

Título: PHYLOGENETIC AND FUNCTIONAL INSIGHTS ON THE GUT MICROBIOTA OF THE LITTER-FEEDING TERMITE *SYNTERMES WHEELERI* (ISOPTERA: TERMITIDAE)

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Abstract:

The gut microbiota of termites allows them to thrive on a variety of recalcitrant materials such as lignocellulose. Their capacity to decompose biomass is essential in tropical savannas, where litter-feeding termites are one of the few active invertebrates during the dry season, thereby providing vital ecosystem services. *Syntermes wheeleri* is a neotropical litter-feeding termite distributed in central and southeastern Brazil. In this study, we describe the gut microbiota of *S. wheeleri*, present in the Cerrado biome, assessed by means of high-throughput DNA sequencing. Amplicon sequencing revealed a greater abundance of Firmicutes that may be related with the voluminous first proctodeal gut segment (putatively alkaline) of this termite. Even though most archaeal OTUs belonged to methanogenic groups, unclassified OTUs of Thaumarchaeota were also detected with low abundance. The fungal classes most abundant was Dothideomycetes, Sordariomycetes, and Eurotiomycetes, which may be related to termites' ability to digest lignocellulose. An ordination analysis of the relative abundance of bacteria taxa showed that the gut bacterial community of *S. wheeleri* did not cluster with any other group of higher termites. This difference suggests that feeding habit and subfamily are variables affecting bacterial microbiota in these termites. All classes of carbohydrate-active enzymes (CAZymes) were detected in *S. wheeleri*: Glycosyl Transferases, Glycoside hydrolases (GH), Carbohydrate Esterases, Polysaccharide Lyases, Auxiliary Activities (AA), and cellulosome components. The functions associated with the most abundant GHs families detected in this termite are involved in cellulosic biomass degradation, plant and bacterial cell wall modification. The low abundance of AA enzymes (1 %) may be associated with restricted oxic environments in the gut of *S. wheeleri*, since they are mostly peroxidases or oxygenases. Taxonomic binning of total WGS sequences and those annotated as CAZymes pointed Firmicutes as the most abundant phylum. However, the first indicated *Clostridium* (8 %) as the abundant genus, and the latter showed *Treponema* (46 %), suggesting that this genus has important players in biomass conversion in this termite. The description of the gut microbiota of *S. wheeleri* can help to understand its ecology and evolution. Not to mention prospect to explore the genetic resource harbored in its gut to biofuel production and other biotechnological processes.

Keywords: biomass conversion, cerrado, gut microbiota, high throughput sequencing, higher termite

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