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LABORATORIUM VOOR KLINISCHE DIAGNOSTIEK N.V.

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Dierenartsenpraktijk
De Meemortel
Meemortel 54
6021 AG Budel
Nederland

Report
No.: 2110-N-15096
Date of arrival: 28-10-2021
Date of report: 03-11-2021

Patient identification:	Dog Duitse Herder	female	* 31.08.20
Owner / Animal-ID:	Stuer, Gerard		
Type of sample:	EDTA		
Date sample was taken:			

Name:	**Tuna van Esblokhof**
Stud book no.:	**LOSH 01320205**
Chip no.:	**967000010307266**
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.

Hyperuricosuria - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for HUU in the SLC2A9-gene.

Trait of inheritance: autosomal-recessive

Coat length I (long or short hair) - PCR

HlHd1 SNP G284T: **L/L**

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.

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 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.

Pituitary Dwarfism - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for Dwarfism in the LHX3-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: German Shepherd, Saarlooswolfdog, Czechoslovakian Wolfdog, Tibetan Terrier, White Swiss Shepherd Dog

*__MDR1 genetic test - PCR__

pending

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.

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).

courier costs

*** END of report ***

Drs. M. Bolumburu

*: test performed by partnerlaboratory