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Report
No.: 1908-W-74770
Date of arrival: 27-08-2019
Testing started: 27-08-2019
Date of report: 20-09-2019
Testing completed: 03-09-2019

Patient identification:	Dog Female Labrador Retriever	* 28.06.18
Owner / Animal-ID:	Brander, Arne	
Type of sample:	EDTA-Blood	
Date sample was taken:	21-08-2019	

Name: **Emshope New Girl In Town**
ZB-Nummer: **DK13451/2018**
Chip-Nummer: **208250000124809**
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.

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

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 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.

*__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

__D-locus D1 (dilution)__

Result: Genotype D/D

Interpretation: The examined animal does not possess the d1 allele. If no other d variant is present, the examined animal is homozygous for the D-allele.

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The test detects the alleles D and d1
Allelic series: D dominant over d1

Please note: Additional d variants have to be considered
to fully evaluate the characteristic of dilution.

Please note:

A further causative mutation for dilution (d2) has been found in the foll
Chow Chow, Sloughi, Thai Ridgeback
The additional mutation might be responsible for dilution in further bree

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

Result: genotype E/e

Interpretation: The dog is heterozygous for the allele E/e at
the E-Locus. That means the coat is not depending on the breed
yellow, lemon, red, cream or apricot in the pigmented areas.
The dog will pass the recessive e-allele onto its offspring
with a probability of 50%.
The currently known mutation has been analysed.

The test is only valid for the submitted sample.

Please note:
A further causative variant in the E lokus (named e2) has been
found in the breed Australian Cattle Dog.
The additional mutation might be responsible for yellow coat colour
in further breeds.

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

The genetic analysis of the B-locus includes the four
recessive, causative variants described so far as the alleles
bd, bc, bs, and b4 as well as the dominant form as allele B.

Variant bd

Result for bd: Genotype B/B
Interpretation: No bd-allele was found for this sample.

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Variant bc
Result for bc: Genotype B/B
Interpretation: No bc–allele was found for this sample.

Variant bs
Result for bs: Genotype B/B
Interpretation: No bs–allele was found for this sample.

Variant b4
Result for b4: Genotype B/B
Interpretation: No b4–allele was found for this sample.

Allelic series: B dominant over bd, bc, bs and b4

If the animal is homozygous for the causative variant, black pigment (eumelanin) is lightened, and the animal appears brown in the areas that were originally black.
If the animal is heterozygous for several causative variants, it is not possible to determine to what degree these will influence the eumelanin. Dark areas may be black or brown.

Presumably, more genetic variants causing brown fur in French Bulldogs, Yorkshire Terriers and similar small breeds exist.
Those variants cannot be analysed by any genetic test yet.

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

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.

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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

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.

Coat length I (long or short hair) - PCR

HlHd1 SNP G284T: **L/L**

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

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

exactly one genotype L/l: The analysed sample is heterozygous for

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the L-allele and the l-allele. The l-allele for long-haired is forwarded to 50% of the dogs offspring.

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

at least one genotype l/l: The analysed sample is homozygous for the l-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, Samoyed
The additional mutations might be responsible for longhair in further breeds.

Sampling:

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

Dyrlaege Nina Haahr

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 17025:2005. (except partner lab tests).

*** END of report ***

Hr.Dr. Beitzinger
Dipl.-Biol. Molekularbiologie

*: test performed by partnerlaboratory