

1. Record Nr.	UNINA9910249958903321
Autore	Svensson-Coelho Maria
Titolo	Diversity, prevalence, and host specificity of avian Plasmodium and Haemoproteus in a Western Amazon assemblage // Maria Svensson-Coelho, John G. Blake, Bette A. Loiselle, Amanda S. Penrose, Patricia G. Parker, and Robert E. Ricklefs
Pubbl/distr/stampa	The American Ornithologists' Union
Disciplina	598.8
Soggetti	Passeriformes - Parasites - Ecuador Host-parasite relationships
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	<p>We used PCR and DNA sequencing to screen for haemosporidian parasites (Haemoproteus and Plasmodium) in 2,488 individual birds from 104 species and 22 families, primarily understory suboscine passerines, captured in a lowland Amazonian forest in Ecuador as a first major step to understanding the transmission dynamics of this cosmopolitan group of parasites in this region. To assess diversity of avian haemosporidia in our study site, we identified putative evolutionary lineages of haemosporidia using the mtDNA gene cytochrome b (cyt b). We sampled birds over 9 years, which allowed us to assess annual variation in haemosporidian prevalence. Additionally, we investigated among-species variation in prevalence and tested relationships between traits of hosts and prevalence of haemosporidia in a comparative analysis. Finally, we estimated host specificity of each recovered parasite lineage and compared several indices with different details of host information. Prevalence of haemosporidia was 21.7% when we combined years and ranged from 5.6% to 91.2% among well-sampled host species. Prevalence varied significantly among years, ranging from 14.5% in 2006 to 33.2% in 2009. The hypothesis that haemosporidian prevalence increases with level of sexual dimorphism</p>

and decreases with foraging height of a host species received some support. We identified 65 unique cyt b haplotypes, some of which we considered variation within the same evolutionary lineage. In total, we defined 45 putative evolutionary lineages based on 363 identified parasites. Fourteen haplotypes were identical to haplotypes found elsewhere, sometimes on different continents. Host specificity varied greatly among parasite lineages. Collectively, our findings indicate that within a local Neotropical assemblage of avian haemosporidia, community organization is highly complex and part of this complexity can be attributed to differences in host life history; diversity, particularly of *Plasmodium* spp., is high; and individual parasite lineages can differ greatly in both abundance and number of host species.
