RESUMO SIMPLES - HELMINTOLOGIA: SISTEMÁTICA, EPIDEMIOLOGIA E CONTROLE

MOLECULAR DETECTION OF FILARIOID NEMATODES (NEMATODA: ONCHOCERCIDAE) IN WILD MAMMALS FROM DIFFERENT BRAZILIAN BIOMES

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Filariasis is defined as a group of diseases caused by parasitic nematodes belonging to the superfamily Filarioidea, which is classified into the families Filariidae and Onchocercidae, considered a relatively small group within the extensive phylum Nematoda. Filarioid nematodes are transmitted by mosquitoes (Culicidae), black flies (Simuliidae), and other blood-feeding arthropods. Several genera and species of filarioid nematodes are known to be

of significant medical and veterinary importance. In humans, they are the primary etiological agents of lymphatic filariasis and river blindness, among other diseases. This study investigated the molecular occurrence of filarioid nematodes in 93 wild mammals from the Amazon, Cerrado, and Pantanal biomes in Brazil, based on analyses of the mitochondrial genes 12S ribosomal DNA (12S rDNA) and cytochrome c oxidase subunit I (COI). Biological samples from free-ranging and captive wild mammals were collected under approval from the Ethics Committee on Animal Use (CEUA) and the Brazilian System of Authorization and Information on Biodiversity (SISBIO). Authorizations were granted for research projects conducted by the wildlife conservation and management group at the Federal University of Mato Grosso do Sul (CEUA protocols: 628/2014, 727/2015, 1035/2019, 1221/2022, and 1355/2024; SISBIO authorizations: 46031-4, 57293-3, 68167-1, 72633-8, and 757626), as well as by the University of São Paulo (CEUA protocol: 74398-2; SISBIO: 6429170220). DNA samples extracted from blood were subjected to conventional polymerase chain reaction (cPCR) targeting the 12S rDNA gene, which yielded positive results in 14.44% (13/93) of the samples: 9.86% of jaguars (7/71), 50% of pumas (1/2), 12.5% of giant anteaters (1/8), 50% of ocelots (1/2), and 60% of crab-eating foxes (3/5). Among the 12S-positive samples, 46% (6/13) also tested positive for the COI gene; however, only one sequence was suitable for further analysis. Phylogenetic analyses based on 12S gene sequences revealed four distinct lineages within the family Onchocercidae. Groups Ia and Ib, composed of Cerrado and Pantanal sequences from jaguars, formed sister clades to Brugia pahangi and Malayfilaria sofiani, respectively. The sequence from the giant anteater (Group Ic) was more divergent, forming a sister clade to species of the genera Malayfilaria, Wuchereria, and Brugia. Group II included sequences closely related to Dirofilaria immitis and D. striata, encompassing samples from crab-eating foxes, ocelots, and one puma. These findings suggest that several wild mammal species may serve as reservoirs for previously uncharacterized Onchocercidae nematodes. Our results expand the existing knowledge on host associations of filarioid nematodes infecting wild mammals from the Pantanal, Cerrado, and Amazon Rainforest.

Palavras-chave: biodversity; filarioidea; south america; zoonosis.