RESEARCH PROGRESS REPORT SUMMARY

Grant 01849: Filling the Gaps in the Canine Genome

Principal Investigator: Dr. Shaying Zhao, PhD

Research Institution: University of Georgia Research Foundation, Inc

Grant Amount: $108,000.00

Start Date: 1/1/2013 **End Date:** 12/31/2014

Progress Report: End-Year 1

Report Due: 12/31/2013 **Report Received:** 12/31/2013

Recommended for Approval: Approved

(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:

The sequencing of the genome of man's best friend in 2005 has provided an invaluable resource to the canine research community, and has reinforced the position of the dog as an important model organism to study human physiology and disease. Unlike the human and the rodent models (the mouse and the rat), very few dog genes, mRNA, and proteins had been sequenced prior to its whole genome sequencing. Consequently, the dog genome has been annotated for its gene content primarily based on mapping the gene-related sequences from the human, the mouse, the rat, and other non-dog species to the dog genome. While providing the community with an unprecedentedly large set of dog genes, the annotation has substantial errors and is missing in dog-specific information in many aspects. This significantly hinders research in many fields, e.g., disease gene discovery and cancer-causative gene mutation identification.

Recently emerged next-generation sequencing (NGS) technologies provide an unprecedented opportunity to correct these errors and to supply the missing information in the current dog gene annotation in a time- and cost-effective fashion. We propose herein to use state of the art NGS strategies to identify genes/transcripts expressed in major dog tissues and cell types. The valuable data, along with more refined sequence alignment between the dog and other species, will be used to build the most accurate and complete annotation of the dog genome for its gene annotation. The project will significantly facilitate research in all 2012 Health Priorities set up by AKC CHF.

Grant Objectives:

1. To perform RNA-seq (transcriptome sequencing) and a small amount of ChIP-seq (chromatin immunoprecipitation sequencing) analyses with major tissues and cell types from Boxer and Labrador retriever, two popular breeds in US and whose genome has been published (Boxer1) or will be published soon (more later).

2. To analyze the data produced by Specific Aim 1 and other data that are publically available to identify alternative splicing, small ncRNAs, and lincRNAs, and to correct sequence/annotation errors described above. Submit all raw data and analyses to public databases.

Publications:

None at this time.

Report to Grant Sponsor from Investigator:

We have finished about 75% of the proposed sequencing experiments with canine tissues which are mostly from Labrador retriever. Meanwhile, we are integrating these data with those generated by the Broad Institute and other scientists to more accurately identify all forms of dog protein-coding genes. We aim to publish the results in several months. We are performing sequencing analysis to identify canine non-coding genes and regulatory regions, which we plan in next few months.