GRANT PROGRESS REPORT SUMMARY

Grant: 01421: *Genomic Resources for the Control of Canine Pyoderma*

Principal Investigator: Dr. Stephen A. Kania, PhD

Research Institution: University of Tennessee

Grant Amount: $42,466.00

Start Date: 1/1/2011 **End Date:** 6/30/2013

Progress Report: Mid-Year 3

Report Due: 6/30/2013 **Report Received:** 6/28/2013

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:

Staphylococcal bacteria are responsible for most canine skin infections as well as other important diseases. Until recently antibiotic therapy was very effective for the treatment of these conditions. However, antibiotic resistance is increasing rapidly and we envision running out of useful antibiotic options. Alternatives to antibiotics may include vaccines or bacterial factors naturally produced by staphylococci that inhibit competing strains. The key to developing these strategies is discovering the genes responsible for antibiotic resistance, bacterial growth inhibitors, and targets for vaccines. The first step in our project is the collection of staphylococci causing skin infections from dogs in designated regions throughout the United States. Unique strains of antibiotic resistant bacteria will be identified and their genes of interest characterized for use in the development of the next generation of therapies for the treatment of canine infections

Grant Objectives:

Objective 1: Identify prevailing clonal populations of methicillin-resistant S.pseudintermedius infecting dogs in North America.

Objective 2: Identify unique S.pseudintermedius antibiotic resistance, virulence, antigen and quorum sensing genes.

Publications:

- S. M. Solyman, C.C. Black, B. Duim, V. Perreten, E. van Duijkeren, J.A. Wagenaar, L. C. Eberlein, L.N. Sadeghi, R. Videla, D.A. Bemis, and S.A. Kania. Multilocus Sequence Typing (MLST) for Characterization of Staphylococcus pseudintermedius J. Clin. Microbiol. published ahead of print 31 October 2012 , doi:10.1128/JCM.02421-12

- Staphylococcus pseudintermedius: population genetics and antimicrobial resistance. Ricardo Videla. December 2012. University of Tennessee. Thesis for the Master of Science Degree.

- Arshnee Moodley, Matthew C. Riley, Stephen A. Kania, and Luca Guardabassi. 2013. Genome sequence of Staphylococcus pseudintermedius strain E140, an ST71 European-associated methicillin resistant isolate. Genome Announcements. 1:1-2. MLST

Report to Grant Sponsor from Investigator:

The emergence of methicillin-resistant staphylococci has made the treatment of canine skin infections with Staphylococcus pseudintermedius a difficult challenge. In fact some of these bacteria are resistant to all available antibiotics. There are many unanswered questions regarding antibiotic resistance and the underlying causes of skin infections. In addition, new strategies are needed to prevent and/or treat infections from these organisms such as vaccines or bacteriophage therapy. The foundation of these approaches rests on identification of the major strains of the bacterial species. To attain this goal we developed a new method of genetic tying and hundreds of bacterial isolates were obtained from all regions of the United States. Each sample was studied with regard to spectrum of antibiotic resistance and genetic background and we have made significant progress toward identifying the entire genome of the major strains of the bacterium. Using the latest technology, genomes have been assembled from two isolates representing the major clonal populations of S.pseudintermedius. We have nearly completed assembling the genomes of three additional genomes and plan to assemble a total of seven genomes. This project has provided important new information by identifying all of the thousands of genes contained within two isolates representing the most frequently occurring type of the bacterium. This information is being used to determine the role of the gene products in infection, to identify new targets for vaccine development, and to better understand the spread of antibiotic resistance between bacteria.