIN EN ISO/IEC 17025:2018. (except partner lab tests).

These results are based on the sample material submitted to our laboratory.

This was suitable if not stated otherwise. The submitter is responsible for the accuracy of the information regarding the sample. This report can only be transmitted in toto and unchanged. Doing otherwise requires written permission from Laboklin GmbH & Co. KG.

*** END of report ***

i.A. Fr. Dipl.-Ing. Christina Dangel
Abt. Molekularbiologie

*: test performed by partnerlaboratory