

ABSTRACT

16S Rrna Gene Amplicon-Based Metagenomic Analysis of Bacterial Communities in the Rhizospheres of Selected Mangrove Species from Mida Creek and Gazi Bay, Kenya

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Prokaryotic communities play key roles in biogeochemical transformation and cycling of nutrients in the productive mangrove ecosystem. In this study, the vertical distribution of rhizosphere bacteria was evaluated by profiling the bacterial diversity and community structure in the rhizospheres of four mangrove species (*Sonneratia alba*, *Rhizophora mucronata*, *Ceriops tagal* and *Avicennia marina*) from Mida Creek and Gazi Bay, Kenya, using DNA-metabarcoding. Alpha diversity was not significantly different between sites, but, significantly higher in the rhizospheres of *S. alba* and *R. mucronata* in Gazi Bay than in Mida Creek. Chemical parameters of the mangrove sediments significantly correlated inversely with alpha diversity metrics. The bacterial community structure was significantly differentiated by geographical location, mangrove species and sampling depth, however, differences in mangrove species and sediment chemical parameters explained more the variation in bacterial community structure. Proteobacteria (mainly Deltaproteobacteria and Gammaproteobacteria) was the dominant phylum while the families Desulfobacteraceae, Pirellulaceae and Syntrophobacteraceae were dominant in both study sites and across all mangrove species. Constrained redundancy analysis indicated that calcium, potassium, magnesium, electrical conductivity, pH, nitrogen, sodium, carbon and salinity contributed significantly to the species–environment relationship. Predicted functional profiling using PICRUSt2 revealed that pathways for sulfur and carbon metabolism were significantly enriched in Gazi Bay than Mida Creek. Overall, the results indicate that bacterial community composition and their potential function are influenced by mangrove species and a fluctuating influx of nutrients in the mangrove ecosystems of Gazi Bay and Mida Creek.

Keywords: 16S rRNA, gene amplicon-based metagenomic, bacterial communities, rhizospheres, mangrove species, Mida Creek, Gazi Bay