

## MICROBIOLOGY

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**Analysis of triatomine midgut bacterial diversity, insect vectors of Chagas disease by next generation sequencing methods (NGS)****Luisa Maria Montoya Porras, Claudia Ximena Moreno-Herrera, Omar Triana-Chavez and Gloria Ester Cadavid-Restrepo**  
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Chagas disease affects more than 6 million people in Latin America, it is a parasitic disease caused by the protozoan *Trypanosoma cruzi*, which is transmitted mainly by bloodsucking insects of the subfamily Triatominae; the study on microbial communities that inhabit the insect gut is important to understand their role in the parasite transmission and development. The aim of this work was to evaluate the gut bacterial composition of two triatomine species from Colombia, using high-throughput sequencing technologies. The insects were collected from housing peridomestic area at Vichada department and wildlife habitat at Magdalena department then they were identified by conventional taxonomy as: *Triatoma maculata* and *Rhodnius pallescens* and their gut were dissected under aseptic conditions in order to obtain total DNA. After DNA quality confirmation, the sequencing of V4 region from 16S rRNA gene was carried out using the Illumina platform MiSeq. The reads thrown were edited and paired obtaining a size of 250 bp. These sequences were analyzed with the RDP-Classifer software and it showed that 13 bacterial genus are present in both species, being *Burkholderia*, *Gordonia*, *Lactococcus* and *Ralstonia*, the most abundant genus. Furthermore, representative genera of each species were found. *Williamsia* and *Kocuria* were the most common in *R. pallescens* and the genus *Curvibacter*, *Dietzia* and *Pelomonas* were only observed in *T. maculata*. This is the first study of microbiota associated with these triatomine species using massive sequencing methods. Some of the genus found in this research, have been reported in previous studies of other species of Chagas disease insect vectors, which may suggest a close association between microbiota and host.

**Biography**

Luisa Maria Montoya Porras is a Biological Engineer of the National University of Colombia, studying Master of Science in Biotechnology. She has worked in the research group Microbiodiversity and Bioprospection for four years in microbial diversity of insect crop pests and insect vector of tropical disease. Currently she is a young Researcher with the "call 706" of the Administrative Department of Science, Technology and Innovation of Colombia (COLCIENCIAS) for the second consecutive year with the project: Analysis of triatomine midgut bacterial diversity, insect vectors of Chagas disease by next generation sequencing methods (NGS). Luisa Maria Montoya Porras is a Biological Engineer of the National University of Colombia, studying Master of Science in Biotechnology. She has worked in the research group Microbiodiversity and Bioprospection for four years in microbial diversity of insect crop pests and insect vector of tropical disease. Currently she is a young Researcher with the "call 706" of the Administrative Department of Science, Technology and Innovation of Colombia (COLCIENCIAS) for the second consecutive year with the project: Analysis of triatomine midgut bacterial diversity, insect vectors of Chagas disease by next generation sequencing methods (NGS).

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