

FIRST RECORD OF *Ornithodoros faccinii* (ACARI: ARGASIDAE) ON TOADS OF GENUS *Rhinella* (ANURA: BUFONIDAE) INFECTED BY A NOVEL *Rickettsia* SPECIES IN MANGARATIBA, RIO DE JANEIRO, BRAZIL

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The fauna of anurans in Brazil is the largest in the world. Less than 10% have been reported to present associations with ticks in this country. Amphibians of the families Bufonidae have been found to act as the main hosts for *Amblyomma* spp., specifically *A. rotundatum* and *A. dissimile*. In addition to hard ticks, two species of soft ticks (Argasidae) such as *Ornithodoros faccinii* and *O. saraivai* have been recently described from the amphibian Cycloramphidae. Here we report the first record of *O. faccinii* parasitizing anurans of the family Bufonidae and the detection of a novel *Rickettsia* species in this tick collected in Mangaratiba, state of Rio de Janeiro. Anurans were caught manually through an active search at dusk, examined for tick infestation and identified according to the system of the Brazilian Society of Herpetology. Larval stages of soft ticks were removed with tweezers and kept in RNA later. For morphological and morphometric analyses, three ticks were slide-mounted and photographed. Specimens were identified to genus level as described by Barros-Battesti et al. (2013). Larval DNA was extracted using the bead-beater/phenol-chloroform method. Subsequently, conventional PCR was performed targeting the *16S rRNA* of the soft tick. The presence of *Rickettsia* species was also tested by PCR using the *16S rRNA*, *htrA*, *gltA*, *ompB*, and *scaD* genes. We captured seven *Rhinella ornata* which yielded 12 larvae, morphologically identified as *O. faccinii* and confirmed by means of molecular analyses, as it showed 100% of similarity with *O. faccinii* (KP861242). The organism detected in *O. faccinii* belongs to the genus *Rickettsia* due to a homology higher than 98.1% and 86.5% for *16S rDNA* and *gltA*, respectively. Also, it is a member of the spotted fever group, as its homology was >98.8% (99.3%) for *16S rDNA*, >92.7% (96.4%) for *gltA*, >85.8% (88.8%) for *ompB*, and >82.2% (90.6%) for *scaD* genes. Finally, the organism exhibited a degree of homology less than 98% for all the studied targets, except for *16S rDNA*, which indicates a novel *Rickettsia* species. This study reported for the first time *O. faccinii* on toads of genus *Rhinella*, and it was the first record of *Rickettsia* species in soft ticks parasitizing anurans.

Keywords: soft ticks, bacteria, cold blooded animals, molecular techniques, PCR.
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