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HV Atlántico
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Report No.:	2209-M-19659
Date of arrival:	28.09.2022
Date of report:	24.10.2022
Testing started:	28.09.2022
Testing completed:	24.10.2022
Status of the report:	Final report

Species:	Dog
Breed:	Pastor alemán
Gender:	Male
Name:	S'Nerzuhl La Légende du Loup Noir
Chip No.:	250268743846041
Date of birth / Age:	19.05.2021
Type of sample:	EB (x2)
Owner / Animal-ID:	Quinta Silfrohn
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.

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

HIHd1 SNP G284T: **1/1**

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.

MDR1 gene variant - PCR

Result: Genotype N/N (+/+)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for MDR in the ABCB1-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Shepherd, Border Collie, Elo, German Shepherd, Longhaired Whippet, McNab, Old English Sheepdog, Rough/Smooth Collie, Shetland Sheepdog, Silken Windhound, Wäller, White Shepherd

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).

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

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).

Classic STR DNA-Profile (ISAG 2006) - PCR

Amelogenin:	Y/X
AHT 121:	102/102
AHT 137:	131/137
AHTH 130:	-/-
AHTH 171:	223/223
AHTH 260:	238/248
AHTK 211:	87/89
AHTK 253:	288/288
CXX 279:	116/126
FH 2054:	152/176
FH 2848:	240/240
INRA 21:	99/99
INU 005:	124/126
INU 030:	146/146
INU 055:	218/218
REN 105 L 03:	227/227
REN 162 C 04:	204/206
REN 169 D 01:	212/216
REN 169 O 18:	162/168
REN 247 M 23:	270/270
REN 54 P 11:	226/226
REN 64 E 19:	143/155

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.

**La probabilidad de que el animal analizado pertenezca a la raza pastor alemán es del 82%.
La probabilidad de que el animal analizado pertenezca a cada una de las razas de nuestra base de datos es <30%.**

Razas de la base de datos:

American staffordshire terrier, border collie, boxer, boyero de berno bullmastiff, bull terrier, chihuahua, collie (de pelo largo y corto), collie barbudo, doberman pinscher, dogo argentino, dogo de burdeos, english springer spaniel, fila brasileño, pastor alemán, braco alemán de pelo duro, golden retriever, gran danés, bichón habanero, labrador retriever, terranova, parson russell terrier, pastor ovejero australiano, perro de presa canario, caniche, carlino, mastín pirineo, rhodesian ridgeback, rottweiler, mastín español, staffordshire bull terrier, weimaraner.

Los valores almacenados en la base de datos se eligen de tal manera que representen un pool genético de la población europea para la respectiva raza.

Interpretación de los hallazgos:

La probabilidad para ser considerado una raza pura debe ser del 80% o más.

Las probabilidades de entre el 40% y el 60% se asocian a perros en los que uno de los progenitores es de raza pura. Una probabilidad menor al 30% es indicativa de que con alta probabilidad el perro no es de raza pura ni es un cruce de las mismas, dentro de las razas de nuestra base de datos. Este valor refleja una probabilidad matemática. Este cálculo se ha basado, entre otras cosas, en el perfil de ADN del animal examinado, así como los datos de todos los animales almacenados en nuestra base de datos hasta la fecha con las frecuencias alélicas calculadas.

Estos resultados se basan en el material de muestra enviado a nuestro laboratorio. Este material es adecuado salvo que se indique lo contrario. El remitente es responsable de la exactitud de la información relativa a la muestra. Este informe solo puede transmitirse íntegramente y sin cambios. Hacer lo contrario requiere el permiso por escrito de Laboratorio Veterinario Laboklin S.L.

*: test performed by partner laboratory

Luisa Murcia Giro - Veterinaria

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



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