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Dynamics of two pathogens in a single tick population

Alexis White

Old Dominion University, awhit130@odu.edu

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Dynamics of two pathogens in a single tick population

Alexis White

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A mathematical model for a two-pathogen, one-tick, one-host system is presented and explored. The model system is based on the dynamics of *Amblyomma americanum*, *Rickettsia parkeri*, and *Rickettsia amblyommii*. The model includes three types of transmission strategies that have been established within the laboratory setting, including vector-borne, transovarial, and cofeeding. The numerical simulations of the model demonstrate the parameter ranges that allow for coexistence. The model is applied to a case study based on a reclaimed swampland field site in southeastern Virginia, and the results pinpoint the thresholds required for persistence of both pathogens in the local tick population. Using field and laboratory data the long term persistence of both *Rickettsia* species is compared to empirical data. Understanding the persistence and coexistence of tick-borne pathogens will allow public health officials increased insight into tick-borne disease dynamics.