German Shepherd lines are genetically different

The German Shepherd is the world's most popular dog breed, with many uses as working dogs, companion dogs, show dogs and pets. The variability of German Shepherds makes the breed an intriguing focus of research for behavioral studies and also raises interesting questions concerning the genetic diversity of the breed as well as the possible differentiation between different breeding lines. These speculations have focused especially on "show lines" and "working lines." White Shepherd Dogs and Long Haired German Shepherds have previously been separated into distinct breeds.

Our research group has various ongoing genetic research projects aiming at the identification of disease genes in the breed, and as part of these projects we have been looking into the genetic differences between different breeding lines. Recognizing these differences is important for the validity of the research findings. According to earlier genetic studies dog breeds differ from each other significantly more than any of the human populations differ from each other. Cultivating purebreds has efficiently differentiated breeds into their own genetic populations. Individual dogs' genomes are often significantly more similar within the breed than between breeds. Considerable genetic differences, forming subpopulations, may also exist within a breed however. This is common in breeds with several different uses and where selective breeding is practiced with these uses in mind. The German Shepherd is a typical example of this type of breed.

We investigated the genetic differences of 62 Finnish German Shepherds from three different breeding lines. The dogs were divided according to the guidelines of a breeding specialist from the Finnish German Shepherd Association into three separate populations: the show line, the mixed line and the working line. A dog was defined as a working-line dog if there were known working dogs in its five-generation pedigree. Similarly, if a dog's pedigree contained known show dogs, the dog was defined as a show-line dog. If both lines were detectable from the pedigree, the dog was defined as being part of the mixed line.

An analysis of 172 000 genetic variants was conducted from the genomes of all 62 dogs in order to measure genetic variation (measuring allele frequencies). A so called similarity matrix was used to compare the genetic similarity between individuals, using the data received from the genome analysis. The results of the analysis are shown in Figure 1. In the figure similarity is represented by distances. Every point represents one dog, and the closer the dogs are to each other genetically the closer together the points are. Based on the results, the show-line dogs and the working-line dogs differ from each other genetically, and form their own clusters in the figure. The mixed-line dogs place in the middle in this figure, but with a closer proximity to the working-line cluster. In the figure one presumed show-line dog and one working-line dog are in opposite clusters, which could be due to an erroneous characterization of the dogs' pedigrees. Most of the mixed-line dogs place close to the working-line dogs, indicating that their genomes are "similar" to each other. A genome-wide analysis shows that these dogs selected from show and working lines differ from each other genetically.

