FIRST MOLECULAR CONFIRMATION OF ZOONOTIC CILIATE PARASITE IN BRAZILIAN TAPIRS

BRENO TORRES DA SILVA[1], CAMILA SOUZA CARVALHO CLASS[1], RODRIGO HIDALGO FRICIELLO TEIXEIRA[2,3,4], MARON GALLIEZ[5], ELAN CARDOZO PAES DE ALMEIDA[1], LAÍS LISBOA CORRÊA[1], LAÍS VERDAN DIB[6], ALYNNE DA SILVA BARBOSA[1]

[1]UNIVERSIDADE FEDERAL FLUMINENSE, RIO DE JANEIRO, BRASIL, [2]PARQUE ZOOLÓGICO QUINZINHO DE BARROS, SÃO PAULO, BRASIL, [3]UNIVERSIDADE PAULISTA JÚLIO DE MESQUITA FILHO, SÃO PAULO, BRASIL, [4]UNIVERSIDADE DE SOROCABA, SÃO PAULO, BRASIL, [5]INSTITUTO FEDERAL DE EDUCAÇÃO, CIÊNCIA E TECNOLOGIA DO RIO DE JANEIRO, RIO DE JANEIRO, BRASIL, [6]FACULDADE DE MEDICINA DE CAMPOS, RIO DE JANEIRO, BRASIL.

Over the years, the mammalian fauna has been declining, with *Tapirus terrestris*, known as the tapir, standing out in this scenario. In Rio de Janeiro, the tapir became extinct, and its reintroduction began in 2017 at the Guapiaçu Reserve (REGUA). Among the various causes for the decline of fauna, parasitic infections are included. This study aimed to investigate gastrointestinal parasites in tapirs, with an emphasis on the Ciliophora Group. Between 2023 and 2024, 41 fecal samples were collected from tapirs kept under human care and in the wild. Of these, 21 samples were obtained from tapirs in six institutions in Rio de Janeiro, São Paulo and Minas Gerais. Furthermore, 20 samples were obtained from the REGUA. The feces were collected from enclosures, trails, and carcass and were subjected to microscopic examinations. Those that exhibited forms of ciliated were inoculated in culture medium and the isolates subjected to molecular analysis. For samples that were not isolated, molecular analysis was performed on DNA extracted from the feces. Samples obtained from the Reserve trails were also analyzed to confirm the host through molecular analysis. In total, 70.7% of the samples tested positive for parasites, with an emphasis on the Ciliophora Group (58.5%), followed by strongyle eggs (31.7%) and coccidian oocysts (19.5%). To date, 20 nucleotide sequences have been generated, all of which were identified as *Balantioides coli*. Of these, 11 were classified as A0, 8 as B0, and one as mixed. Both *B. coli* type A0 and B0 sequences were identified in tapirs in Rio de Janeiro, both under human care and in the wild. Only type A0 was identified in the samples from São Paulo. It is worth noting that the A0 variant of *B. coli* has been identified in humans, where it can cause serious dysenteric infections. The results of this study indicate, for the first time, that the tapir serves as a host for *B. coli* and may contribute to the maintenance of this zoonotic parasite in the wild.

Keywords: Wild animals, *Balantioides coli*, Intestinal parasite

Supported By: Faperj, CNPQ.