

DETECTION OF PHLEBOTOMINAE TRANSMITTED BUNYAVIRALES COINFECTIONS IN DOGS WITH VISCERAL LEISHMANIASIS IN RIO DE JANEIRO, BRAZIL

Daniel Marcos J. Agostinho ¹, José Vitorino dos Santos ¹, Mariana Boité ², Elisa Cupolilo ², Ulisses Gazos Lopes ¹

1- Laboratory of Molecular Parasitology, Institute of Biophysics Carlos Chagas Filho, Federal University of Rio Janeiro, Brazil. 2 Laboratory of Leishmaniasis Research, Institute Oswaldo Cruz, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil.

Abstract

Leishmaniasis is a parasitic disease caused by protozoans of the Genus *Leishmania*. The disease is widespread worldwide, and in some countries, it is a significant healthcare concern. The Phlebotominae vectors of *Leishmania* may transmit Phleboviruses and Pacuvirus from the Bunyavirales Order. These viruses also pose a health risk to humans and livestock, causing symptoms such as thrombocytopenia and fever. Previous studies in our lab have shown that coinfection, both in vitro and in vivo, increases both the parasite load and the viral titer of the sample, suggesting an association between more severe cases of leishmaniasis and coinfections with viruses from the Bunyaviricetes order. Dogs are the main reservoir for *L. infantum* transmission, and we hypothesized the existence of coinfection in transmission foci of Visceral Leishmaniasis with *Leishmania* and Bunyavirales. To test this hypothesis, we searched for sequences of segment L, the most conserved region of the genomes of both Phleboviruses and Pacuviruses. We focused on sequences found in the New World transmitted sand fly Bunyavirales genomes and designed two sets of PCR primers to detect these viruses. We tested bone marrow and sera samples from 25 VL-positive dogs from the Municipality of Rio de Janeiro. We detected by RT-PCR in 8 animals, thus suggesting that dogs are coinfecting with Bunyavirales and *Leishmania*. Our data show, for the first time in Brazil, the coinfection in VL foci adds a layer of complexity to the understanding of the factors enrolled in *L. infantum* transmission.

More samples from Rio de Janeiro and from other States in Brazil are currently in progress

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