**TIBETAN TERRIER HEALTH & WELFARE FOUNDATION**

In October 2010, the TTHWF helped to fund a AKC CHF grant to identify the genes associated with Canine Autoimmune Hemolytic Anemia (AIHA) through the University of Manchester.

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**Grant No. 1268**

Investigation to identify genes associated with canine immune-mediated haemolytic anaemia

**Abstract:**

Background: Immune-mediated haemolytic anaemia (IMHA) is the most common immune-mediated disease of the dog, representing a major health concern to this species. There are several breeds that are predisposed to developing IMHA, including the Cocker Spaniel, the English Springer Spaniel and the Clumber Spaniel. The researchers have previously identified an association of IMHA with some immune function genes, and have also performed a genome wide search for other genes involved in the disease. This has identified several other regions of the genome that are statistically associated with IMHA. Objective: The researchers aim to confirm these findings, investigate these areas further, and identify other potential susceptibility genes. The identification of one or several genes associated with IMHA could be used to develop a screening test that could indicate the risk of an individual dog developing IMHA. This would be of great importance to owners and breeders of dog breeds that are susceptible to this devastating disease.

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GRANT PROGRESS REPORT REVIEW 2-2011

Grant: *01268: Investigation to identify genes associated with canine immune-mediated haemolytic anaemia*

**Principal Investigator: Dr. Lorna J. Kennedy, PhD**

**Report to Grant Sponsor from Investigator:**

Previously the AKC gave us some funding for a pilot study on immune-mediated haemolytic anaemia (IMHA). This involved doing a whole genome scan comparing healthy cocker and springer spaniels withaffected dogs, in order to identify regions of the genome that might be associated with IMHA. A preliminaryanalysis revealed several potential regions of interest.

We have now performed a replication study testing those regions for associations using a larger group of over300 dogs. Disappointingly, none of the markers were confirmed in the replication study as having anassociation with IMHA.

We have obtained extra data for control dogs of both breeds and reanalysed the original data, hoping that this increased power would reveal some stronger associations. New analysis methods are being developed all the time, and there is, as yet, no standard method for such analyses. We have contacted many collaborators, and are testing out various different approaches.

We cannot proceed with fine mapping based on these results, as there is no strong evidence for one region of the genome to investigate. We therefore propose to test some extra cases on the high de sity array, to increase the power of the experiment.

We are also part of a large European study (known as the LUPA project) investigating canine diseases. We have seen many of the early studies within LUPA starting with low sample numbers on low density arrays and unable to identify associated markers, which have gone on to test additional cases on the high density array, and then found some strong associations.