

# A novel mitovirus from the sand fly *Lutzomyia longipalpis* shows sRNA profiles consistent with siRNA pathway activation

Flavia Viana Ferreira, Felipe Ferreira da Silva, Liliane Santana Oliveira Kashiwabara, João Trindade Marques, Aristóteles Góes-Neto, Eric Roberto Guimarães Rocha Aguiar, Arthur Gruber, Paula Luize Camargos Fonseca

*UNIVERSIDADE TECNOLÓGICA FEDERAL DO PARANÁ, UNIVERSIDADE FEDERAL DE MINAS GERAIS, UNIVERSIDADE DE SÃO PAULO, UNIVERSIDADE ESTADUAL DE SANTA CRUZ*

## Abstract

Hematophagous insects act as major reservoirs of infectious agents due to their intimate contact with a large variety of vertebrate hosts. *Lutzomyia longipalpis* is the main vector of *Leishmania chagasi* in the New World, but its role as a host of viruses is poorly understood. In this work, publicly available *L. longipalpis* RNA libraries were subjected to progressive assembly using viral profile HMMs as seeds. A viral sequence presented a size distribution of small RNAs consistent with the activation of the siRNA pathway. This sequence 2,697-bp corresponds to a monopartite ssRNA(+) genome of a virus called Lul-MV-1. A single ORF encoding an RNA-directed RNA polymerase covers almost the entire genome and uses a typical organellar genetic code with tryptophan being mostly coded by UGA. A phylogenetic analysis positioned Lul-MV1 in a monophyletic clade composed of mitoviruses mostly found in fungal, but also in crustaceans. To determine whether the virus was infecting a fungus from the sand fly microbiota or the phlebotomine itself, we analyzed some molecular characteristics of the genome. Dinucleotide composition and codon usage showed profiles similar to mitochondrial DNA of invertebrate hosts. Also, base preference and size of sRNAs were analogous to those observed in viruses that infect sand flies, suggesting that *L. longipalpis* is the putative host. Finally, RT-PCR of different insect pools confirmed the presence of Lul-MV-1 in seven out of eight tested samples. Concluding, the strategy used in this work permitted to identify and characterize for the first time of a mitovirus infecting an insect host.

Funding:

Link to Video: