
Bacterial community composition response to nutrients and other environmental factors in an urban river, China

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Introduction

An excess of nitrogen and phosphorus from anthropogenic sources can alter the nutrient pool in an aquatic system, causing eutrophication and ecosystem deterioration (Angel et al. 2010). Surface-associated bacterial populations in rivers play an important role in the biodegradation of allochthonous substance (Araya et al. 2003). The information about how nutrients affect communities, enhances our understanding of how changes in nutrient concentrations and stoichiometry may effect aquatic ecosystems (Melissa A. 2007). The determination of bacterial community composition and their activities in nature is fundamental but has long been a challenge to microbial ecologists (Kenzaka et al. 2001). In recent years, various molecular techniques have been used to identify environmental samples bacterial species (Joo et al. 2010). T-RFLP analysis is a widely used tool for studying microbial communities because it is relatively rapid and technically simple (Marsh et al. 2000).

Beiyun River, which is the most important drainage river in Beijing, is seriously polluted by organic substances and ammonia nitrogen. Here we investigated the spatial distribution of nutrient and bacterial communities, and site-specific differences in the interaction between bacterial communities and environmental factors. Bacterial communities were investigated by terminal restriction fragment length polymorphism (T-RFLP) in water collected at Beiyun River with different nutrient input.

2. Materials and Methods

Water samples were collected at 10 stations in the winter and summer 2010. Part of water was used for physicochemical analysis, and another part was filtered through 0.22 μm -pore-size filters for molecular analysis. DNA was extracted from the filters using the FastDNA spin kit for environmental sample. The primers used for amplification of the 16S rDNA genes were 27F-5'FAM and 1492R. Purified PCR product from each of the amplification was digested separately for 6h at 37 °C with HaeIII. The T-RFLP patterns were analyzed with ABI analyzer.

3. Results

3.1 Variation in water quality

Ecological parameters determined were pH, DO, ORP, temperature, Chl. a, TP, TN, NH_4^+ , NO_3^- , NO_2^- , COD, BOD, DOC. The concentrations of TN and NH_4^+ were significantly higher than in other study areas. NH_4^+ range from 10.5 mg/L –17.6 mg/L that account for 78% of TN. The concentration of TN at NO.9 site was higher than that at other sites and the concentration of TP was highest at the NO.2 site.

3.2 Variation in bacterial community

At least thirty-four terminal restriction fragments (T-RFs) were detected in all samples. The 10 samples had different bacterial compositions and predominant types. However, the Shannon-Weiner diversity in all the samples was low; the highest value was two, which indicated that the ecological status of Beiyun River was fragile. The richness, diversity, and evenness in sample NO.2 and NO.3 were generally lower than other samples (Figure 1.1). The dominant T-RFs were 37bp, 38bp, 39bp, 67bp and 218bp in natural water environment, they are widely distributed and quantity relatively stable. The BBCs of 10 samples could be divided into five clusters. The bacterial communities in closed water areas like reservoir and floodgate have large differences with flux in Beiyun River.



Figure 1.1 Analysis of the gene diversity of bacterial communities

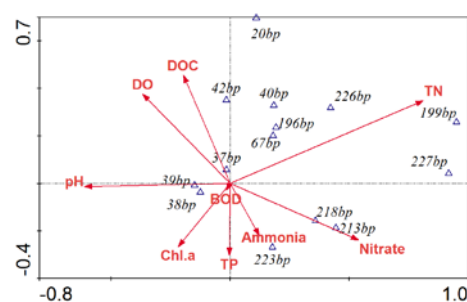


Figure 1.2 DCCA plot showing species in relation to the environmental factors

3.3 Major environmental variables regulating bacterial community

The distribution of species showed the bacterial community composition in each sample. The results of detrended canonical corresponding analysis (DCCA) illuminated that the differences in bacterial communities in 10 samples are related to environmental factors (Figure 1.2). A Monte Carlo Permutation Test demonstrated that nine environmental variables selected manually were correlated significantly with first canonical axis (< 0.05) and all canonical axes (< 0.05). In the present study, TN was the most important nutrient affecting the bacterial community. NO_3^- , pH, TP and DOC contributed significantly to variance in bacterial communities.

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