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39 and Me: The Evolution of Dogs through the Study of Genomics

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Introduction

- Dog breeds have been created by humans through artificial selection, developing their unique genetic history.
- Contrasting genetics within a breed allows us to reconstruct a large amount of phylogenetic data (Parker et al. 2017).
- Modern molecular tools allow us to recreate the genetic history of different breeds, their traits, and diseases.
- Our lab focuses on the hovawart breed (Fig. 1) to better understand the evolution of breed-specific traits and potential mutations leading to genetic predisposition to diseases.
- We will achieve our goals by using highly variable genetic markers called single nucleotide polymorphisms (SNPs).

Figure 1. Hovawart dogs, a German breed, the focus of this study.

Objectives

- Screen a large dataset (~350 dogs) of hovawarts by obtaining their genotypes using SNPs distributed across their genome.
- Correlate genotypes and phenotypes within the dogs. Specifically, the SOD1 gene, which is linked to degenerative myelopathy. Hovawarts show a unique gene insertion within this gene (Turba 2017).
- Determine the genetic origin of this breed based on their genetic variability contrasted to other canids (coyotes and foxes).

Materials And Methods

- DNA samples were extracted from buccal swabs or blood using the Qiagen DNeasy kit.
- The EP1 Fluidigm SNP system was used to genotype samples.
- Statistical analyses completed with the R statistical program using the LEA package (Frichot and François 2015) and Structure software V2.0 (Pritchard et al. 2003).
- RFLP analysis was used to genotype samples for the SOD1 gene mutation (Chang et al. 2013).

Results

- 329 hovawart samples and other canids were genotyped across 192 loci.
- Four loci were removed from analyses as they were monomorphic.
- Dogs of similar ancestries grouped together into clusters. Five clusters were obtained across hovawarts (Figs. 2 and 3).
- Distribution of ancestral clusters was mapped across American and European populations (Fig. 4).
- Evidence of an insertion near the SOD1 gene was visible in gel images of PCRs (Figs 5 and 6).

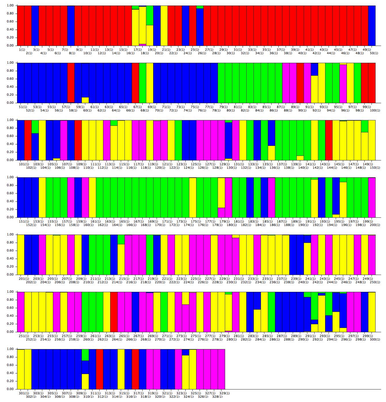


Figure 2: Bar plot from Structure indicating that hovawarts branch into 5 ancestral genetic clusters, distinguishing American and European samples.

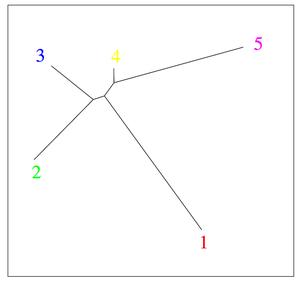
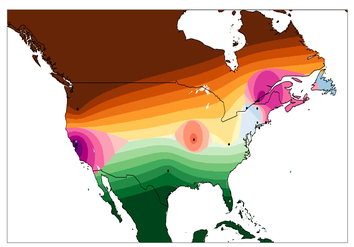


Figure 3: Ancestral tree from Structure shows the phylogenetic relationships between the groups of samples.



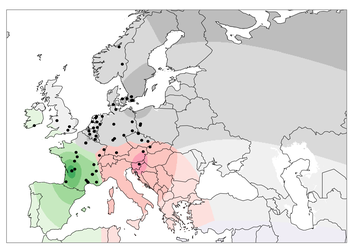


Figure 4. Geographical maps of the ancestral groupings from R statistics.

Conclusions

- Clusters mostly reflect geographical origins. To improve genetic variability, it is important to breed dogs that are from different countries.
- Our multigenerational samples also show the passing of traits down familial lines. This also includes genetic insertion observed in the SOD1 gene associated with degenerative myelopathy.
- By assessing local genetic variability among hovawarts from different localities we will be able to advise breeders on best mating practices avoiding introgression.

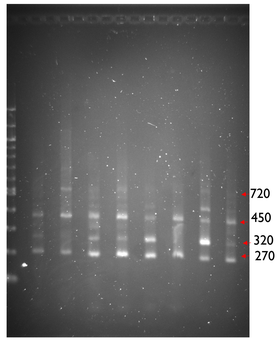


Figure 5. Gel electrophoresis image of a polymerase chain reaction for the SOD1 gene. Bands of different sizes/intensities reflect the variability among the samples.

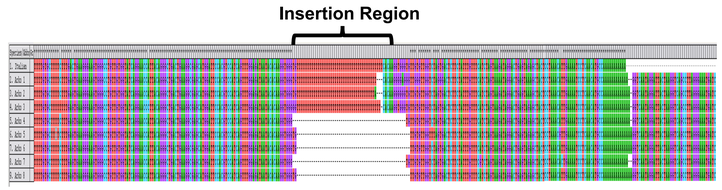


Figure 6. Insertion in the SOD1 gene is displayed here, consisting of variable lengths of a poly T repeat.

Future Goals

- Use publicly available datasets to expand to dozens of other breeds and create a more thorough assessment of genetic variability.
- Conduct an GWAS with the extended dataset to associate traits with genes.
- Further explore the effects of the insertion near the SOD1 gene with regards to degenerative myelopathy.

References

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Acknowledgements

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