EVOLUTION OF AVIAN MALARIAL PARASITES IN GEOGRAPHICALLY STRUCTURED HOST SPECIES: A PHYLOGENETIC APPROACH

J. M. Moser and Garth M. Spellman
Biology Department
Black Hills State University
Spearfish South Dakota 57799

ABSTRACT

Avian malarial parasites are a diverse group of protozoans (*Plasmodium* and *Haemoproteus*) that are globally distributed and transmitted by several different families of blood-feeding dipteran vectors. Modern molecular techniques (DNA sequences) have significantly increased our understanding of the speciation and transmission of these parasites within their hosts across broad geographic scales. Phylogenetic studies of malarial parasite DNA sequences have revealed a substantial number of cryptic species which can be identified within traditionally recognized morpho-species of parasites and that these lineages can have unique ecological properties and varied evolutionary histories. The revelation of these cryptic species challenges previous hypotheses of high transmission rates of these parasites via long distance migration, and instead suggests allopatric speciation and host switching within geographic areas strongly influence parasite evolution. In this study, we examined avian malarial parasite diversity (using malarial cytochrome *b* sequence data) within several geographically structured avian species from North American pine and oak woodlands. This was done by using a PCR-based assay to detect parasite lineages in their host then analyzing these lineages using traditional phylogenetic techniques. Our study shows that both traditional (high transmission rates via long distance migration) and modern (allopatric speciation and host-switching in restricted geographic areas) hypotheses can explain the evolution of malarial parasites in North American pine and oak woodland birds. The high transmission rates observed in long distance migrants suggest that disease can be transported easily over great distances in avian hosts, and a cause for concern if these birds were to come in contact with diseases that pose a threat to human health.