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## **BACTERIAL COMMUNITY STRUCTURE IN THE NANMING RIVER, CHINA AND THEIR RELATIONS TO ENVIRONMENTAL FACTORS**

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### **Abstract**

Microbial communities play an important role in water quality regulation and biogeochemical cycling in river ecosystems. However, there is a lack of research on the effects of environmental factors on bacterial community structure in karst urban rivers. In this study, 16S rRNA gene high-throughput sequencing was used to explore the bacterial community structure in the Nanming River, China and analyze the extent to which it is influenced by environmental factors. The results showed that the water quality was alkaline and the content of dissolved oxygen (DO) was relatively high. The concentration of chemical oxygen demand (COD) fluctuated between 2.2 and 17.0 mg/L and ammonia nitrogen varied little among sampling sites. At the phylum level, the dominant bacterial community were Actinobacteriota, Proteobacteria and Bacteroidota. Flavobacterium had the highest abundance, followed by Limnhabitans and hgcl\_clade at the genus level. Water temperature, DO, oxidation-reduction potential, and total phosphorus (TP) were environmental factors with significant correlation to Actinomycetes, Bacteroides, and Proteobacteria. Water temperature and pH were positively correlated with Shannon index and Simpson index, while COD, TP and chlorophyll a were significantly correlated with Chao1 index. At present, Nanming River is in a state of eutrophication. This study can provide theoretical basis and data support for the regulation of karst urban rivers in the future.

*Key words:* bacterial diversity, environmental drivers, high throughput sequencing, Nanming River, water eutrophication

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