



## Comparison of the effects of two municipal sewage treatment process discharge on receiving rivers in plateau habitats

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### ABSTRACT

Microbiological and metabolomic analyses based on Illumina MiSeq high-throughput sequencing technology were carried out on the receiving rivers in upland habitats to compare the impacts of effluent discharges from two urban wastewater treatment processes on the receiving rivers. The results showed that microbial diversity increased in the lower reaches of the receiving rivers, but the overall microbial diversity of the rivers in the plateau habitat was lower than that in the plains. *Proteobacteria* (47.4%–57.04%) and *Sphingorhabdus* (25%–32.19%) were both the most abundant phylum and genus in the upper and lower reaches of the two feeder rivers. The effects of anaerobic-anoxic-aerobic (AAO) vs. artificial wetland (CW) effluent discharge on microbial community abundance showed either an increase or a decrease, but analysis of *Luteolibacter*, an indicator bacterium of good water quality, found that abundance increased by 4.01% downstream of the AAO receiving river. Analysis of the downstream trend of dominant genera abundance suggests that the AAO receiving river has a stronger self-purification of pollutants and recovery of dominant genera. In terms of carbon, nitrogen, and phosphorus metabolic pathways and gene expression, AAO and CW treatment processes showed different significant effects on the receiving rivers and even had completely opposite effects on some functional modules. In addition, the AAO receiving river showed better recoverability in terms of carbon and phosphorus metabolic pathways. This study reveals the microbiological and carbon, nitrogen, and phosphorus metabolomic responses of the receiving rivers to sewage discharge in plateau habitats and provides a new practical idea and perspective for the selection of sewage treatment processes and sewage discharge in plateau towns.

**Keywords:** Receiving rivers; Plateau habitats; Microbial communities; Metabolic pathways

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