

Contribution ID: 59

Type: **Oral Presentation**

Signatures of within-host dynamics of dengue at a population level

Monday, 9 July 2018 10:30 (30 minutes)

Vector-borne diseases cause worldwide concern with hundreds of millions of new cases and over a million deaths reported annually. Mathematical models are a key tool in the study of the spread of diseases such as malaria and dengue. In particular, transmission models have been successful at determining the most promising intervention strategies, despite the fact that many of these models assume all individuals experience identical infections. Within-host dynamics of infections, however, vary widely among individuals. In the case of dengue, within-host dynamics differ between primary and secondary infections, where secondary infections with a different virus serotype typically last longer, produce higher viral loads, and induce more severe disease. Here, we build upon models of variable within-host dengue virus dynamics resulting in mild dengue fever and severe dengue hemorrhagic fever by coupling them to a population-level model. The resulting multiscale model examines the dynamics of between-host infections in the presence of two circulating virus strains that involves feedback from the within-host and between-hosts scales. We analytically determine a threshold under which infections persist in the population.

Primary authors: NIKIN-BEERS, Ryan (Virginia Tech); BLACKWOOD, Julie (Williams College); CHILDS, Lauren (Virginia Tech); CIUPE, Stanca (Virginia Tech)

Presenter: CHILDS, Lauren (Virginia Tech)

Session Classification: Advances in mathematics of infectious diseases

Track Classification: Minisymposium: Advances in Mathematics of Infectious Diseases