Infectious disease in cattle production remains a significant threat to productivity, profitability, animal welfare, and food safety. Concerns regarding the development of resistant bacterial populations associated with antimicrobial use in food-producing animals and the limitations of biocontainment and biosecurity procedures in contemporary production systems underscore the need for novel approaches to disease control. One of the opportunities to mitigate infectious disease threats is to use genetic selection for cattle with natural resistance to infectious disease.

Resistance to infectious diseases is controlled in large part by the immune system, which includes a complex array of immune cells and cytokines, all of which are regulated by genetic factors. Progress in our understanding of the bovine genome and rapidly expanding technologies for genotyping cattle and analyzing complex genetic data have opened the door for identification of markers associated with disease resistance for use in marker-assisted selection. Further, expanded knowledge of the role of genetics in resistance to infectious disease improves our understanding of the underlying pathophysiology of these infections.

Paratuberculosis, commonly referred to as Johne’s disease, is an inflammatory bowel disease of cattle caused by Mycobacterium avium subsp. paratuberculosis (MAP). There are no effective therapies for treating cattle with Johne’s disease and vaccines are currently not available to prevent infection. These challenges to disease control make Johne’s disease an ideal target for studies of genetic resistance to infection. Researchers at Texas AgriLife Research and in the College of Veterinary Medicine and Biomedical Sciences have been studying Johne’s disease for several years and have been recognized internationally for their expertise in the disease in beef cattle. Completed research has identified familial associations with the development of anti-MAP antibody and has developed methods for describing familial aggregation of Johne’s disease in beef cattle populations of unknown pedigree.

Objectives
- To identify genetic polymorphisms associated with Johne’s disease in cattle for use in marker-assisted selection
- To differentiate genetic regulation of resistance to MAP infection from the development of antibody response to Mycobacterium spp. exposure
- To develop methods for the analysis of complex genotyping data in cattle including arrays with thousands of genetic markers
- To estimate the effect of marker-assisted selection on disease transmission and reduction of populations at risk of infection