RESEARCH PROGRESS REPORT SUMMARY

Grant 02553: Targeted Next Generation Sequencing Panel for Comprehensive Testing of Vector-borne Pathogens

Principal Investigator: Rebecca Wilkes, DVM, PhD

Research Institution: Purdue University

Grant Amount: $103,245

Start Date: 2/1/2019 **End Date:** 1/31/2021

Progress Report: End-Year 1

Report Due: 1/31/2020 **Report Received:** 1/29/2020

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

Original Project Description:

Diagnosing vector-borne disease (VBD) in dogs can be difficult for a number of reasons. First, there are many different disease-causing agents that can be transmitted from ticks/fleas, and the clinical signs caused by these agents in dogs can overlap. Additionally, because ticks/fleas can harbor more than one agent at a time, multiple pathogens may be passed to a dog with a single vector bite, resulting in co-infections. VBD infections can initially present with non-specific signs, such as fever, lethargy, vomiting, diarrhea, and/or respiratory signs. Severe cases can be associated with neurologic signs. These signs can be a diagnostic conundrum. While initial blood work can be helpful and suggest VBD, it does not determine the infecting agent. This study will develop a comprehensive next generation sequencing panel to detect and identify major VBD agents known to cause disease in dogs and to aid in diagnosis of active infections. Additionally, through parallel sequencing with this method, this panel will incorporate testing for additional infectious diseases that may cause GI, respiratory, or neurologic signs in dogs. The comprehensive nature of this sequencing panel should be a useful tool for surveillance of infectious diseases in the canine population for rapid identification of VBD in dogs and protection of pet owners from such zoonotic diseases.

Publications: None at this time.

Presentations: None at this time.

Report to Grant Sponsor from Investigator:

We proposed to develop a comprehensive method for detection of infectious diseases of dogs, taking the guesswork out of determining which tests to use for diagnosis, and potentially improving disease surveillance because of the comprehensive nature of the test. This method takes advantage of the amount of data that can be generated with next-generation sequencing (NGS) but will be performed in a way to keep costs down and maintain adequate turn-around time for diagnostic use. We proposed a combined PCR/NGS method called targeted NGS. With funding generously provided by AKC CHF, we will build on this assay, which was originally begun with internal funding from a university, by including additional targets, particularly for vector-borne pathogens. To date, we have found regions in the sequences of these vector-borne pathogens that can be used for assay development. The development work is complete and these targets have been added to our assay, which now includes 488 primer sets for detection of pathogens of both dogs and cats. We are now starting testing with type/validated samples of vector-borne pathogens and clinical samples from dogs with diagnosed vector-borne diseases to determine how well the assay works. We have hired a postdoc with grant funds to help with the bench work required for the study. We are very grateful for the support to do this work.