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Report

No.: 2208-N-09312
Date of arrival: 03-08-2022
Date of report: 25-08-2022

Patient identification:	Dog	male	* 14.10.21
	Australian Labradoodle		
Owner / Animal-ID:	Bakker, Patty		
Type of sample:	Swab		
Date sample was taken:			

Name: **Mischa's Doodles Bakker Billy**
Stud book no.: ---
Chip no.: **528257000162871**
Tattoo no.: ---

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.

Exercise Induced Collapse (EIC) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for EIC in the DNMT1-gene.

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Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Boykin Spaniel, Cheseapeake Bay Retriever, Clumber Spaniel, Curly Coated Retriever, Labrador Retriever, Old English Sheepdog, Pembroke Welsh Corgi and Wirehaired Pointer

Hereditary nasal parakeratosis (HNPK) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for HNPK in the SUV39H2-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Labrador Retriever

Dwarfism (Skeletal Dysplasia 2) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for SD2 in the COL11A2-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Labrador Retriever

Neonatal Encephalopathy - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for NEWS in the ATF2-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and

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symptoms of the disease in the following breeds: Standard Poodle

vWD Type I

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for vWD Type I in the vWF-gene.

Trait of inheritance: autosomal-dominant with variable penetrance

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Bernese Mountain Dog, Coton de Tulear, Doberman, Drentse Patrijshond, German Pinscher, Kerry Blue Terrier, Kromfohrlander, Manchester Terrier, Papillion, Pembroke Welsh Corgi, Poodle and Stabyhoun

Hereditary myopathy (CNM) - PCR

Result: Genotype N/N

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

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Labrador Retriever
Other forms of myopathy cannot be excluded by this test.

***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

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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 Lapphund, Silky Terrier, Spanish Water Dog, Swedish Lapphund, Wäller, Yorkshire Terrier.

Progressive Retinal Atrophy (rcd4 PRA) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for rcd4-PRA in the C2orf71-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, English Setter, Gordon Setter, Irish Setter, Irish Red&White Setter, Old Danish Pointing Dog, Polish Lowland Sheepdog, Polish Tatra Sheepdog, Poodle, Small Munsterlander, Tibetan Terrier

Notice: It is assumed that other, until now unknown, mutations exist as app. 10% of ill Irish and Gordon Setters and 80% of ill Tibet Terriers do not carry this mutation.

B-locus (brown, chocolate, liver(nose))

This genetic analysis of the B-locus includes the three variants bd, bc and bs described for all breeds so far, as well as the corresponding wildtypes as allele N.

Variant bd

Result for bd: Genotype N/bd (before B/bd)

Interpretation: One bd-allele was found for this sample. The animal is heterozygous for this variant.

Variant bc

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Result for bc: Genotype bc/bc

Interpretation: The animal is homozygous for the bc-allele.

Variant bs

Result for bs: Genotype N/N (before B/B)

Interpretation: No bs-allele was found for this sample.

When one of the variants is found homozygous, dark pigment (eumelanin) changes in colour accordingly. When several variants of the B-locus are found in heterozygous state, it is not possible to directly determine the influence on the eumelanin.

The overall genotype for the B-locus-complex can only be deduced if all known variants on the B-locus (bd, bc, bs, b4 and be) are analysed. Some of these alleles only exist in specific breeds.

Please note: The nomenclature of the results has been changed due to harmonizing efforts for genetic tests.

D-locus D1 (dilution)

Result for d1: Genotype N/N (before D/D)

Interpretation: No d1-allele was found for this sample.

The overall genotype for the D-locus-complex can only be deduced if all known variants on the D-locus (d1, d2 and d3) are analysed. Some of these alleles only exist in specific breeds.

Please note: The nomenclature of the results has been changed due to harmonizing efforts for genetic tests.

E-locus e1 (apricot, cream, lemon, red, yellow) - PCR

Result for e1: Genotype N/e1 (before E/e)

Interpretation: One e1-allele was found for this sample.
The animal is heterozygous for this variant.

