

# