



Shift in the microbial community composition of surface water and sediment along an urban river

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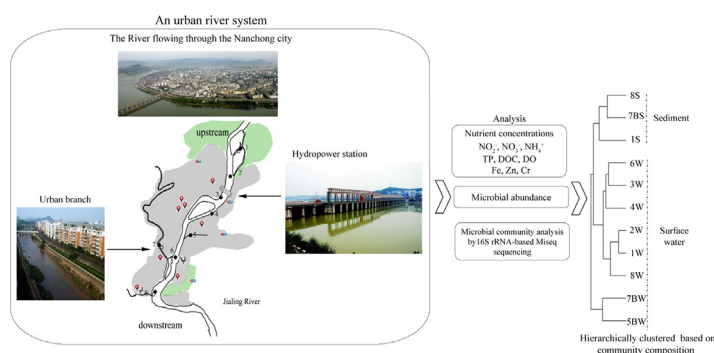
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HIGHLIGHTS

- Microbial community in the urban river exhibited spatial variations due to the joint influence of chemical variables
- The microbial OTUs richness decreased in the urban area
- TP, NO₃ and metals (Zn, Fe) were the most determining factors impacting the surface water microbial compositions
- Higher abundance of genes associated with xenobiotic metabolism were observed in the urban surface water and sediments

GRAPHICAL ABSTRACT



ARTICLE INFO

Article history:

Received 25 September 2017

Received in revised form 4 January 2018

Accepted 20 January 2018

Available online 3 February 2018

Editor: Henner Hollert

Keywords:

Urban river

Microbial community

Miseq sequencing

PICRUSt metabolic prediction

Sewage pollution

ABSTRACT

Urban rivers represent a unique ecosystem in which pollution occurs regularly, leading to significantly altered of chemical and biological characteristics of the surface water and sediments. However, the impact of urbanization on the diversity and structure of the river microbial community has not been well documented. As a major tributary of the Yangtze River, the Jialing River flows through many cities. Here, a comprehensive analysis of the spatial microbial distribution in the surface water and sediments in the Nanchong section of Jialing River and its two urban branches was conducted using 16S rRNA gene-based Illumina MiSeq sequencing. The results revealed distinct differences in surface water bacterial composition along the river with a differential distribution of *Proteobacteria*, *Cyanobacteria*, *Actinobacteria*, *Bacteroidetes* and *Acidobacteria* ($P < 0.05$). The bacterial diversity in sediments was significantly higher than their corresponding water samples. Additionally, archaeal communities showed obvious spatial variability in the surface water. The construction of the hydropower station resulted in increased *Cyanobacteria* abundance in the upstream (32.2%) compared to its downstream (10.3%). Several taxonomic groups of potential fecal indicator bacteria, like *Flavobacteria* and *Bacteroidia*, showed an increasing trend in the urban water. PICRUSt metabolic inference analysis revealed a growing number of genes associated with xenobiotic metabolism and nitrogen metabolism in the urban water, indicating that urban discharges might act as the dominant selective force to alter the microbial communities. Redundancy analysis suggested that the microbial community structure was influenced by several environmental factors. TP ($P < 0.01$) and NO₃⁻ ($P < 0.05$), and metals (Zn, Fe) ($P < 0.05$) were the most significant drivers determining the microbial community composition in the urban river. These results highlight that river microbial communities exhibit spatial variation in urban areas due to the joint influence of chemical variables associated with sewage discharging and construction of hydropower stations.

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1. Introduction

Rivers or streams flowing through cities always serve as an important sink for waste materials, urban sewage, and storm water run-off. They are also the main source of drinking or industrial water in cities, especially those along the river. Microorganisms inhabiting these ecosystems are one of the crucial players in the biogeochemical cycling of organic matter and nutrients, biodegradation and biotransformation of pollutants, and the recovery and maintenance of ecosystem health and balance (Bai et al., 2014; Kirchman, 1994; Ruiz-González et al., 2015). Although there has been an increasing awareness of water quality and great efforts are being taken to ensure greater sustainability of urban rivers, the accelerating development of cities, commonly in developing countries, inevitably leads to an increase in river deterioration (Suthar et al., 2010) due to high-load discharge and water front construction. Meanwhile, the water microbial properties, particularly the diversity and community structure, could be susceptible influenced by the spatial variability of the physicochemical and biotic parameters, which can be used as an indicator of environmental conditions (Kostanjsek et al., 2005; Lundgaard et al., 2017; Tiquia, 2010). Most previous laboratory and field studies assessing the impact of urban human activity on surface water and sediments have focused on physicochemical indexes such as heavy metals (Vink et al., 1999; Zheng et al., 2008), hydrocarbons (Yunker et al., 2002) or nutrients (Howarth et al., 2000), and algal characters (Biggs, 2000; Flynn et al., 2013). The in-depth understanding of microbial community diversity in the flowing urban river is still lacking, and is less explored than that of marine or lake ecosystems (Zinger et al., 2012).

