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Research Article

RESEARCH ARTICLE

Shotgun metagenomics reveals a heterogeneous prokaryotic community and a wide array of antibiotic resistance genes in mangrove sediment

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One sentence summary: Mangrove sediments around the globe harbour a highly heterogeneous microbial community and antibiotic resistome in contrast with several other ecosystems.

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ABSTRACT

Saline tolerant mangrove forests partake in vital biogeochemical cycles. However, they are endangered due to deforestation as a result of urbanization. In this study, we have carried out a metagenomic snapshot of the mangrove ecosystem from five countries to assess its taxonomic, functional and antibiotic resistome structure. Chao1 alpha diversity varied significantly ($P < 0.001$) between the countries (Brazil, Saudi Arabia, China, India and Malaysia). All datasets were composed of 33 phyla dominated by eight major phyla covering >90% relative abundance. Comparative analysis of mangrove with terrestrial and marine ecosystems revealed the strongest heterogeneity in the mangrove microbial community. We also observed that the mangrove community shared similarities to both the terrestrial and marine microbiome, forming a link between the two contrasting ecosystems. The antibiotic resistant genes (ARG) resistome was comprised of nineteen level 3 classifications dominated by multidrug resistance efflux pumps (46.7 ± 4.3%) and BlaR1 family regulatory sensor-transducer disambiguation (25.2 ± 4.8%). ARG relative abundance was significantly higher in Asian countries and in human intervention datasets at a global scale. Our study shows that the mangrove microbial community and its antibiotic resistance are affected by geography as well as human intervention and are unique to the mangrove ecosystem. Understanding changes in the mangrove microbiome and its ARG is significant for sustainable development and public health.

Keywords: mangroves; environment; microbial ecology; antibiotic resistance; metagenome; next generation sequencing

INTRODUCTION

Mangrove forests are one of the most endangered ecosystems although they host one of the most complex and diverse microbial communities in the natural environment. Mangrove sediments are significantly richer in total organic carbon, N, P and K than the surrounding sandy area. The rich organic sediments and the regular physiochemical fluctuation brought about by tidal waves enrich a wide array of microbial populations that perform crucial biogeochemical cycles. The microbial community, as a precursor, is consumed by protists and invertebrates (Alongi 1994). This leads to a larger food chain, forming a self-sustaining forest that protects the land from sea and shelters a variety of insects, fish, reptiles, birds, etc. Although several conservation campaigns have been successful, the rate of mangrove forest destruction continues at an alarming rate

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