



RESEARCH PROGRESS REPORT SUMMARY

Grant 02172-MOU: Understanding Hereditary Deafness in Dogs

Principal Investigator: George Strain, MS, PhD

Research Institution: Louisiana State University

Grant Amount: \$105,091.05

Start Date: 11/1/2015 **End Date:** 10/31/2018

Progress Report: FINAL

(The content of this report is not confidential and may be used in communications with your organization.)

Original Project Description:

Hereditary deafness associated with white pigmentation occurs in numerous dog breeds. 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, and previous studies to determine the mode of inheritance and locate the causative gene(s) have thus far been unsuccessful. Using a modified twin study approach, full-sibling littermates will be clinically and genetically evaluated. Like human twins, full siblings should have very similar DNA, which will reduce the variability of their DNA 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, markers will be compared between the sibling pairs, and differences between siblings at individual markers will thus be identified. Using this approach candidate deafness genes can be identified and will advance the current understanding of this heritable disorder.

Funding for the research is provided through the efforts and generosity of the Australian Cattle Dog Health, Education, and Welfare Inc., Australian Cattle Dog Club of America, Dalmatian Club of America, and the Dalmatian Club of America Foundation. The AKC Canine Health Foundation supports the funding of this effort and will oversee grant administration and scientific progress reports.

Publications: None at this time.

Presentations:

Strain, G.M. 2015. Hereditary deafness in the ACD: What we know and where we're heading. Australian Cattle Dog Club of America National Specialty, Gray Summit, MO.



Report to Grant Sponsor from Investigator:

Samples for DNA analysis were collected from 501 Australian Cattle Dogs (ACD), Dalmatians (Dal), and English Setters (ES), more than in any previous study (228 hearing, 149 unilaterally deaf, and 124 bilaterally deaf). Genome-wide association studies (GWAS) were performed using Illumina microarrays to identify single nucleotide polymorphisms (SNPs, or DNA markers) significantly associated with deafness, which in turn would point to nearby causative genes. Very few SNPs approached a significant association, when analyzed for individual breeds (allowing for different mechanisms among the three breeds) or all dogs combined (assuming a common mechanism for all three breeds). This may have been the result of insufficient numbers of dogs, or complex hereditary mechanisms. Not all genetic disorders can be identified by GWAS studies.

We have also generated the whole genome sequence for 11 deaf and hearing dogs: 2 deaf and 1 hearing ACD, 4 deaf and 1 hearing Dal, and 2 deaf and 1 hearing ES. The problem of deafness is of sufficient importance in the breeds of this study (and others) to justify continued studies to provide a solution that can lead to identifying carrier dogs and reducing disease prevalence.