Quantifying Heterogeneity in Within-Mosquito Malaria Parasite Dynamics

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The malaria parasite *Plasmodium falciparum* requires a vertebrate host, such as a human, and a vector host, the *Anopheles* mosquito, to complete a full life cycle, with sexual reproduction occurring in the vector host. This sexual stage of the parasite life cycle creates opportunities for the production of genetically novel parasites. In the meantime, a mosquito's biology creates bottlenecks in the infecting parasites' development. In previous work, we developed a two-stage stochastic model of the generation of parasite diversity within a mosquito, and were able to demonstrate the importance of heterogeneity amongst parasite dynamics across a population of mosquitoes on estimates of parasite diversity. Empirical data confirms the presence of this heterogeneity in mosquitoes infected in the lab. We use Bayesian inference techniques with simple models of within-mosquito parasite dynamics and experimental data to estimate a posterior distribution of parameter estimates to (1) determine the identifiability of model parameters, (2) estimate the degree of heterogeneity in parameters associated with parasite expansion and different life-stage transitions within mosquitoes, and (3) investigate possible density-dependent relationships between transition rates and parasite densities.

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