MALARIAL PARASITE INFECTION AND MHC VARIABILITY IN THE WHITE WINGED JUNCO

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ABSTRACT

Avian malarial parasites play an important role in the study of human malaria, being a stimulus for the development of medical parasitology. Malarial parasites’ use in epidemiological and ecological investigations has led to many new insights into the evolution of host-parasite-vector interactions. These parasites are one of the most well known and well studied groups of parasitic protists. With the introduction of molecular screening techniques, the diversity of avian malaria parasites has increased from what was previously thought. In this study, we examined the impacts of seasonality, sex, body condition, and genetic variation at immune related major histocompatibility class I alleles on malarial infection rates in the white-winged junco (Junco hyemalis aikeni), a subspecies of the dark-eyed junco endemic to the Black Hills. We found that the diversity of malarial parasite lineages in this species changes. Malarial infection rates in males were significantly higher than in females. There was also a significant association with malaria infection and body condition as measured by mass, indicating infection adversely impacts health. To further elucidate the impacts of the malarial parasites, we are now examining loci of the major histocompatibility complex (MHC) in the Black Hills junco. Previous studies have shown that parasite and pathogen diversity promotes diversifying selection in MHC loci. Thus, individuals with higher heterozygosity at MHC loci should have lower infection rates, possibly indicating increased immune function.