ABSTRACT

TITLE:	Development of Q-Pcr Technique for Determining Bartonella Infection in Wild Deer Mice (Peromyscus Maniculatus)
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ABSTRACT: Sin Nombre virus (SNV) is a North American hantavirus that causes Hantavirus Pulmonary Syndrome (HPS) in humans, an acute and rapidly progressing disease with high (~40%) mortality rates. Deer mice (Peromyscus maniculatus) are the primary mode of human HPS infection; humans become infected with SNV via inhalation of virus particles shed through deer mouse excrement. It is unknown whether chronic infection with SNV impacts the ability of deer mice to respond to other immune challenges. This has significant implications for the deer mouse - SNV system, as deer mice with reduced immunocompetence may shed greater amounts of SNV, increasing the likelihood of human SNV infection. Thus, our objective was to develop a protocol in which we could quantify Bartonella, a bacterial pathogen that is endemic in wild rodents, through Q-PCR. Similar to SNV, Bartonella has low pathogenicity, but requires that deer mice mount a chronic, low-level immune response post infection. For the development of a Q-PCR assay, we are using the forward and reverse primers BhC5781p (5'-GGGGACCAGCTCATGGTGG-3') and BhCS1137n, (5'-AATGCAAAAAGAACAGTAAACA-3' respectively. Q-PCR trials were completed using serum and whole blood; however, we were unable to isolate and amplify Bartonella DNA using serum and whole blood alone. DNA isolation appears to be a necessary step to detect the presence of Bartonella DNA in the deer mouse whole blood samples. The further development of this protocol will allow us to determine the extent to which SNV and Bartonella infections are correlated. This research will ultimately improve our ability to predict human patterns of infection with zoonotic pathogens.