TITLE: PHYLOGENOMIC ANALYSIS OF NEW ACHOLEPLASMA SPECIES FOUND IN AN ENDEMIC TERMITE (*SYNTERMES WHEELERI*) FROM BRAZILIAN SAVANNAH

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ABSTRACT:

Termites represent the most abundant arthropods in tropical ecosystems, contributing greatly to the recycling of organic matter. These organisms cooperate with microbiota that provides protection against foreign microorganisms or pathogens, dietary resources, and depolymerize recalcitrant plant biomass. However, the roles of some symbionts such as members of phylum Tenericutes remain unrecognized. Therefore, the aim of this study is to do a phylogenomic description of three new Tenericutes and investigate their roles in an endemic Termite (Syntermes wheeleri) from Brazilian Savannah. To that end, metagenomics sequences from the hindgut P3 segment of S. wheeleri were obtained using the Illumina HiSeq platform. These sequences were binned based on GC content, coverage, and taxonomy. These genomes were annotated for metabolic reconstruction and Fluorescence in situ hybridization (FISH) was performed. The bacterial community was dominated by Firmicutes 72%, followed Spirochaetes 5%, Bacteroidetes 4%, Tenericutes 2%, Proteobacteria 2%. Within Tenericutes, Mollicutes is the most abundant class composed by Acholeplasmatales 1.26%. Three Tenericutes genomes were recovered from this sample, named rkP31 [0.805 Mbp], rkP32 [1.338 Mbp], rkP33 [0.673 Mbp]. Phylogenetic analysis placed the genomes in a sister group of Acholeplasma. ANI values calculated between the genomes of this study and their closest members were never higher than 69%, suggesting the occurrence of different species from those in the literature. Metabolic reconstruction reveals that these genomes are mainly involved in the fermentative process of acetate and lactate. They lack genes that encode for the tricarboxylic acid cycle, cytochromes, and guinones. Were also detected genes involved in plant biomass degradation, xylose isomerase, xylan $1,4-\beta$ -xylosidase, pectinesterase, and endoglucanase. Visual identification by FISH confirmed these organisms present in the gut content as circle-shaped cells among other tagged Bacteria. Unexpectedly, the three genomes encode for β-lactamase, which are possibly acting against b-lactam antibiotics produced by foreign microorganisms. Our data suggest that these bacteria are present in lower concentrations in the termite gut and are involved in plant biomass degradation, acetate production, and protection against damages caused by foreign microorganisms.

Keywords: FISH, termite gut, host association, genome-resolved metagenomics

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