Microbial community structure and antibiotic resistance genes distribution in the hyporheic zone of effluent-receiving rivers

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Antibiotic resistance is posing potential threats to human health, and therefore, antibiotic resistance genes (ARGs), an emerging pollutant, gain increasing attention. Wastewater treatment plants are the hot spot for the detection of ARGs, and the mitigation and control of ARGs in effluent-receiving rivers are of great importance. The hyporheic zone in the river mediates the interaction of the surface water and groundwater, being the area with high microbial activities and pollutants attenuation. However, the microbial community structure and ARGs distribution in the hyporheic zone of effluent-receiving rivers are not well understood. In this study, two rivers with effluent accounting for the high proportion of flow were selected to investigate the effects of the hyporheic zone on the mitigation of ARGs. The sediment samples were collected at three depths including 0-10 cm, 20-30 cm, and 30-50 cm. After DNA extraction, the metagenomic sequencing technique was applied to analyze the microbial community structure and characteristics of ARGs distribution. Results showed that the microbial community and ARGs composition in two rivers were different, indicating that environmental selection showed a strong influence on their distribution. In the vertical direction, the ARGs composition in the top layer was different from those in the other two layers, and the relative abundances of ARGs showed a decreasing trend. Multidrug resistance genes were the most abundant types, probably because of the various selection pressures in wastewater treatment plants effluent. In summary, the hyporheic zone can reduce the relative abundance of ARGs in the hyporheic zone of effluent-receiving rivers and more efforts could be made to enhance the removal effects of the hyporheic zone.