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LABOKLIN
LABORATORIUM VOOR KLINISCHE DIAGNOSTIEK N.V.

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Mevr.
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Nederland

Report
No.: 2306-N-06364
Date of arrival: 07-06-2023
Date of report: 19-06-2023

Patient identification:	Dog	female	* 21.03.22
	Australian Labradoodle		
Owner / Animal-ID:	Bakker, P.		
Type of sample:	Swabs		
Date sample was taken:			

Name: **Australianlabradoodle brabant bakker lilly**
Stud book no.: ---
Chip no.: **528246003142850**
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 DNM1-gene.

Trait of inheritance: autosomal-recessive

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

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

lock
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, Irish Setter, Terrier, KromfohrlΣnder, Manchester Terrier, Papillion, Pembroke Welsh Co

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 - 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.

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

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

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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/Kb

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

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

A-locus (agouti) ASIP analysis û PCR

ASIP haplotype analysis

ASIP haplotype: Genotype BB1/BB1

Interpretation: The genotype BB1/BB1 has been found for the submitted samples ASIP haplotypes. The corresponding dog is homozygous for the BB1 allele for black back 1.

a variant genetic analysis

Result for the a allele: Genotype N/N

Interpretation: The results for the submitted sample show the genotype N/N for the a allele. The corresponding dog is homozygous for the wildtype allele and not carry an a variant for recessive unicolour in the pigmented areas of the fur. The ASIP haplotypes determine the phenotype.

VP variants genetic analysis

Result for the VP alleles: Genotype VP2/VP2

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HCP variants genetic analysis

Result for the HCP alleles: Genotype HCP3/HCP3

The genotypes for the variants VP and HCP logically determine two ASIP haplotypes (DY, SY, AG, BS, BB1-3) each. Together with the knockout variant a the final genotypes of the A-locus can be calculated.
The allelic row of the ASIP haplotypes can be found in the table attached or with the following link: www.labogen.com/en/asip

S-Locus

Result: Genotype S/S

Interpretation: The examined animal is homozygous for the S-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.

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

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breeder association:	---
name:	**Australianlabradoodle brabant bakker lilly**
stud book no.:	---
tattoo no.:	---
chip no.:	**528246003142850**

ZB-Nr.:	---
Tattoo-Nummer:	---
Chip-Nr.:	**528246003142850**
Amelogenin:	**X/X**
AHT 121:	**100/108**
AHT 137:	**141/147**
AHTH 130:	**121/127**
AHTH 171:	**219/219**
AHTH 260:	**244/248**
AHTK 211:	**87/87**
AHTK 253:	**288/288**
CXX 279:	**116/124**
FH 2054:	**156/168**
FH 2848:	**240/240**
INRA 21:	**91/95**
INU 005:	**110/124**
INU 030:	**144/150**
INU 055:	**210/214**
REN 105 L 03:	**233/241**
REN 162 C 04:	**208/208**
REN 169 D 01:	**216/218**
REN 169 O 18:	**168/170**
REN 247 M 23:	**268/268**
REN 54 P 11:	**226/232**
REN 64 E 19:	**-/-**

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.

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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.

Sampling:

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

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 ***

Robin Maes, DVM MSc

*: test performed by partnerlaboratory