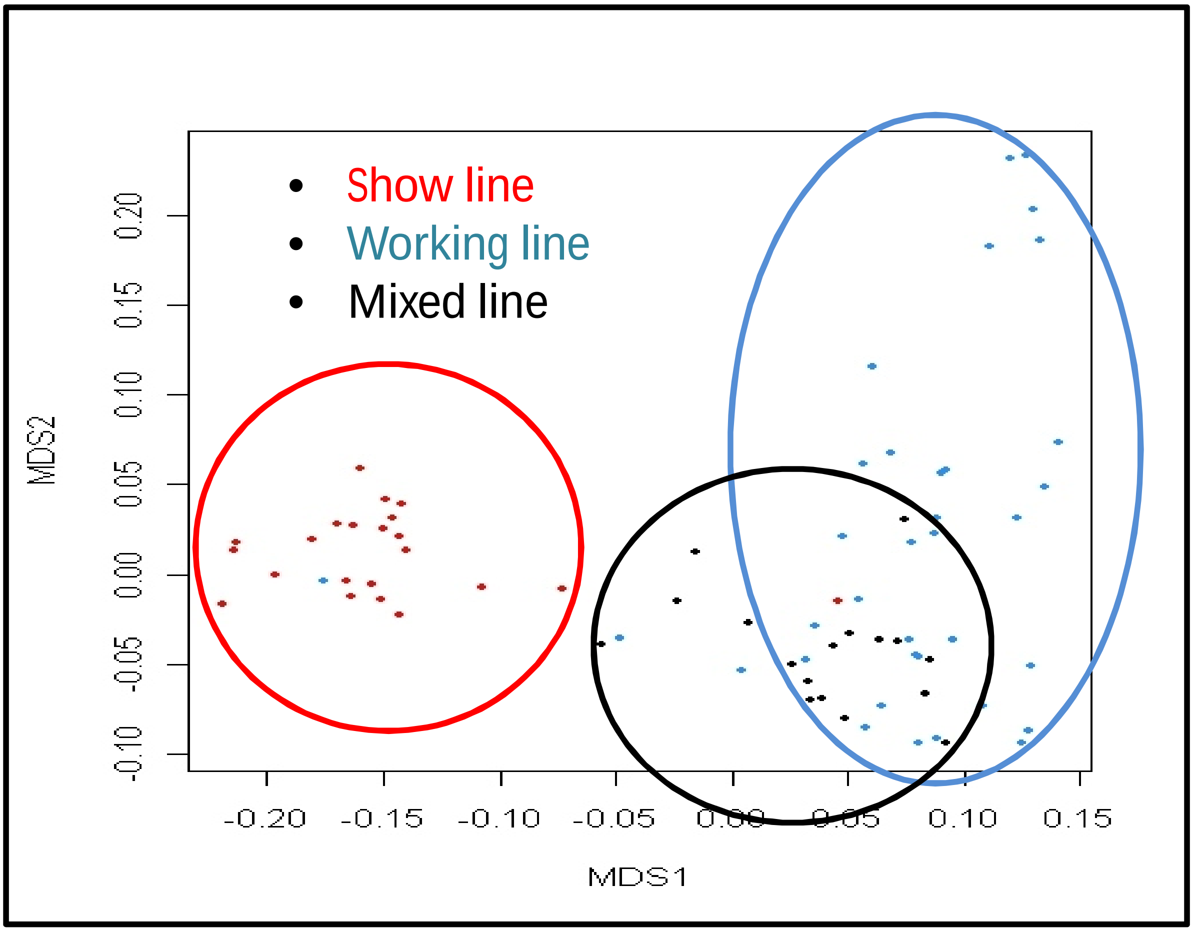

Figure 1. The genetic differences of a German Shepherd population. Based on pedigrees and uses 62 German Shepherds were selected from three different lines for a genome-wide analysis in order to detect possible genetic differences. The results indicated that show-line dogs (red points) and working-line dogs (blue points) differ from each other genetically. The mixed-line dogs (black points) place between the two other lines with a closer proximity to the working-line dogs.

After a similarity-matrix analysis was performed, we predicted the genetic probability for each of the dogs to belong to a specific population, based on the genome-wide marker data and the population division. The results of this analysis have been presented in Figure 2. The results were again surprisingly clear: all dogs predicted to belong to the show line did so also according to this analysis. The mixed-line and the working-line dogs had similar probabilities, but even there the division was relatively clear. (Figure 2.) The results indicate that the show-line dogs are clearly separated into their own population. In the mixed and working lines the probabilities vary, reflecting the actual “degree of mixing.”

In the future, the analysis can be taken even further by locating those gene regions where populations differ from each other most clearly and calculating different physical quantities which would indicate to what degree the populations have differentiated from each other. However, the division between the lines is clear in also this study, and based on this sample we were able to see a clear genetic interpopulation variation. The results of the genome analysis confirm the hypothesis of the existence of also a genetic intrabreed division into show and working lines. The different appearance and behavioral traits between the lines are another indication of this. Working line dogs are often bred with other individuals of the same line.

