RESEARCH PROGRESS REPORT SUMMARY

Grant 02172-MOU: Understanding Hereditary Deafness in Dogs

Principal Investigator: Dr. George M. Strain, PhD

Research Institution: Louisiana State University

Grant Amount: $120,015.00

Start Date: 11/1/2015 **End Date:** 10/31/2017

Progress Report: End-Year 1

Report Due: 10/31/2016 **Report Received:** 10/28/2016

(Content of this report is not confidential. A grant sponsor's CHF Health Liaison may request the confidential scientific report submitted by the investigator by contacting the CHF office. The below Report to Grant Sponsors from Investigator can be used in communications with your club members.)

Original Project Description:

Hereditary deafness associated with white pigmentation occurs in numerous dog breeds. Because of quality-of-life concerns and in an effort to reduce the prevalence of deafness within breeds, many bilaterally deaf puppies are euthanized by breeders. The breeds most affected are the Dalmatian (Dal, 22% unilaterally deaf, 8% bilaterally deaf) and the Australian cattle dog (ACD, 11.4% and 3%). The mechanism of inheritance is unknown, but does not appear to be simple Mendelian: breeding of two bilaterally deaf Dals produced puppies that heard in both ears. Numerous studies to determine the mode of inheritance and locate the causative gene(s) have thus far failed.

The proposed work will use a modified twin study approach. Full-sibling littermates will be identified within the two breeds, where one puppy has normal hearing and one is deaf. Like human twins, full siblings should have very similar DNA, which will reduce the variability of the DNA samples when compared to studies of unrelated dogs. Using the Illumina CanineHD Beadchip, which contains 172,115 DNA markers (SNPs) spread uniformly across the canine chromosomes, activity at the markers will be compared between the sibling pairs, and differences in activity between siblings at individual markers will be identified. These differences will be tallied for 50 Dal pairs and 50 ACD pairs. The chromosome locations of the markers are known, and genes located close to each marker are known because of the sequencing of the canine genome, so candidate deafness genes can be identified and provide the basis for more detailed study.

Publications:

None at this time.

Report to Grant Sponsor from Investigator:

Saliva samples have been collected for DNA isolation from 114 Dalmatians plus 25 samples archived with the OFA, giving 139 samples, above our goal of 100 samples (50 sibling pairs). Saliva samples have been collected for DNA isolation from 87 Australian cattle dogs (ACD) to date, below our goal of 100 (50 sibling pairs), but samples are continuing to be collected. In anticipation of finding a significant marker for deafness in the Dal and ACD dogs, we have also collected saliva samples for DNA isolation from small numbers of dogs in other breeds with pigment-associated deafness to look for a similar significant marker; these include 4 Old English sheepdogs, 4 Dogo Argentinos, and 8 Jack Russell terriers. We will continue to collect as many Dal and ACD samples as possible to increase the statistical power of the DNA analyses in these breeds, and limited numbers of samples from other affected breeds to assess whether one genetic mechanism is associated with hereditary deafness in piebald breeds, or whether multiple mechanisms exist. Identification of a single unified mechanism will significantly increase the impact of the findings on the pure dog breed world.

DNA isolation from the collected samples has been completed and the DNA has been delivered to Cornell University where the Illumina microbead array assays will be performed and the subsequent analyses will be performed. Further DNA samples will be conveyed to Cornell as they become available. Genome sequencing studies will be performed with DNA from selected dogs based on findings from the Illumina array analyses.