

# SUMMARY OF GENETIC DIVERSITY in FINNISH MAGYAR AGÁR POPULATION

Finnish Magyar Agár Association organized a genetic diversity testing at UC Davis University Veterinary Genetics Laboratory (later VGL) in Spring 2017. 26 Magyar Agárs currently living in Finland participated. Some siblings and parent-descendant pairs were included, and therefore, some bloodlines are overrepresented in the study material.

In this project, the number of tested Magyar Agárs (later MAs) is small, and therefore, we can't and surely won't make any analysis concerning the whole population. We emphasize, that in this summary, we will only focus on Finnish MA test population and it's results. We received a short report of the results from VGL and will summarize it here. The results will most likely change when more MAs will be tested.

## DLA-diversity

Diversity of the major histocompatibility complex (MHC) was examined by testing DLA class I and II haplotypes. This area includes many of the functional genes of the immune system, thereby making it a candidate region for involvement in immune-mediated disorders.

From the 26 tested MAs, 11 different haplotype combinations were found. These 11 haplotypes are composed of 11 class I and 6 class II haplotypes. Only two of the tested dogs were homozygous, which means that these dogs inherited the same haplotype from the sire and the dam. The two dogs were homozygous for different DLA haplotypes (Avenina's Elszánt Erzsebet and Puszták Vadásza Kele).

### *DLA haplotype distribution in the Finnish Magyar Agár Association project*

| <i>Haplotype</i>              | <i>Amount</i> | <i>Frequency</i> |
|-------------------------------|---------------|------------------|
| 1 1033 (DLA I) 2006 (DLA II)  | 8             | 0,15             |
| 2 1003 (DLA I) 2001 (DLA II)  | 8             | 0,15             |
| 3 1066 (DLA I) 2047 (DLA II)  | 6             | 0,12             |
| 4 1054 (DLA I) 2017 (DLA II)  | 6             | 0,12             |
| 5 1104 (DLA I) 2017 (DLA II)  | 6             | 0,12             |
| 6 1163 (DLA I) 2016 (DLA II)  | 4             | 0,08             |
| 7 1015 (DLA I) 2012 (DLA II)  | 4             | 0,08             |
| 8 1052 (DLA I) 2017 (DLA II)  | 3             | 0,06             |
| 9 1164 (DLA I) 2012 (DLA II)  | 3             | 0,06             |
| 10 1162 (DLA I) 2006 (DLA II) | 3             | 0,06             |
| 11 1161 (DLA I) 2001 (DLA II) | 1             | 0,02             |

Statistics of DLA haplotypes can be found in the VGL site

<https://www.vgl.ucdavis.edu/services/dog/GeneticDiversityInMagyarAgarSTRInfo.php> This page will be updated when more MAs are tested.

From the 11 DLA class I haplotypes, five most common are represented in 66 % of tested MAs. Only three of the tested MAs have none of the most common class I DLA haplotypes (Avenina's Amans Aenea, Hajnali Tejeskává and Puszták Vadásza Kele). From the 6 DLA class II haplotypes, three most common are represented in 67 % of the tested MAs. Only a few DLA class II haplotypes were found in comparison to other breeds. However, the incidence of the class II haplotypes is quite even in the test group. The number of rare DLA haplotypes may rise when more MAs are tested.

VGL has studied genetic diversity in 329 Italian Greyhounds from North-America, Europe and Russia Italian Greyhounds using the same method. 28 different DLA haplotype combinations composed of 18 class I and 17 class II haplotypes were found. Despite of the quite high number of haplotypes, three most common DLA class I and II haplotypes were presented in 66 % of the Italian Greyhounds tested.

## **Genetic diversity examined using STR markers**

Genetic diversity was studied between individuals and within the tested group using 33 genomic STR (Short Tandem Repeat) markers. These markers represent the whole genomic diversity and heterozygosity. According to VGL, there are no shockingly high frequencies for any allele. However, each marker has one or two obviously common alleles which will make it hard to avoid homozygosity in breeding.

Updated frequencies of the STR markers in MAs are available

<https://www.vgl.ucdavis.edu/services/dog/GeneticDiversityInMagyarAgarSTRInfo.php>

The Internal Relatedness value (IR value) is a measure of genetic diversity within an individual. IR value takes into consideration both heterozygosity of alleles at each STR loci and their relative frequency in the population. Heterozygosity over homozygosity and uncommon alleles over common alleles are preferred. IR value is unique for each dog and cannot be compared between dogs. Two dogs may have same IR values but very different genetic makeups.

New test result will most likely change the IR values and therefore, the IR values in this summary can be comparable only within the MA group tested before 15<sup>th</sup> July 2017. The most diverse MA was Balaton Nyitnikék Bársonyos with IR value -0,23. Highest IR value 0,13 was calculated for Csaba Öhungerikum. Average IR value in this test group was -0,03.

In the large population study of 329 individuals, genetic difference between Italian Greyhounds from Europe and North America was observed using STR markers. North American population harbored more different STR alleles but heterozygosity was shown to be lower than in European dogs.

## **How to proceed?**

Obviously, there are several aspects breeders should consider in breeding dogs, but we should also pay attention to maintaining the genetic diversity. Genetic research is one piece of the puzzle where we should first compare the DLA haplotypes and after that the STR markers. If future parents are different in these genetic areas, next generations will stay more diverse. Dogs with rare haplotypes or alleles should be preferred since there is a better chance to save genetic diversity and increase frequencies of rare haplotypes and alleles in the population. On the other hand, a single or even some DLA haplotypes might be associated to immunological diseases or disorders.

However, DLA haplotyping does not reflect at any level inheritance of other inherited disorders or disease susceptibility.

IR value represents only a status of an individual dog as a measure of inbreeding. If you put together two dogs with very low IR value but representing the same genotypes, the progeny will have much higher IR value and lower genetic diversity than parents. A dog with high IR value might not be a bad choice for breeding when mated with a partner with a different genetic makeup. Homozygous genetic regions may allow recessively inherited disorders to appear. This can be avoided by preferring pairings where genetic diversity will be high and therefore IR values low.

Excel file in <http://files.unkarinvintikoirat.com/200000681-5f9ee60992/DLA-tulokset%202017.xls> includes all the results of the 26 MAs tested in order to help to compare DLA haplotypes, STR markers and IR values. When you compare the results, you have to remember that each parent will contribute the puppy with one copy of DLA haplotype and each STR marker allele – so it's like a lottery which one to which puppy. This is easily visible in the test group since there are MAs whose both parents are tested also. VGL provides a mating calculator in their website <https://www.vgl.ucdavis.edu/index.php> . You create first a free account on the website on the left side "Login" and "Create account". After you have logged in, click "Order tests" and then "Dog tests". On the left you will find "Mating evaluation" which has a link to the calculator. From our Excel file, you can find for all the 26 tested MAs a "Case number" which you will need to write on the calculator.

We hope that owners and breeders would become inspired for testing more MAs. It would increase the value and usability of the available test results also. We would like to give warm thanks to every owner with their MAs who participated in this project! Huge thanks go to several veterinary clinics around Finland, they helped us in proper sampling of the dogs:

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If you have any questions about this summary, please contact secretary of the association via [sun.sihteeri@gmail.com](mailto:sun.sihteeri@gmail.com)

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