

Huxley M. Makonde, Hamadi I. Boga, **Romano Mwirichia**, Lucy M. Mackenzie, Markus Göker, Hans-Peter Klenk (2013). 16S-rRNA-based analysis of bacterial diversity in the gut of fungus-cultivating termites (*Microtermes* and *Odontotermes* species)", 10.1007/s10482-013-0001-7

Abstract

The interaction between termites and their gut symbionts has continued to attract the curiosity of researchers over time. The aim of this study was to characterize and compare the bacterial diversity and community structure in the guts of three termites (*Odontotermes somaliensis*, *Odontotermes* sp. and *Microtermes* sp.) using 16S rRNA gene sequencing of clone libraries. Clone libraries were screened by restriction fragment length polymorphism and representative clones from *O. somaliensis* (100 out of 330 clones), *Odontotermes* sp. (100 out of 359 clones) and *Microtermes* sp. (96 out 336 clones) were sequenced. Phylogenetic analysis indicated seven bacterial phyla were represented: Bacteroidetes, Spirochaetes, Firmicutes, Proteobacteria, Synergistetes, Planctomycetes and Actinobacteria. Sequences representing the phylum Bacteroidetes (>60 %) were the most abundant group in *Odontotermes* while those of Spirochaetes (29 %) and Firmicutes (23 %) were the abundant groups in *Microtermes*. The gut bacterial community structure within the two *Odontotermes* species investigated here was almost identical at the phylum level, but the *Microtermes* sp. had a unique bacterial community structure. Bacterial diversity was higher in *Odontotermes* than in *Microtermes*. The affiliation and clustering of the sequences, often with those from other termites' guts, indicate a majority of the gut bacteria are autochthonous having mutualistic relationships with their hosts. The findings underscore the presence of termite-specific bacterial lineages, the majority of which are still uncultured.