

**Molecular phylogenetic study of fungal symbionts of fungus-growing termites and  
DNA barcoding of termites for biodiversity assessment in Kenya**

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## ABSTRACT

Termites are among the most important decomposers in tropical ecosystems. Their taxonomy to the species level mostly relies on characters of soldiers. The workers are morphologically uniform, and thus exhibit only few traditional taxonomic characters for species identification. However, they are the most frequently sampled caste during field sampling. Therefore, the diversity of termites is poorly understood. Recently, the use of DNA-sequences (barcoding) has become more important for inventory and biodiversity assessment of hyperdiverse taxa and those which are difficult to identify. An approach towards establishing a DNA barcode library for termite species identification and biodiversity assessment using sequences of the mitochondrial COII gene is presented in this study. At least 16 termite species were observed in Kakamega Forest by morphological identification whereas at least 22 species (MOTUs) were found by molecular species delimitation. This study highlights the advantage that molecular based species delimitation reveals some morphological cryptic species. Furthermore, termite workers can be assigned to their respective phylogenetic clusters.

Recent studies on fungus-growing termites based on genetic markers have largely increased knowledge about the evolutionary history of the symbiosis between fungus-growing termites and their fungi. Studies focusing on interaction specificity have been conducted elsewhere in Africa but none so far has been done on Eastern Africa despite the high generic richness of host termites in this area. The phylogenetic relationship among *Termitomyces* sampled in Kenya showed strong sequence divergence among host termite genera, showing high interaction specificity. However, within the clade associated with the host genus *Macrotermes*, fungi lineages occurred in several species indicating low host

specificity. Furthermore, same lineages occurred across steep environmental gradients. Therefore, the association of the fungal lineages with several host species is not the result of an allopatric distribution of fungi among climatic regions.