Modeling Within-Vector Viral Kinetics in a Multi-Scale Vector-Host Model

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A current challenge for disease modeling and public health is understanding pathogen dynamics across scales since their ecology and evolution ultimately operate on several coupled scales. This is particularly true for vector-borne diseases, where within-vector, within-host, and between vector-host populations all play crucial roles in diversity and distribution of the pathogen. Despite recent modeling efforts to determine the effect of within-host virus-immune response dynamics on between-host transmission, the role of *within-vector viral dynamics* on disease spread is overlooked. Here we formulate an age-since-infection structured model where epidemic model parameters are governed by ODE systems describing within-host immune-pathogen dynamics and within-vector viral kinetics. We define the *basic reproduction number*, $\mathcal{R}_0$ and study the threshold dynamics of the system. Numerical results suggest that within-vector-viral kinetics may play a substantial role in epidemics. Finally, we address how the model can be utilized to better predict the success of control strategies such as vaccination, or Wolbachio-based biocontrol.