



Canine Genetics Progress Report

Breed: Siberian Huskies

Condition: Hereditary Cataract

Date: 29.07.2009

Funding:

- Funding Body:* Canine Health Foundation (American Kennel Club)
Amount: \$100,000
Start Date: July '08, 24 months

This project is a collaboration between Cathryn Mellersh (Animal Health Trust, UK) and Hannes Lohi (University of Helsinki, Finland).

Sample Collection

Sample collection for project has started well, with samples from 138 huskies being submitted to the AHT to date. Of these 33 samples are from dogs with a cataract in at least one eye, 58 are from dogs that have been declared free of cataracts at their last eye examination and the remaining samples were not accompanied by any eye information. Additional samples have also been collected by our Finnish collaborators.

Current Progress

At the end of last year we extracted DNA from 19 dogs that we were confident had hereditary cataracts (judging from the clinical description of their cataracts) and from 22 dogs that were clear of cataracts at their last eye examination and were over the age of 5 years when they were examined. Those samples were sent to our collaborators in Finland where, along with DNA samples from Finnish Huskies, they

were each genotyped with approximately 22,000 markers from all over the canine genome (called a Whole Genome Scan). In total we genotyped samples from 21 cases and 21 controls. The DNA we extracted was of very good quality and the genotyping worked extremely well (i.e. we received information about almost every marker we investigated for every DNA sample we analysed).

The data generated has been analysed to try to identify a region of the genome that is shared between all affected dogs and different in the unaffected dogs; this would be the region where the HC mutation was located. We have tried many different forms of analysis, for example modelling the condition as dominant or recessive, and we have identified a small number of chromosomal regions that are more likely to harbour a cataract mutation than others. Unfortunately none of these regions are associated with HC to a statistically significant level. We have investigated the genes that are located in the suggested regions, to see if any of them might reasonably be expected to play a role in cataract development, based on what is known about the gene function. None of the genes are sufficiently provocative candidates to warrant further investigation at this stage.

The number of samples we have analysed (21 cases and 21 controls) has been sufficient to successfully identify regions associated with other diseases our laboratory has investigated. The fact that no significantly associated regions have been identified for the Husky thus far suggests HC in this breed is probably caused by mutations in more than one gene and we will need to analyse more samples. The data we already have will not be wasted; we will keep it and add it to the additional genotyping data we will now aim to generate.

Additional Samples

Although we have collected sufficient samples to initiate research we now need to collect samples from more HC affected and unaffected Huskies with a view to undertaking a new Whole Genome Scan when we have collected sufficient additional samples. We put an emphasis on collecting samples from dogs of any age diagnosed with bilateral cataracts (i.e. cataracts in both eyes) and dogs over the age of 5 years that are clear of cataracts. We currently have samples from 24 dogs with bilateral cataracts; we would like to increase this number to 48. Similarly we currently have samples from dogs that were clear of cataracts over the age of 5 years; we would like to increase this number to 48 also.

Acknowledgements

We would like to thank all owners who have submitted samples and information from their dogs – without either of these we would be unable to make any progress with this project.