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## DNA Barcoding: A Method of Diversity Assessment of Termite Communities in Kakamega Forest, Kenya

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### Abstract

Termites are among the keystone species of tropical ecosystems and contribute to ecosystem processes and carbon and nitrogen cycles. The role of termites for soil processes depends strongly on the species composition and their feeding habits. Termite workers are morphologically rather uniform, and thus exhibit only few traditional taxonomic characters for species identification and yet they dominate in ecological surveys. Therefore, the diversity of termites is poorly understood, especially in tropical forests which are hotspots of biodiversity and threatened by disturbances. 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. Kakamega forest is the remnant of the Congo-Guinean Forest reaching Kenya. This isolated forest is a hotspot of biodiversity which is threatened by the increasing human population. Depending on the land use, along a gradient from primary rain forest to farmlands, the species composition among the termites varied greatly, dominated by termite species feeding on wood in the primary forests and by grass feeding termites in farmlands. Hence, to interpret the role of termites in different land-use habitats the species composition needs to be understood. Here we present termite biodiversity assessment using sequences of the mtCOII gene. At least 16 termite species were observed in Kakamega Forest by morphological determination whereas at least 22 species (MOTUs) were found by molecular species delimitation. This highlights the advantage that molecular based species delimitation and reveals some morphological cryptic species.

**Keywords:** DNA barcoding, Kenya, termites