Emergence and maintenance of malaria parasite diversity across scales

Lauren Childs

Virginia Tech

The deadliest human malaria parasite, Plasmodium falciparum, exhibits high genetic diversity in many contexts despite evolutionary mechanisms that one would expect to limit diversity, such as severe bottlenecks in population size at several points in the parasite life cycle. To address this conundrum, we develop an individual-based multi-scale model mathematical model of malaria transmission specifically accounting for the within-human and within-vector population dynamics as well as representative genetic sequences. The model is an expansion of previous work focused on the within-vector genetic and population dynamics, that showed that diversity greatly increases within the mosquito despite the restrictive bottleneck within the oocyst stage. Using large-scale stochastic simulations, we generate synthetic data to assess the role of various evolutionary pressures (e.g., acquired immunity, drug resistance, transmission intensity) on the emergence and maintenance of parasite genetic diversity. Furthermore, we compare parasite diversity, using metrics including population richness and nucleotide diversity, at different scales (e.g., within-vector, within-human, community level, population level) to assess evolution at different scales.

In Special Session 64 on Dynamics of Infectious Diseases: From Within-host to Population-level at the Mathematical Congress of the Americas 2025.

MCA 2025 internal code: SS64-T01