Article

Microbial Community Structure and Bacterial Lineages Associated with Sulfonamides Resistance in Anthropogenic Impacted Larut River

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Abstract: Anthropogenic activities often contribute to antibiotic resistance in aquatic environments. Larut River Malaysia is polluted with both organic and inorganic pollutants from domestic and industrial wastewater that are probably treated inadequately. The river is characterized by high biochemical oxygen demand, chemical oxygen demand, total suspended solids, ammonia, and heavy metals. In our previous study, sulfonamides (SAs) and sulfonamide resistance genes (*sul*) were detected in the Larut River. Hence, in this study, we further examined the microbial community structure, diversity of sulfonamide-resistant bacteria (SARB), and their resistance genes. The study also aimed at identifying cultivable bacteria potential carriers of *sul* genes in the aquatic environment. Proteobacteria (22.4–66.0%), Firmicutes (0.8–41.6%), Bacteroidetes (2.0–29.4%), and Actinobacteria (5.5–27.9%) were the most dominant phyla in both the effluents and river waters. SARB isolated consisted only 4.7% of the total genera identified, with SAR Klebsiella as the most dominant (38.0–61.3%) followed by SAR Escherichia (0–22.2%) and Acinetobacter (3.2–16.0%). The majority of the SAR Klebsiella isolated from the effluents and middle downstream were positive for *sul* genes. *Sul* genes-negative SAR Escherichia and Acinetobacter were low (<20%). Canonical-correlation analysis (CCA) showed that SAs residues and inorganic nutrients exerted significant impacts on microbial community and total *sul* genes. Network analysis identified 11 SARB as potential *sul* genes bacterial carriers. These findings indicated that anthropogenic activities exerted impacts on the microbial community structure and SAs resistance in the Larut River.

Keywords: anthropogenic water pollution; Larut River; microbial community structure; sulfonamide resistance genes

1. Introduction

The increasing community-acquired infections of antibiotic-resistant bacteria (ARB) and occurrence of environmental ARB and their resistance genes (ARGs) have raised concern about antibiotic resistance in natural environments [1–4]. Aquatic environments are suffering from different types and levels of anthropogenic antibiotic pollution, including discharge of untreated and crudely treated municipal, hospital, agricultural, livestock, and pharmaceutical industries wastewaters [5]. Subsequently, aquatic environments may represent the origin, amplifier, and/or reservoir of the environmental, human, and/or animals ARB and ARGs as well as act as a bioreactor facilitating the emergence and dissemination of ARGs transfer between the pathogenic and non-pathogenic bacteria [6–8].