

**AGRICULTURAL RESEARCH FOUNDATION
FINAL REPORT
FUNDING CYCLE 2013 – 2015**

TITLE: *Chlamydia abortus* genome sequencing and analysis

RESEARCH LEADER: Daniel D. Rockey

COOPERATORS: The project is a collaboration between my group, Chuck Estill of the OSU CVM Clinical Sciences Department, and Bernhard Kaltenboeck of Auburn University.

SUMMARY: Ovine Enzootic Abortion (OEA) is a disease associated with infection of pregnant ewes by the bacterial pathogen *Chlamydia abortus*. The pathogen is present in sheep flocks in most countries, including the USA, and can be a substantial burden both in terms of sheep health and economic productivity. In some areas, this disease is a major limitation to profitability.

Using culture-independent technologies, recently developed in our laboratory, we have isolated and whole-genome sequenced 12 strains of *C. abortus* sourced from infected placenta tissues from farms, and acquired and sequenced 6 historical strains. Using comparative genomics we have obtained a broad view of the variation in genomic structure in populations of the pathogen across a large geographical region.

OBJECTIVES: Generate genome sequence analysis form uncultured *Chlamydia abortus* specimens, and determine the level of variability among strains in the Western United States.

PROCEDURES: Sample acquisition from producers and diagnostic laboratories, use commercial kits to purify DNAs, use the OSU CGRB to generate raw sequence data, us contemporary bioinformatics programs to assemble and compare the genomes.

SIGNIFICANT ACCOMPLISHMENTS: Our results demonstrated that the species is highly conserved across the western USA, perhaps as conserved as any species should be expected to be. We have generated a useful collection of genome sequences that will be of interest to individuals in the research community.

Our sequencing was conducted by my graduate student Tim Putman and served as a major aspect of his thesis. He delivered a poster on this subject at the recent Chlamydia Basic Research Society meeting and we are in the later stages of a manuscript describing the results. Tim has moved onto a postdoctoral position in San Diego, and this project was an important contributor to his competitiveness for success in his search for employment.

BENEFITS & IMPACT: The basic science applications in the previous section, plus the ability to evaluate whether or not contemporary vaccines that are used in preventing this disease are similar enough to be globally useful to sheep farmers. The sequence data says that it is likely the vaccine is similar to most strains causing problems in the Western United States.

ADDITIONAL FUNDING RECEIVED DURING PROJECT TERM: **none**

FUTURE FUNDING POSSIBILITIES: This is a developing project and we hope to turn our work into preliminary data for a federal research grant proposal.