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Changes in the relative abundances of clones in genetically complex *Plasmodium* infections

Malaria parasites (*Plasmodium* species) are a major public health concern and socio-economic burden in many areas of the world, causing severe illness in human populations and killing millions of people each year. These species have also been implicated in major wildlife die-offs. The genetic diversity of parasite populations has significance for studies of infection dynamics, clonal interactions, and gametocyte sex ratios. A study of human malaria conducted in Papua New Guinea demonstrated an apparent cycling of dominant parasite species over the course of mixed-species infections. It is not known, however, whether similar changes in relative abundances occur among genotypes in single-species, multi-clonal *Plasmodium* infections. Using simulated genetically complex *P. mexicanum* and *P. falciparum* infections and three variable microsatellite markers, we have developed a novel method of quantifying shifts in relative clonal proportions based on electropherogram peak heights. This technique will be used to follow experimentally induced *P. mexicanum* infections of known parasite density in western fence lizards. We will investigate the hypothesis that the relative abundances of co-infecting parasite clones in the blood of a host fluctuate over time due to either competitive or cooperative clonal interactions. We will consider infections that continuously increase in parasite density, eventually leading to the death of the lizard host, and those that reach a certain parasitemia and remain at that level of infection. We expect to see continuous shifting of relative clonal proportions both during periods of increasing parasitemia and during periods when parasitemia remains constant, which will suggest clonal interactions rather than random fluctuations in the reproduction rates of individual genotypes.