



MOLECULAR CHARACTERIZATION OF BACTERIAL COMMUNITIES OF *Amblyomma aureolatum* AND *Ornithodoros brasiliensis* TICKS USING rRNA 16S MARKER SEQUENCING

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Ticks are among the main vectors of diseases for humans and animals, but little is known about the interactions of these arthropods with their microbiota. It is known that the microbiota plays a key role in physiology of its host either by preventing infection by pathogens or by synthesis of compounds necessary for the survival of the host organism. Therefore, the objective of this work was to investigate the bacteria associated with two tick species of human and veterinary health importance from Southern Brazil: *Amblyomma aureolatum* and *Ornithodoros brasiliensis*. Specimens of *A. aureolatum* were collected from free-ranging Crab-eating fox (*Cerdocyon thous*), captured in two areas of environmental preservation of the Pampa biome, Refúgio de Vida Silvestre Banhado dos Pachecos (RVSBP) and Área de Proteção Ambiental do Ibirapuitã (APA Ibirapuitã). Adults and nymphs of *O. brasiliensis* were collected in their natural environment in Atlantic rainforest biome. The specimens were classified in males, females, fed and unfed nymphs. The DNA was extracted and amplification of the bacterial 16S rRNA V4 region was performed. Sequencing was done on MiSeq™ (Illumina) platform using a 500-cycle v2 kit. Raw FASTQ files were analyzed in the Mothur software and the data analysis was conducted using the statistical language R. The OTUs generated were compared with the ribosomal RNA database Silva. The mean number of raw reads obtained per sample was 313,515 (100,548 to 765,590) and after quality control was 276,052 (91,728 to 665,380). In *A. aureolatum* the predominant bacterial genera were *Francisella* (97.01%), *Spiroplasma* (0.70%), *Wolbachia* (0.51%), *Candidatus* Midichloria (0.25%) and *Alkanindiges* (0.13%). Bacterial diversity was higher in RVSBP compared to APA Ibirapuitã. In *O. brasiliensis* the predominant bacterial genera were *Coxiella* (87.71%), *Nocardioides* (1.73%), *Saccharopolyspora* (0.54%), *Marmoricola* (0.42%) and *Staphylococcus* (0.40%). Greater diversity was found in fed nymphs. We evaluated, for the first time, the bacterial diversity of two tick species native from Brazil. This work may serve as a basis for new studies that may focus on manipulation of the tick microbiota to vector population control and prevention of outbreaks of tick-borne diseases.

Keywords: Argasidae; Ixodidae; microbiome; *Francisella*; *Coxiella*.

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