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Hayriye Gulbudak* (hayriye.gulbudak@louisiana.edu), Lafayette, LA. *An Immuno-Epidemiological Vector-Host Model with Within-Vector Viral Kinetics*. Preliminary report.

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. Here we formulate an age-since-infection structured epidemic model coupled to nonlinear ordinary differential equations describing within-host immune-virus dynamics and within-vector viral kinetics, with feedbacks across these scales. We first define the *within-host viral-immune response and within-vector viral kinetics dependent* basic reproduction number \mathcal{R}_0 , and then investigate the threshold dynamics of the system. Furthermore, we numerically show that within-vector-viral kinetics and dynamic inoculum size may play a substantial role in epidemic spread. Finally, we address how the model can be utilized to better predict the success of control strategies such as vaccination and drug treatment. (Received January 21, 2020)