RESUMO SIMPLES - PROTOZOÁRIOS E AGENTES TRANSMITIDOS POR VETORES DE IMPORTÂNCIA EM SAÚDE

MOLECULAR DETECTION OF HAEMOSPORIDA PARASITES IN WILD AQUATIC BIRDS FROM LAGO AÇU, UFRRJ, RIO DE JANEIRO, BRAZIL

Nelson Meireles Da Silva (meirelesvet3@gmail.com)

Andressa Kagohara (de.kagohara@gmail.com)

Carla Alves Rabello (carlaalves.rabello@gmail.com)

Karina Cristina Paes Galdino (karinapaes2@gmail.com)

Laís Feliciano De Souza (laisfelicici@gmail.com)

Anieli Vidal Stocco (anielistocoo@gmail.com)

Luiz Ricardo De Oliveira Roberto (luiz_ricardoroberto@yahoo.com.br)

Ana Elisa Barros Medeiros (anamedeiros.aem@gmail.com)

Daniel De Almeida Balthazar (danielbalthazar@yahoo.com.br)

Huarrisson Azevedo Santos (huarrisson@yahoo.com.br)

Avian haemosporidians of the genera Plasmodium, Haemoproteus and Leucocytozoon are vector-borne protozoans that infect a wide range of bird species, playing important roles in host ecology and parasite diversity studies. Despite their relevance as indicators of ecosystem health, information on Haemosporida diversity in wild birds from southeastern Brazil remains limited. This study aims to detect and molecularly identify Haemosporida species infecting aquatic birds from Lago Açu, located on the campus of the Federal

Rural University of Rio de Janeiro (UFRRJ), Seropédica, Rio de Janeiro, Brazil. A total of 22 birds were sampled using mist nets positioned along the lakeside area, including Neotropical cormorants (Phalacrocorax brasilianus), great and snowy egrets (Ardea alba, Egretta thula), cattle egret (Bubulcus ibis), striated herons (Butorides striata), roseate spoonbills (Platalea ajaja), wattled jacanas (Jacana jacana), and a ringed kingfisher (Megaceryle torquata). All sampling procedures were conducted in accordance with institutional ethical guidelines (CEUA nº 8856050525, ID 003003). Blood samples were collected on FTA cards and stored for molecular analysis. DNA extraction was performed using the Invitrogen kit, and Haemosporida detection was conducted by nested PCR, targeting the mitochondrial cytochrome b gene for Plasmodium, Haemoproteus, and Leucocytozoon. Amplicons were visualized on agarose gels and sequenced using the Sanger method. Sequence identity was verified through BLAST comparisons with GenBank data. Four of the twenty-two analyzed samples (18.18%) tested positive for Haemosporida, revealing the presence of Plasmodium nucleophilum, Plasmodium sp. isolate UR050 (OP087640.1), Plasmodium sp. (GQ141569.1), and Haemoproteus sp. (MN150702.1). Positive samples were obtained from one snowy egret (Egretta thula), one cattle egret (Bubulcus ibis), one striated heron (Butorides striata), and one roseate spoonbill (Platalea ajaja). The first three were infected by Plasmodium spp., while Haemoproteus sp. was found exclusively in the spoonbill. No samples were positive for Leucocytozoon. The observed infection rate suggests active circulation of Haemosporida in aquatic birds from Lago Açu. Sampling and laboratory processing are still ongoing, and additional data are expected to expand the molecular database for local Haemosporida lineages. For this reason, the phylogenetic analysis has not yet been completed, but it will be conducted to clarify the genetic relationships and potential host specificity of the detected parasites. These preliminary results contribute to the understanding of avian blood parasite diversity in southeastern Brazil and highlight the importance of continued molecular and ecological surveillance in anthropogenic wetland environments.

Palavras-chave: avian malaria; molecular diagnostics; sequencing.