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The Role of Variation in Mate Choice and Wolbachia Infection on *Aedes Aegypti* Population Dynamics

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The Role of Variation in Mate Choice and Wolbachia Infection on *Aedes Aegypti* Population Dynamics

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MTBI

Wolbachia, an endosymbiont bacteria, is common in various invertebrates and known for host reproductive manipulation strategies as well as for slowing the replication of certain viruses. When infected by Wolbachia, *Aedes aegypti* mosquitoes become resistant to transmitting some mosquito-borne diseases (MBD) such as dengue, diseases prevalent in tropical and subtropical regions.

Releasing a large number of Wolbachia infected mosquitoes in the environment is assumed to be a more effective strategy than other various methods to control the spread of MBD. However, evaluation of such Wolbachia-based interventions over a long term temporal scale is limited in the literature. Moreover, the Wolbachia's host manipulation strategy, cytoplasmic incompatibility (CI), benefits the Wolbachia in the form of decreasing the number of non-infected mosquitoes. Additionally, Changes in mating preference could impact the benefit from CI, as it requires that infected males mate with uninfected females.

We developed and analyzed models that capture the life cycle and mating preference of mosquitoes with and without Wolbachia. Our research primarily focuses on the effects of non-random mating on the population dynamics of mosquitoes. The analysis of models suggest that Wolbachia persists in the mosquito population as long as a sufficiently large Wolbachia infected mosquito population (critical population size) is released. This critical population size is a function of mating-related factors and stage progression rates.

We hope that the results of this modeling study will help in identifying significant change to the dynamics which could better inform us about the effectiveness and sustainability of this method to combat MBD.

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