Ornithological Monographs
Volume (2013), No. 76, 1–47
© The American Ornithologists' Union, 2013.
Printed in USA.

DIVERSITY, PREVALENCE, AND HOST SPECIFICITY OF AVIAN *PLASMODIUM* AND *HAEMOPROTEUS* IN A WESTERN AMAZON ASSEMBLAGE

Maria Svensson-Coelho,[1,2] John G. Blake,[1,3] Bette A. Loiselle,[1,3] Amanda S. Penrose,[1] Patricia G. Parker,[1] and Robert E. Ricklefs[1]

[1]*Department of Biology, University of Missouri–St. Louis, One University Boulevard, St. Louis, Missouri 63121, USA*

Abstract.—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 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. *Received 15 August 2012, accepted 1 March 2013.*

Key words: avian blood parasites, avian malaria, community ecology, compound community, Neotropics, parasite diversity, parasite prevalence.

DIVERSITY, PREVALENCE, AND HOST SPECIFICITY OF AVIAN *PLASMODIUM* AND *HAEMOPROTEUS* IN A WESTERN AMAZON ASSEMBLAGE

Resumo.—Nós usamos PCR e sequenciamento de DNA para identificar infecções de parasitas hemosporídeos (*Haemoproteus* e *Plasmodium*) em 2.488 indivíduos pertencentes a 104 espécies e 22 famílias de aves (primariamente passeriformes suboscines) em uma localidade

[2]Present address: Departamento Genética e Biologia Evolutiva, Instituto de Biosciências, Universidade de São Paulo, Edifício André Dreyfus, Rua do Matão, 277, São Paulo, Brazil. E-mail: mariasve@usp.br

[3]Present address: Department of Wildlife Ecology and Conservation and Center for Latin American Studies, 110 Newins-Ziegler Hall, P.O. Box 110430, University of Florida, Gainesville, Florida 32611, USA.

Ornithological Monographs, Number 76, pages 1–47. ISBN: 978-0-943610-95-5. © 2013 by The American Ornithologists' Union. All rights reserved. Please direct all requests for permission to photocopy or reproduce article content through the University of California Press's Rights and Permissions website, http://www.ucpressjournals.com/reprintInfo.asp. DOI: 10.1525/om.2013.76.1.1.