Canine Genetics Progress Report

Breed: **Standard Poodles**

Condition: **Sebaceous Adenitis**

Date: **March, 2011**

Sample Collection

Since our last report in September 2008 (AKC Acorn Grant funded) the AHT has received an additional 32 samples from Standard Poodles, 10 of which were from dogs affected with Sebaceous Adenitis ("cases"). We would like to thank Molly Windebank for her hard work in encouraging owners to send in samples. However these numbers were not sufficient by themselves for a second whole genome scan. Luckily in 2010 we were contacted by Dr Niels Pedersen who suggested a collaboration involving pooling of our samples.

Collaboration with University of California Davis

Dr. Niels Pedersen at the Veterinary Genetics Laboratory at the University of California Davis (UC Davis) and Dr. Mike Boursnell in Dr Cathryn Mellersh's Canine Genetics Group at the Animal Health Trust in the United Kingdom (AHT) have entered into a collaboration centred round the genetics of Sebaceous Adenitis in Standard Poodles (SPs). Dr Pedersen had selected a batch of US SP samples for genotyping, and kindly offered to genotype some SP samples from the AHT. It was hoped that this larger sample set would provide more useful information than either set alone. The data would be analysed both by UC Davis and the AHT, each providing their own experience to the analysis.

The data.

The US set included 35 samples from affected dogs ("cases") and 22 samples from unaffected dogs ("controls"). The UK samples included 23 cases and 16 controls. Some of the UK samples had been previously genotyped using the old Canine array (22,362 SNPs), and were re-genotyped on the new Canine HD array (173,662 SNP markers). All samples were successfully genotyped, with high call rates, indicating that the DNA was of good quality. This type of "Whole Genome Scan" is used to search for regions of the genome that are consistently shared among cases but different in controls. Such regions are likely to be associated with the disease and may contain mutations in genes that are involved with Sebaceous Adenitis.

Current Progress

The data from the genotyping is currently being analysed at UC Davis and at the AHT. Initial analysis has been carried out, but there is still a great deal to do, and possible follow up experiments to be conducted. The first stage of the analysis has confirmed the results of the previous smaller whole genome scan with the old Canine SNP array, namely that there is no evidence for a single mutation causing the disease. In fact the data further strengthen our belief that SA is a more complex condition with perhaps several genes involved.

Some other interesting facts emerge from the first stage of the analysis. Firstly that the US and the UK sample sets are clearly distinct genetically. In addition the regions of the genome that are most associated with the disease are also different in the two data sets. This latter observation raises the possibility that some of the genetic factors causing the disease are different in the US population than in the UK population. If true, this would be interesting scientifically but obviously makes identifying a clear cause a bit more problematical.

On the positive side, the association of some regions of the genome with the disease is more clear cut than with the previous smaller sample set. This is probably due in part to the new combined data set arising from the collaboration, and also from the use of the new high density SNP marker array. This gives us encouragement to follow up these results with further analysis and experimentation.

Future work

The enormous amounts of data that we have obtained in this new Whole Genome Scan means that there is still some way to go in completing the analysis. We will try to make sense of the differences that we see between the US and the UK populations, and also to look to see if there are any connections or interactions between the separate associated genome regions. To try to test whether each of these regions are genuinely significant we will need to analyse a limited number of SNP markers in as many more samples as we can find. If we can validate these regions in a large number of extra dogs, then we can be more confident that they are associated with the disease.