BLOOD MEAL SOURCES, TRYPANOSOMATID INFECTION AND MICROBIOTA IN TRIATOMINES COLLECTED FROM A CHAGAS DISEASE OUTBREAK LOCALITY IN PERNAMBUCO, BRAZIL THROUGH HIGH-THROUGHPUT SEQUENCING

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The interactions of vectors, parasites, microbiota composition, and blood meal source (BMS) species constitute a dynamic process in the success of parasite transmission. In this study, we investigated these elements through High-Throughput sequencing (HTS) in triatomines from Ibimirim municipality, Pernambuco, a locality where a Chagas disease (CD) outbreak occurred in 2019. *Triatoma pseudomaculata* nymphs (n=28) were collected in bird nests (peridomestic ecotope) and tree barks (wild ecotope). DNA extracted from intestinal contents was submitted to the 12S rDNA, 18S rDNA, and 16S rDNA PCR to detect BMS, *Trypanosoma cruzi*/DTUs infection, and microbiota composition, respectively. A mix of the markers of 6/28 specimens was submitted to HTS on a MiSeq Platform (Illumina). The dataset obtained was processed using a genomic pipeline based on AdapterRemoval, SeqKit, and Blast for removing adapters and low-quality bp, following the comparison consensus to a custom-built reference database. BMS results revealed humans, *Felis catus*, *Mus musculus*, *Didelphis albiventris*, and *Carollia perspicillata*. The 5 BMS were detected in a single vector, and 2/6 vectors were *T. cruzi* positive. Nymphs from the peridomestic ecotope had the highest BMS and microbiota diversity. Vectors that fed on >1 BMS also had greater microbiota diversity. *Didelphis albiventris,* and *C. perspicillata*, ancient and significant reservoirs of *T. cruzi*, were identified in both wild and peridomestic environments. The recognition of opossums and bats suggests their role in sustaining the cycle of the parasite, which may have implications in the outbreak scenario. In the same way, the *M. musculus* and *F. catus*, proposed to actively link domestic and peridomestic environments, could had established the role of connector with humans. Microbiota specific profiles associated to BMS or *T. cruzi* infection were not observed. The study provided additional data for understanding the transmission scenario of the CD outbreak.

Supported by: FAPERJ, CNPq, IOC, LPIP-IOC/FIOCRUZ, CAPES.

Keywords: *Trypanosoma cruzi;* HTS, *Triatoma pseudomaculata*