

Terça 11:00 às 12:00

Auditório 1

ASSEMBLAGE OF AVIAN HAEMOSPORIDIAN IN TWO ECOSYSTEMS OF NORTHEAST BRAZIL

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We studied the assemblages of avian haemosporidian parasites in three protected areas of the Caatinga (Raso da Catarina Ecological Station, RCES) and Atlantic Forest (Restinga de Cabedelo National Forest, RCNF and Guaribas Biological Reserve, GBR). Extracted DNA was screened for Plasmodium/Haemoproteus by amplifying a segment of mtDNA. For the positive samples, a fragment of ~550-600 bp was amplified from cytochrome b (cyt b) and sequenced. We considered each haplotype as an independent lineage and analyzed variation in prevalence and 'well-sampled' host species among the phylogeographic domain, protected areas and vegetation type sampled using the G-test adjusted for small sample size. Overall, 699 individuals from 104 species in 33 families were analyzed, of which 126 (18.0%) yielded parasite cyt b sequence from 41 host species. The overall prevalence was similar between phylogeographic domain, protected areas and vegetation type. Prevalence was significantly heterogeneous among species ($G_{adj}=111.4$, $df=15$, $p<0.001$), ranging from zero (*Thamnophilus pelzelni*, *Hemitriccus margaritaceiventer*, *Elaenia cristata*, *Cnemotriccus fuscatus*, *Myiothlypis flaveola*) to 88.24% (*Columbina talpacoti*). Prevalence of Plasmodium as higher at RCNF (22.2%; $G_{adj}=4.8$, $df=1$, $p=0.03$) and GRB (11.5%; $G_{adj}=9.0$, $df=1$, $p=0.003$) than at RCES (4.4%), and Atlantic Forest (12.3%) than Caatinga (4.4%, $G_{adj}=11.1$, $f=1$, $p=0.0009$). Forested habitats presented lower prevalence of Haemoproteus (5.8%, $G_{adj}=8.8$, $df=1$, $p=0.003$) than opened habitats (13.4%). It might be related to the behavior, presence, and density of vectors and to the presence and abundance of competent hosts. Fifteen cyt b sequences showed multiple infections with unrecognized lineage. Haemoproteus prevalence was 8.9% and Plasmodium prevalence was 7.0%, representing 49 mitochondrial lineages: 26 of Plasmodium and 23 of Haemoproteus. One morphospecies, Plasmodium nucleophilum, and 37 new lineages were recovered. Numerous lineages were obtained in this study, following the pattern of other Brazilian ecosystems, which might be associated with high host diversity, in conjunction with the heterogeneity of environments.

Financiamento: CNPq

