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March 18, 2011

SRC Application Abstract

Project Title: Dynamics of clonal diversity within natural infections of a malaria parasite, *Plasmodium mexicanum*

Abstract:

Infections of *Plasmodium spp.*, the causative agent of malaria, can exist within a host as a genetically uniform population of asexually dividing clones, or as mixture of genetically distinct clones which could potentially compete for resources and affect the evolution of virulence. Studies of the dynamics of clonal diversity within infections of *Plasmodium* have appeared over the past decade; however, the methods allowing for the quantification of relative proportions of various clones within an infection, and thus the nature of competitive interactions, have been developed only recently. The present study follows the relative proportions of genetically distinct populations of *P. mexicanum* clones coexisting in their natural lizard host, *Sceloporous occidentalis*. A total of 27 free ranging lizards were selected from two mark-recapture studies. One study followed individual lizards over the course of two summers from 1996 to 1997 and the other was performed over a single summer in 2010. I extracted *P. mexicanum* DNA from blood samples taken from studied lizards and amplified two polymorphic microsatellite loci using PCR which were then analyzed by capillary electrophoresis. The resulting electropherograms were used to score the number of alleles present, and thus number of clones, as well as the relative proportion of each clone. Preliminary results indicate a high level of stability of diversity within infections both with regards to clone identity and relative proportions. Loss of clones as well as superinfection by novel clones also appear to be uncommon. This is the first study to follow relative proportions of clones of a *Plasmodium* species in natural infections over long periods and opens a new window into the biology of malaria parasites.

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