It is well-understood that microbial communities are taxonomically distinct at different spatial and temporal scales in river systems (García-Armisen et al., 2014; Savio et al., 2015; Zhi et al., 2015). Urban rivers are rather spatially heterogeneous ecosystems that are mainly influenced by the terrestrial environment. Sewage from the residential areas containing organic and inorganic pollutants notably alters the basic parameters of freshwater, such as pH, temperature, dissolved oxygen content, and light penetration, which could further reshape the bacterial community structure (García-Armisen et al., 2014; Lindström et al., 2005; Mark Ibekwe et al., 2012). The sewage system seems to be an eutrophic environment for stimulating the growth of microorganisms which are likely to be physiologically adapted to this environment. In addition, sewage also introduces microbiological contamination to the river which can have a key impact on the diversity and function of the bacterial community (Drury et al., 2013). To some degree, the spatial distribution of river bacterial communities is also associated with the landscape topography and hydrology (Crump et al., 2007; Lindström and Bergström, 2004). The variations in valley width, hydrologic connections, and flow can directly influence the water residence time and water dilution capacity. These factors are related to the balance process between the bacteria from terrestrial or sewage source, and indigenous communities, and the stabilization of the communities by predation or competition (Crump et al., 2007; Lozupone and Knight, 2007; Read et al., 2015; Székely et al., 2013), which might indirectly or directly affect the microbial community function. As a result, it is essential to understand the microbial communities in the context of their spatial distribution and microbial diversity in a river to monitor the ecosystem health and function. Recently, a growing number of nations have highlighted the development of small hydropower resources (Karki, 2007; Li et al., 2009; Yüksel, 2007). The construction of hydropower stations could exert a significant influence on altering the upstream and downstream water quality (Zhang et al., 2005). These changes can greatly affect the microbial communities in the aquatic system (Sekiguchi et al., 2002; Yan et al., 2015). Several studies have described the impact of hydropower stations on phytoplankton (Sow et al., 2016; Ye et al., 2006; Zhou et al., 2011) and other related environmental changes (Zhang et al., 2005). However, there exists little data regarding their effects on microorganisms. Therefore, an attempt to determine the shift in microbial

communities caused by hydropower projects has also been emphasized in the present study.

We hypothesized that addition of high nutrient elements from anthropogenic sources associated with urbanization is an important impetus for altering the microbial communities in the surface water and sediment of urban rivers. In the current study, the Jialing River (Nanchong section), which is the second longest tributary of the Yangtze River impacted by urbanization and a small hydropower station, was chosen as a model to gain insight into the variation of bacterial communities in the urban river. We performed 16S rRNA gene-based high-throughput sequencing on the microbial communities of eight surface water samples (two of which were collected from the urban branches) and three representative sediments. The objectives of the study are as follows: (i) to study the spatial variations in bacterial communities along the urban river; (ii) to reveal the main environmental factors leading to the altered dynamics change of microbial communities; and (iii) to identify the response of microbial communities to urban discharge and the construction of a hydropower station in terms of microbial composition and metabolic prediction analysis.

2. Material and methods

2.1. Description of sampling sites

The Jialing River is the second longest tributary of the Yangtze River in China, and stretches over 1120 km from Qinling Mountain to Chongqing city (Zhang et al., 2008). Nanchong is located in the low reach of the Jialing River, and the river runs through Nanchong city. The flow direction throughout Nanchong City is from the north to the south. The area is highly urbanized with a population of over 7.6 million. Jialing River is the main source of drinking and household water, and also the main industrial and agricultural water supply for the city. Nanchong is an important light industrial city in the Sichuan Basin. With the development of the society and economy, river pollution has become an increasingly serious problem in recent years. The major sources of pollution are sewage runoff, dumpsites, contaminated grounds, and storm water runoff. Besides, the increasing anthropogenic alteration of the river bank and construction of a hydropower station construction has also had a great impact on the health of the Jialing River ecosystem. In total, eight sample sites were chosen in Jialing River from the upstream to downstream of Nanchong city. Samples were collected from the following sites: upstream of the Nanchong City (1W), upstream of the hydropower station (2W), downstream of the hydropower station (3W), a site near a drain outlet (4W), an urban branch of the river (5BW), midstream of the urban river (6W), an urban branch of the river (7BW), and downstream of Nanchong City (8W). Some of these sites are hard to reach to collect the corresponding sediment samples for the reason that there are two meters-high fences with barbed wire, or high concrete walls around the river bank. Three sediments were sampled from site 1, 7, and 8, and were respectively named as 1S, 7BS, and 8S. The sample site locations are indicated in Fig. 1 and Table S1.

2.2. Sample collection

Sampling was carried out on 17th September 2016. Surface water samples were collected manually by lowering sterile Schott bottles to a depth of 20 cm. All sampling sites were at 10 m from shore. Triplicate river water samples or sediments were collected by filling three 20 L carboys or plastic bags ($N = 3$). The three subsamples from each site were randomly obtained at an interval of 5 m. The collected samples were analyzed for various physicochemical parameters in triplicate. The pH and temperature of the water were determined immediately after sampling. Sediment samples from site 1, 7, and 8 were obtained using a stainless-steel shovel, from the shore in <1.5 m depth of water. Sediment samples were collected and transferred to plastic bags. Excess

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