

Title: Diversity of the gut microbiota of Triatominae bugs, vectors of Chagas disease, using 16S rRNA metagenomics

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Abstract:

Bugs of the subfamily Triatominae (Hemiptera: Reduviidae) known in Brasil as “barbeiros” are the vectors of flagellate *Trypanosoma cruzi* the causative agent of the Chagas disease. The study of the Triatominae gut microbiota has gained relevance in the last years due to the possible use of genetic modified bacteria to block the development of the insects or the parasites. However, for the application of these methods a good understanding of the host-microbiota-pathogen interactions is required, including the microbiota distribution within the body, its mode transmission, the effect of the infection in the microbiota composition, and the phylogenetic and genomic diversity of these bacterial communities. Most bacteria known to inhabit the digestive system of Triatominae have been identified by culturing methods, but the real diversity of uncultivated species is still unknown. The most complete approach for characterizing a bacterial communities is by metagenomics, where high throughput genomic techniques are applied to the study of microbial communities directly in their natural environments, without the need for isolation and cultivation. In order to better understand the composition and dynamics of the Triatominae microbiota, we used high throughput sequencing of the 16S rRNA to analyze the gut microbiota of colony-reared individuals of six representative species of the genera *Triatoma*, *Panstrongylus* and *Rhodnius*, comparing between experimental infected and uninfected insects. In addition, to study a possible vertical transmission mode, we sequenced the microbiota associated to the gonad tissue. After filtering out short (<200 bp), and repeated sequences, and underrepresented OTUs, we found a microbiota dominated by at least one or few bacteria taxa in every genus: *Arsenophonus* in *Triatoma*, *Staphylococcus*, *Pectobacterium* and *Arsenophonus* in *Panstrongylus*, and *Pectobacterium*, *Rhodococcus* and *Staphylococcus* in *Rhodnius*. *Pectobacterium* had been previously found in *Rhodnius* by other methods, but misclassified as *Candidatus Rohrkolberia cinguli*. *Rhodococcus* is underrepresented in the gonads while the other bacterial taxa consistently appear in both tissues. Although our preliminary analyses suggest a difference between infected vectors and controls, statistical analyses are underway to evaluate the possible effect of parasite infection on the diversity and composition of the vector microbiota.

Keywords: Triatominae, *Trypanosoma cruzi*, Gut microbiota, *Pectobacterium*, *Rhodococcus*

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