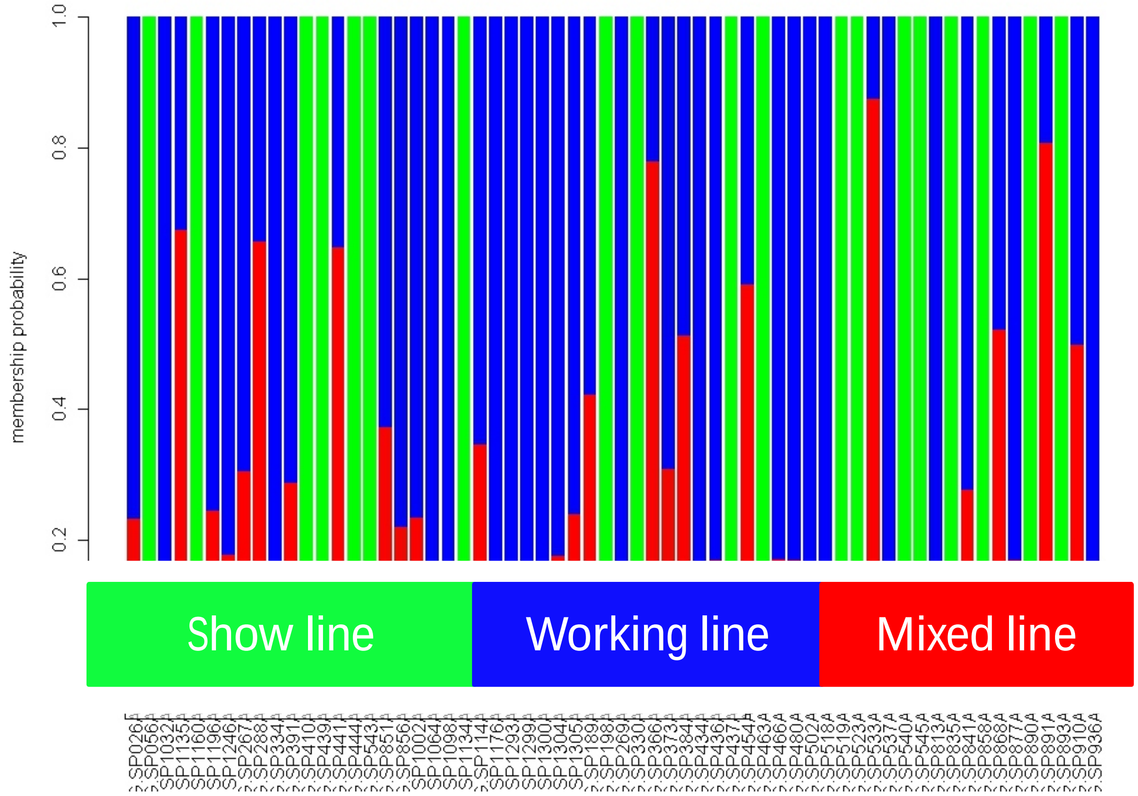

Figure 2. The probability of German Shepherds to belong to a predicted line. Samples from altogether 62 German Shepherds were examined in a genome-wide analysis (~172 000 markers) and based on the data received and an earlier population division (Figure 1.) the probability of each dog to belong to one of the three given lines was predicted. In the figure each dog has its own vertical bar and the probability (0-1) has been marked with different colors according to the corresponding line. Based on the genetic data all show-line dogs were predicted correctly (green bars, possibility of 1 = 100%). With the mixed-line and the working-line dogs the probabilities varied according to the “degree of mixing.”

This study conducted on a small data set opens up interesting avenues for further research into the German Shepherd breeding lines. The genetic differentiation of the breed by appearance and behavior (possibly also by diseases) into different populations enables a closer mapping of the genes related to these traits in a bigger data set. As a result of selected breeding the show line has developed genetic variants different from the working line and vice versa. In a larger study more specific genetic regions connected to the different lines could be identified from the genetic data. Some of the genes in these genetic regions explain the typical appearance and behavioral characteristics of the different lines.

German Shepherds have a significant role as working dogs in for example the police force and the border guard. These working dogs are required to have specific qualities necessary for each type of service in order to learn and manage the given assignment. Although dog training plays a vital role, there are differences in different dogs' learning abilities and behavioral character traits, and some of these differences can be explained by genetics. Our particular area of interest for follow-up studies is to find out whether genetic analyses could help separate the potentially "extraordinary" working dogs from the good working dogs. If we were to successfully develop this kind of tool we could help select young dogs with the best potential to be trained as working dogs. In addition to domestic populations, the test could help identify dogs for breeding purposes in also international German Shepherd populations, which in turn would be a positive step towards increasing diversity in the breed. We are now investigating, together with the German Shepherd breed association and different working dog associations, possibilities for further studies. The research requires samples from dogs, but also technical equipment as well as reliable information on the participating dogs.

The research group would like to thank the more than a thousand dog owners who have participated in the study, as well as breeders and contact persons for breed associations for their support. Without your help the research could not go forward.

With warm autumn wishes,

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