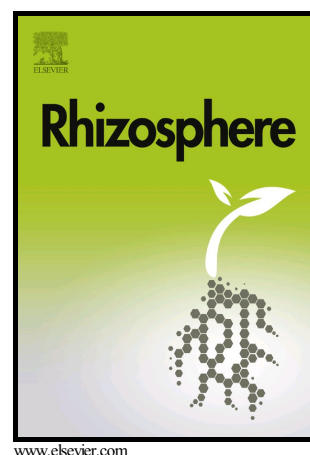


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Rhizosphere of water hyacinth as a niche for multidrug resistant *Aeromonas taiwanensis* and *Paenibacillus taiwanensis*: a study from a tropical wetland of South India

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Abstract

The present study highlights the prevalence of multidrug resistant bacteria in the rhizosphere of a floating nuisance weed, water hyacinth growing in a tropical wetland of South India. The isolated strains from the rhizosphere were subjected to 16S rRNA gene sequence analysis and identified as *Aeromonas taiwanensis* and *Paenibacillus taiwanensis*. The identified strains were tested for the multidrug (13 antibiotics) resistance and pathogenicity. Both *A. taiwanensis* and *P. taiwanensis* were found to be multidrug resistant and only *A. taiwanensis* showed the pathogenicity. The present study is the first report on the prevalence of *A. taiwanensis* and *P. taiwanensis* in the rhizosphere of water hyacinth.

Keywords: *Aeromonas taiwanensis*, *Paenibacillus taiwanensis*, rhizosphere, water hyacinth, multidrug resistance, Kuttanad

Introduction

Wetlands have been called as 'kidneys of the landscape' because of their ability to accumulate, assimilate and transform contaminants through various biogeochemical processes (Keddy, 2000). The aquatic plants of wetlands have specialized mechanisms to remediate the pollution load by accumulating the inorganic contaminants in different parts. Rhizosphere, the complex and active zone of root-microbe association having considerable potential for plant growth promotion and detoxification of hazardous compounds (Arti et al., 2017). Water hyacinth (*Eichhornia crassipes* (Mart.) Solms), a fast growing aquatic perennial herb is considered as the worst weed in the tropics, which is floating freely on the surface of water or it can also be anchored in mud (Bhattacharya et al., 2015). It has well developed fibrous root system with 20 to 40 cm length and due to its colonized growth, the under layer of the floating biomass provides a specialized habitat for many organisms (John et al., 2009) including human pathogenic microorganisms (Pratap, 2014). Antibiotic resistance is an emerging environmental issue due to the overuse and misuse of antibiotics in health and agriculture (Ventola, 2015). The development and spread of antibiotic resistance among bacteria is considered as a threat to human, animal and environmental health (Ivone et al. 2014). Bacteria have a notable genetic capability that allows them to respond to a wide range of environmental pressures, including the presence of antibiotic molecules that may threaten their existence. Antibiotic resistance genes can be present within the bacteria or extracellularly as naked DNA. Bacteria adapt two major genetic strategies to prevent the antibiotic "attack", i) mutations in gene(s) often associated with the mechanism of action of the compound ii) acquisition of foreign DNA coding for resistance determinants through Horizontal Gene Transfer (HGT) by conjugation, transformation or transduction (Jose and Cesar, 2016; Davies & Davies, 2010). The improper disposal of unused or expired antibiotics in the environment eventually reaches to the wetlands through land run off and causes the emergence of multidrug resistant microorganisms in wetlands.

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