ABSTRACT

454 Pyrosequencing-Based Assessment of Bacterial Diversity and Community Structure in Termite Guts, Mounds and Surrounding Soils

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Termites constitute part of diverse and economically important termite fauna in Africa, but information on gut microbiota and their associated soil microbiome is still inadequate. In this study, we assessed and compared the bacterial diversity and community structure between termites' gut, their mounds and surrounding soil using the 454 pyrosequencing-based analysis of 16S rRNA gene sequences. A wood-feeder termite (Microcerotermes sp.), three fungus-cultivating termites (Macrotermes michaelseni, Odontotermes sp. and Microtermes sp.), their associated mounds and corresponding savannah soil samples were analyzed. The pH of the gut homogenates and soil physico-chemical properties were determined. The results indicated significant difference in bacterial community composition and structure between the gut and corresponding soil samples. Soil samples (Chao1 index ranged from 1359 to 2619) had higher species richness than gut samples (Chao1 index ranged from 461 to 1527). The bacterial composition and community structure in the gut of Macrotermes michaelseni and Odontotermes sp. were almost identical but different from that of Microtermes and Microcerotermes species, which had unique community structures. The most predominant bacterial phyla in the gut were Bacteroidetes (40–58 %), Spirochaetes (10–70 %), Firmicutes (17–27 %) and Fibrobacteres (13 %) while in the soil samples were Acidobacteria (28–45 %), Actinobacteria (20–40 %) and Proteobacteria (18–24 %). Some termite gut-specific bacterial lineages belonging to the genera Dysgonomonas, Parabacteroides, Paludibacter, Tannerella, Alistipes, BCf9-17 termite group and Termite Treponema cluster were observed. The results not only demonstrated a high level of bacterial diversity in the gut and surrounding soil environments, but also presence of distinct bacterial communities that are yet to be cultivated. Therefore, combined efforts using both culture and culture-independent methods are suggested to comprehensively characterize the bacterial species and their specific roles in these environments.

Keywords: Termites gut symbionts, 454 Pyrosequencing, OTUs, Macrotermitinae