This project has allowed us to conclude that current diagnostic tools used in veterinary medicine are not providing an accurate diagnostic for Lyme disease, giving many false negatives (66% of the cases) as well as false positives (25% of the cases). The statistical analysis of all three serological testing methods used (IFA, Western Blot, and ELISA) led us to the conclusion that P66 a surface antigen of the bacterium *Borrelia burgdorferi*, the causative agent of Lyme disease, is a better candidate for the development of a more sensitive diagnostic tool. The development of this test will result in better diagnostics to be used in veterinary medicine to detect vector borne zoonotic diseases, having a high impact not only on animal but also on human health. Specifically, with better diagnostic tests, the efficacy of available treatments in both animal and human medicine will increase considerably. The preliminary maps generated with this study start pointing a distribution of veterinary Lyme disease very similar to that observed in the human population, with the added value that the animal Lyme disease is closer to the natural areas where the infection happens. Additionally, by using the same diagnostic tools in both human and veterinary medicine comparative studies and more accurate predictions of distribution and dissemination of the disease in areas where this disease is not well understood will arise. Consequently, when using the same techniques, we observed that most of the human and animal cases are reported around the big metropolitan areas in Texas (Austin, Dallas, Fort Worth, and Houston) and along the border of Mexico. This observation might be due to the fact that both physicians and veterinarians in those urban metropolitan areas are more aware of the disease than those practicing in rural areas. In addition to this study, our laboratory is collecting ticks from different areas in Texas in order to correlate the presence of Lyme disease in human and animals to the areas in the state that might be maintaining the pathogen in nature, and can be consider as the areas with high risk for infection with the disease. In addition, a diagnostic test that is not host species specific will be of great value when establishing surveillance programs, because it avoids the generation of reagents for each specific animal species to be monitored. The methodology we are trying to develop will decrease the amount of errors that occur from the current testing method. This project is still a work in progress. Due to time constraints we have only been able to test dog serum thus far,
making it our animal model. However, other animal (cattle, horses, and white tail deer) sera will be analyzed following the same methodology. By testing a larger number of samples and a variation of species, this testing method will improve diagnostic tests and the surveillance of Lyme disease in states where the distribution of the disease and its maintenance in nature is not well understood.

This work in currently being done at the Department of Veterinary Pathobiology, College of Veterinary Medicine and Biomedical Sciences at Texas A&M University by two students Erin McGregor and Juang M Pavey participating in an Undergraduate Math Biology Program funded by NSF. Dr. Maria Esteve-Gassent (Mentor and Lead investigator), Dr. May Bogges (statistician), and Sandy Rodgers (at the Texas Veterinary Medical Diagnostic Laboratory). The work has been funded by the State of Texas AgriLife seed grants. 112th Annual General Meeting of the American Society for Microbiology, June 16th-19th 2012, San Francisco, CA.