

In this talk, the speaker will present recent theoretical results from the dynamics of a two-vector, two-pathogen, single host model. A system of ordinary differential equations is used to model the dynamics of two vector-borne pathogens (*Rickettsia parkeri* and *Rickettsia amblyommii*) that are increasingly found within tick populations of Virginia spread by two species of ticks (*Amblyomma maculatum* and *Dermacentor variabilis*), within a single host system. Three methods of transmission are included in the model: vector-borne, transovarial, and co-feeding. Results of numerical simulations are presented and determine a range of parameter values which lead to coexistence of the two pathogens and values which lead to the extinction of one pathogen and persistence of the other.