

Presented in this talk is a system of ordinary equations used to model the prevalence of *Rickettsia amblyommii*, a member of the Spotted Fever Group, and *Ehrlichia chaffeensis*, the pathogen responsible for Human Monocytic Ehrlichiosis, within a single-vector, (*Amblyomma americanum*, the Lone star tick), two-host (*Odocoileus virginianus* - the White-tailed deer – and *Procyon lotor* – the North American Raccoon) environment. Though a number of models exist describing dynamics of pathogens within a host-vector system this will be the first to incorporate multiple hosts and a full tick life stage. This talk will focus on the equation development and contain a short parameter exploration. Emphasis will be on the free parameters and their effects on the system when modified from a baseline case.