Reducing Mathematical Models for *Wolbachia* Transmission in Mosquitoes to Control Mosquito-borne Diseases

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We develop and analyze a reduced model for the spread of *Wolbachia* bacteria infection in wild mosquitoes. *Wolbachia* is a natural parasitic microbe that can reduce the ability of mosquitoes to spread mosquito-borne viral diseases such as dengue fever, chikungunya, and Zika. It is difficult to sustain an infection of the maternally transmitted *Wolbachia* in a wild mosquito population because of the reduced fitness of the infected mosquitoes and cytoplasmic incompatibility limiting maternal transmission. The infection will only persist if the fraction of the infected mosquitoes exceeds a minimum threshold. This threshold can be characterized as a backward bifurcation for a system of nine ordinary differential equations modeling the complex maternal transmission of the bacteria infection in a heterosexual mosquito population. Although the large system of differential equations capture the detailed transmission dynamics, they are difficult to extend to account for the spatial heterogeneity of *Wolbachia* infection when releasing the infected mosquitoes into the wild. We derive a seven-equation, a four-equation and a two-equation system of differential equations that are formulated in terms of the more accurate nine-equation model and capture the important properties of the original system. The reduced models preserve the key dimensionless numbers, such as the basic reproductive number, and accurately capture the backward bifurcation threshold. We are extending the differential equation model to account for the spatial heterogeneity of the *Wolbachia* infection when mosquitoes are released into the wild to better understand when local high infection region will grow or shrink.

⋆Mini-Symposium: Density dependence in mosquito populations: implications for control