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Metagenomic insights into the antibiotic resistome of mangrove sediments and their association to socioeconomic status*

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abstract

Mangrove sediments are prone to anthropogenic activities that could enrich antibiotics resistance genes (ARGs). The emergence and dissemination of ARGs are of serious concern to public health worldwide. Therefore, a comprehensive resistome analysis of global mangrove sediment is of paramount importance. In this study, we have implemented a deep machine learning approach to analyze the resistome of mangrove sediments from Brazil, China, Saudi Arabia, India, and Malaysia. Geography ($R_{ANOSIM} = 39.26\%$, $p < 0.005$) as well as human intervention ($R_{ANOSIM} = 16.92\%$; $p < 0.005$) influenced the ARG diversity. ARG diversity was also inversely correlated to the human development index (HDI) of the host country ($R = 0.53$; $p < 0.05$) rather than antibiotics consumption ($p > 0.05$). Several genes including multidrug efflux pumps were significantly ($p < 0.05$) enriched in the sites with human intervention. Resistome was consistently dominated by rpoB2 (19.26 ± 0.01%), multidrug ABC transporter (10.40 ± 0.23%), macB (8.84 ± 0.36n%), tetA (4.13 ± 0.35%), mexF (3.26 ± 0.19%), CpxR (2.93 ± 0.2%), bcrA (2.38 ± 0.24%), acrB (2.37 ± 0.18%), mexW (2.19 ± 0.17%), and vanR (1.99 ± 0.11%). Besides, mobile ARGs such as vanA, tet(48), mcr, and tetX were also detected in the mangrove sediments. Comparative analysis against terrestrial and ocean resistomes showed that the ocean ecosystem harbored the lowest ARG diversity (Chao1 = 71.12) followed by mangroves (Chao1 = 258.07) and terrestrial ecosystem (Chao1 = 294.07). ARG subtypes such as abeS and qacG were detected exclusively in ocean datasets. Likewise, rpoB2, multidrug ABC transporter, and macB, detected in mangrove and terrestrial datasets, were not detected in the ocean datasets. This study shows that the socioeconomic factors strongly determine the antibiotic resistome in the mangrove. Direct anthropogenic intervention in the mangrove environment also enriches antibiotic resistome.

Credit author statement

Madangchanok Imchen, Data curation, Writing- original draft preparation, Visualization, Software. Ranjith Kumavath, Supervision, Conceptualization, Methodology, Editing, reviewing, Investigation.

1. Introduction

Antibiotic resistance is the ability to resist the inhibitory effect(s) of an antibiotic. Such resistance has made the treatment of bacterial infections extremely difficult. Over 700,000 deaths related to antibiotic resistance are reported globally which is projected to rise sharply in the coming decades (Friedrich, 2019). Antibiotic resistance has become an acute global concern. For instance, the mortality due to methicillin-resistant Staphylococcus aureus (MRSA) alone is comparable to that of HIV (Coates et al., 2011). Multidrug resistant bacteria are not only confined to the hospital environments but also in environmental soil, wastewater treatment plants, gut microbiome, etc. (Diaz et al., 2017). The prevalence of ARGs in the environment could lead to the dissemination of the clinically relevant ARGs to the surroundings and distant locations (Zeng et al., 2019b). Rapid and exponential dissemination of ARGs is not only confined at the local or national level but also spreads on a global scale. Although antibiotic resistance is a global issue, the consequences of antibiotic resistance are more severe in developing countries (Klein et al., 2018). Infections caused by multidrug-resistant (MDR) microbes are also associated with higher

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