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Mr. & Mrs.
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Report No.:	**2304-W-74602**
Date of arrival:	18.04.2023
Date of report:	09.05.2023
Testing started:	18.04.2023
Testing completed:	25.04.2023
Status of the report:	Final report

Species:	Dog
Breed:	Labrador Retriever
Gender:	Male
Name:	Labrander Hodja
Stud book No.:	DK05927/2020
Chip No.:	208250000140031
Date of birth / Age:	31.03.2020
Type of sample:	EDTA-Blood
Sampler:	Pia Bjerre Pedersen
Owner / Animal-ID:	Brander, Arne
IT No. / Report-ID:	---

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

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Hereditary nasal parakeratosis (HNPK) - PCR

Result: Genotype N/HNPK

Interpretation: The examined animal is heterozygous for 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

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.

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Retinal dysplasia (OSD) - PCR *

Result: Genotype N/N

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

Trait of inheritance: autosomal-dominant

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

STGD-PRA (Stargardt disease) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype allele. It does not carry the causative mutation for STGD in the ABCA4 gene.

Trait of inheritance: autosomal recessive

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

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/N (before B/B)

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

Variant bc

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

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

Variant bs

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

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

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.

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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.

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

Genetic analyses A-Lokus Agouti (PCR)

Result: Genotype at/a

Interpretation: The examined animal is heterozygous for the at- and a-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.

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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.

Coat length I (long or short hair) - PCR

Parameter	Value
HIHd1 SNP G284T:	**L/L**

Interpretation:
The test detects the alleles L (shorthair) and I (longhair) in the FGF5 gene.

Allelic series: L dominant over I
solely genotype L/L: The analysed sample is homozygous for the L-allele for short-haired.

exactly one genotype L/I: The analysed sample is heterozygous for the L-allele and the I-allele. The I-allele for long-haired is forwarded to 50% of the dogs offspring.

multiple Genotypes L/I: The analysed sample is heterozygous for the L-allele and the I-allele on more than one gene-locus. The dog inherits the I-allele for long-haired to it's offspring.

at least one genotype I/I: The analysed sample is homozygous for the I-allele for long-haired.

Please note:
Further causative mutations for longhaired have been found in the
following breeds:
Afghan Hound, Akita Inu, Alaskan Malamute, Chow Chow, Eurasian, French Bulldog, Husky, Prague Rattler, Shar Pei, Samoyed The additional mutations might be responsible for longhair in further breeds.

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).

Breeding club discounts were granted for discountable services!

Sampling:

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

Pia Bjerre Pedersen

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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.

LABOKLIN is an officially accredited laboratory according to DIN EN ISO/IEC 17025:2018, DAkkS No. D-PL-13186-01-01 and D-PL-13186-1-02. The accreditation applies to all test procedures listed in the accreditation certificate.

*: test performed by partner laboratory

Fr.Dipl.-Biol. Bärbel Gunreben
Abt. Molekularbiologie

***** END of report *****

Laboklin App

***** News from the laboratory *****

PCR detection of Devriesea agamarum in lizards is now available (test ID 8826). This gram-positive bacterium can cause dermatitis, cheilitis and septicaemia in lizards.