

RESUMO - PROTOZOOLOGIA E PATÓGENOS TRANSMITIDOS POR
VETORES

**MOLECULAR DETECTION AND CHARACTERIZATION OF PIROPLASMIDS
IN WILD MAMMALS FROM THE BRAZILIAN CAATINGA, WITH A
DESCRIPTION OF A PUTATIVE NOVEL CLADE INFECTING KERODON
RUPESTRIS AND THRICHOMYS APEREOIDES**

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Piroplasmids are tick-borne protozoan parasites of global importance, and key species like *Babesia* and *Theileria* have a widespread distribution, primarily

infecting mammalian hosts and potentially causing disease and economic losses. In the present study we investigated the molecular occurrence of Piroplasmida agents in mammalian blood samples collected from April 2025 to February 2026 in the Monumento Natural Grota do Angico (Mona), a Caatinga preservation area located in the state of Sergipe, northeastern Brazil. We sampled a total of 46 animals: 26 rock cavies (*Kerodon rupestris*), 13 common Punarés (*Thrichomys apereoides*), 4 crab-eating foxes (*Cerdocyon thous*), 2 white-eared opossums (*Didelphis albiventris*) and one black rat (*Rattus rattus*). DNA was extracted and a cPCR based on the mammalian endogenous gene (*gapdh*) was performed to confirm the absence of inhibitors. All samples (46/46; 100%) were positive for this assay and were subsequently submitted to a molecular screening for piroplasmids based on the 18S rRNA genic region. A total of 30/46 (65.2%) samples were positive in that assay [24/26 (92.3%) *K. rupestris*; 6/13 (46.1%) *T. apereoides*; 2/2 (100%) *D. albiventris*]. Those positive samples were then submitted to molecular characterization of piroplasmids, using PCR assays based on distinct molecular markers: 18S rRNA, *hsp70*, *cytB*, *cox-1*, and *cox-3*. The 18S rRNA, *cytB* and *cox-1* sequences obtained from *D. albiventris* showed a high similarity (>99.5%) and were phylogenetically related to *Babesia* sp. sequences from the South America Marsupialia clade previously detected in *D. albiventris* and associated *Amblyomma dubitatum* ticks from Brazil. The sequences (18S rRNA, *cytB* and *cox-1*) obtained from *K. rupestris* and *T. apereoides* showed a higher identity (94.2 to 96.1%) to Piroplasmida sp. sequences from the Phyllostomidae and South America Rodentia clades previously detected in *Phyllostomus discolor* bats and *Thrichomys pachyurus* from the Brazilian Cerrado, respectively. Phylogenetic analyzes based on the 18S rRNA, *cytB* and *cox-1* molecular markers revealed that our sequences clustered together in the same subclade, which was a sister clade to the subclade containing the South America Rodentia and Phyllostomidae bat-associated Piroplasmida sequences, with high bootstrap support values (100 for 18S rRNA, 98 for *cytB* and *cox-1*). These findings suggest that new species of Piroplasmida, positioned in a new piroplasmid clade, occur in rodents from the Brazilian Caatinga, as well as expand the geographical distribution of South American Marsupialia group in the Brazilian territory.

Palavras-chave: piroplasmida; caviidae; rodents; marsupials.