



GRANT PROGRESS REPORT REVIEW

Grant: 00632: *MicroRNAs and Canine Lymphoma*
Principal Investigator: Dr. William C Kisseberth, DVM PhD
Research Institution: Ohio State University
Grant Amount: \$98,766.00
Start Date: 10/1/2005 **End Date:** 9/30/2010

Progress Report: 66 month
Report Due: 3/31/2010 **Report Received:** 3/30/2010

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.)

Original Project Description:

Lymphoma is one of the most common cancers in the dog. The current classifications of lymphoma do not explain or predict its changing clinical behavior. Much of the progress in diagnosis, prognosis, and treatment of lymphoma and other cancers in people has been the result of advances in "genomics." Recently the canine genome has been sequenced, providing the opportunity to apply new genomic approaches to better understand and treat cancer in the dog. MicroRNAs (miRNA) are small non-protein coding molecules that have been linked in humans as having an important role in cancer and a variety of other diseases. In this study, the researchers will identify miRNAs using bioinformatic methods. The researchers will then use miRNA microarrays to study normal canine tissues and canine lymphoma biopsies. These results (miRNA expression profiles) will be linked with previous diagnosis and clinical restrictions. The goals of this study are to identify canine miRNAs and their normal patterns of expression and to determine if specific subtypes of lymphoma are characterized by unique miRNA expression profiles, if specific miRNAs have predictive importance, and to identify potential goals for future investigation and therapies. This study will also generate new tools for future miRNA investigation in the dog.

Original Grant Objectives:

Hypothesis: A custom canine miRNA microarray can be used to determine miRNA expression profiles in canine lymphoma. Canine lymphomas can be classified based upon their miRNA expression profiles. Individual and coordinately regulated miRNAs may have diagnostic, prognostic, and/or therapeutic significance.

Objective 1: Identify canine miRNAs and characterize their expression in canine tissues.

Objective 2: Determine the miRNA expression profiles of canine lymphomas using a modified custom oligonucleotide microRNA microarray.

Publications:

None Reported. Information about the Canine miRNA will not be published until after the university has completed filing the patent/intellectual property.

Report to Grant Sponsor from Investigator:

A new technology has become available to us, "next generation" sequencing, that offers several advantages over microarrays for miRNA profiling, especially for species other than human and mouse, where few miRNAs have been experimentally validated. Briefly, with next generation sequencing a sequencing library is constructed from size fractionated small RNAs and the entire library is then sequenced. The number of each unique RNA transcript is then determined. The major advantage of this technological approach is that it makes no a priori assumptions about what RNAs will be present in the sample; perfect for canine samples where little is currently known or validated regarding miRNA expression. We have recently converted to this technology for performing our canine miRNA profiling studies, although we will use the second-generation canine microRNA microarray for the independent validation of a subset of samples run on the first generation array. Currently, the researchers are constructing sequencing libraries for canine lymphoma samples.