The overall genotype for the E-locus-complex can only be deduced if all known variants on the E-locus (e1, e2, e3, eA, eg, eh and EM)

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are analysed. Some of these alleles only exist in specific breeds.

Please note: The nomenclature of the results has been changed due to harmonizing efforts for genetic tests.

I locus (pheomelanin intensity) - PCR

Result: Genotype I/I

Interpretation: The examined animal is homozygous for the I-allele.

The test detects the alleles I and i.
Allelic series: I dominant over i

Genetic analysis K-Lokus (PCR)

Result: Genotype Kb/ky

Interpretation: The examined animal is heterozygous for the Kb- and ky-allele.

The test detects the alleles Kb and ky.
Allelic series: Kb dominant over ky

Genetic analyses A-Lokus Agouti (PCR)

Result: Genotype at/at

Interpretation: The examined animal is homozygous for the at-allele.

The test detects the alleles Ay, Aw, at and a.
Allelic series: Ay dominant over Aw, Aw dominant over at, at dominant over a

S-Locus

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the N-allele.

The test detects the alleles N and S.
The color is inherited in a semidominant trait.

Please note: there are more genetic variants leading to Piebald which are not tested at the moment.

K locus (brindle)

Please note: LABOKLIN offers no longer shipment of samples for the brindle gene test. There is the possibility to test for the K locus at LABOKLIN, but this test only for the alleles KB and ky. From this result, no statement about the presence or absence of kbr (brindle) allele can be made.

Curly1 - PCR:

Result: Genotype NC/C1

Interpretation: The examined animal is heterozygous for the NC- and C1-allele.

The test detects the alleles NC (non-curly) and C1 (curly).

Curly2 - PCR:

Result: Genotype NC/NC

Interpretation: The examined animal is homozygous for the NC-allele.

The test detects the alleles NC (non-curly) and C2 (curly).

Improper Coat - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the N-allele.

The test detects the alleles N and IC (improper coat).

Allelic series: N dominant over IC

Classic STR DNA-Profile (ISAG 2006) - PCR

breeder association: **WALA**
name: **Mischa's Doodles Bakker Billy**
stud book no.: ---
tattoo no.: ---
chip no.: **528257000162871**

ZB-Nr.: ---
Tattoo-Nummer: ---
Chip-Nr.: **528257000162871**
Amelogenin: **Y/X**

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AHT 121:	98/108
AHT 137:	137/143
AHTH 130:	119/121
AHTH 171:	219/221
AHTH 260:	244/246
AHTK 211:	91/91
AHTK 253:	290/292
CXX 279:	118/124
FH 2054:	148/168
FH 2848:	238/240
INRA 21:	97/101
INU 005:	126/126
INU 030:	150/150
INU 055:	214/214
REN 105 L 03:	231/233
REN 162 C 04:	202/206
REN 169 D 01:	202/216
REN 169 O 18:	162/168
REN 247 M 23:	266/278
REN 54 P 11:	226/226
REN 64 E 19:	145/155

Nomenclature is based on ISAG comparison test 2006 standards.

The results are only for the sample material submitted to the laboratory. Responsibility for the accuracy of the information on the sample provided lies with the submitter. No warranty obligation for that information is provided. Damage claim liabilities, if legally permissible, are limited to the invoice value of the testing done. We are also only liable for intentional and gross negligence, if legally possible. Additional genetic modifications which might also influence the development of the disease/trait, cannot be ruled out. Testing was carried out according to current general scientific knowledge.

The laboratory is accredited for the tests listed in this report according to DIN EN ISO 17025:2018.

In the requested DNA profile an issued Certificate is included (not for breed classifications) if the sample has been collected by a veterinarian. Please thoroughly verify the animal and owner data provided to you. Any corrections afterward can only be carried out in accordance with prior written confirmation from the veterinarian. Please note that an extra charge will be invoiced separately upon changes to an already issued certificate.

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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).

*** END of report ***

Drs J. Vis

*: test performed by partnerlaboratory