microorganisms

Article

Insights into Antagonistic Interactions of Multidrug Resistant Bacteria in Mangrove Sediments from the South Indian State of Kerala

Madangchanok Imchen [1], Ravali Krishna Vennapu [1], Preetam Ghosh [2] and Ranjith Kumavath [1,*]

[1] Department of Genomic Science, School of Biological Sciences, Central University of Kerala, Tejaswini Hills, Periya (P.O) Kasaragod, Kerala 671316, India; anokimchen@gmail.com (M.I.); ravalikrishna224@gmail.com (R.K.V.)

[2] Department of Computer Science, Virginia Commonwealth University, Richmond, VA 23284, USA; preetam.ghosh@gmail.com

* Correspondence: RNKumavath@gmail.com or RNKumavath@cukerala.edu.in; Tel.: +91-854-764-8620

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Abstract: Antibiotic resistance is a global issue which is magnified by interspecies horizontal gene transfer. Understanding antibiotic resistance in bacteria in a natural setting is crucial to check whether they are multidrug resistant (MDR) and possibly avoid outbreaks. In this study, we have isolated several antibiotic-resistant bacteria (ARB) (n = 128) from the mangroves in Kerala, India. ARBs were distributed based on antibiotics ($p = 1.6 \times 10^{-5}$). The 16S rRNA gene characterization revealed dominance by Bacillaceae (45%), Planococcaceae (22.5%), and Enterobacteriaceae (17.5%). A high proportion of the isolates were MDR (75%) with maximum resistance to methicillin (70%). Four isolates affiliated to plant-growth promoters, probiotics, food, and human pathogens were resistant to all antibiotics indicating the seriousness and prevalence of MDR. A significant correlation (R = 0.66; $p = 2.5 \times 10^{-6}$) was observed between MDR and biofilm formation. Antagonist activity was observed in 62.5% isolates. Gram-positive isolates were more susceptible to antagonism (75.86%) than gram-negative (36.36%) isolates. Antagonism interactions against gram-negative isolates were lower (9.42%) when compared to gram-positive isolates (89.85%). Such strong antagonist activity can be harnessed for inspection of novel antimicrobial mechanisms and drugs. Our study shows that MDR with strong biofilm formation is prevalent in natural habitat and if acquired by deadly pathogens may create havoc in public health.

Keywords: multidrug resistance; mangrove; biofilm; antibiotic-resistant genes; antagonism

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1. Introduction

The discovery of antibiotics has been a breakthrough in the medical field, which has saved millions of lives. However, the emergence of antibiotic resistance over time has rendered pathogenic microbes resistant to single and multidrugs. Such evolution has made the treatment of infectious diseases extremely difficult. Given the importance of pathogenic microbes in public welfare, most of the research has focused mainly on the human, agricultural, and veterinary pathogens. However, there is an increasing evidence of several non-pathogenic drug-resistant microbes in the environmental microbial community. This is of serious concern since those non-pathogenic microbes could serve as a reservoir of antibiotic-resistant genes, which could ultimately spread to pathogens through horizontal gene transfer and give rise to numerous super bugs. Despite such threats, the natural environment microbial community resistome has received relatively less focus [1]. Antibiotic resistance of a bacterium in clinical terms is classified into breakpoints such as susceptible, intermediate, or resistant [2]. However,