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genetic laboratory

Result certificate #012345

Detection of a SINE insertion in the SILV gene causing merle coat color

Customer: Jan Novák, Dlouhá 1, 30000 Plzeň, Czech Republic
Sample:
Sample: 21-12345
Date received: 01.02.2021
Sample type: blood

Information provided by the customer
Name: Lassie DEMO
Breed: Plemeno
Tattoo number: 1392013
Microchip: 123 456 789 012 345
Reg. number: REGQ12345
Date of birth: 1.1.2020
Sex: female
Date of sampling: 01.02.2021
The identity of the animal has been checked.

Result: m/Mc (Mc ~ 222A)

Explanation

Presence or absence of SINE insertion in SILV gene was tested. The insertion causes the inability of cells to produce normal eumelanin. The degree of expression in the phenotype is associated with the variable length of the inserted polyA sequence (a chain of repeating base pairs that is part of the SINE insertion). The longer the inserted polyA sequence is, the greater degree of merle expression in the phenotype can be observed.

Merle alleles:
- m non-merle (wild type, no SINE insertion)
- Mc cryptic merle (length of polyA 200 – 230 bp)
- Mc+ cryptic merle + (length of polyA 231 – 246 bp)
- Ma atypical merle (length of polyA 247 – 254 bp)
- Ma+ atypical merle + (length of polyA 255 – 264 bp)
- M merle (length of polyA 265 – 268 bp)
- Mh harlequin merle (length of polyA 269 – 280 bp)

There are 28 possible merle genotypes: m/m, m/Mc, Mc/Mc, Mc/Mc+, m/Mc+, Mc+/Mc+, m/Ma, Mc/Ma, Mc+/Ma, Ma/Ma, m/Ma+, Mc/Ma+, Mc+/Ma+, Ma/Ma+, Ma+/Ma+, m/M, Mc/M, Mc+/M, Ma/M, Ma+/M, M/M, m/Mh, Mc/Mh, Mc+/Mh, Ma/Mh, Ma+/Mh, M/Mh, Mh/Mh.

A total of 14 allelic combinations cause deletion of the pigment to white color: Mc+/Ma+, Ma/Ma+, Ma+/Ma+ Mc+/M, Ma/M, Ma+/M, M/M, m/Mh, Mc/Mh, Mc+/Mh, Ma/Mh, Ma+/Mh, M/Mh, Mh/Mh.

There is a risk of health problems with 8 allelic combinations: M/M, m/Mh, Mc/Mh, Mc+/Mh, Ma/Mh, Ma+/Mh, M/Mh, Mh/Mh.

The dog can also be a merle mosaic, i.e. can carry several types of merle alleles in its cells. The result lists all detected major and minor alleles in the tested sample. Minor alleles are shown in brackets [].

Method: SOP176-merle, fragment analysis

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Approved by: Mgr. Martina Šafrová, Laboratory Manager

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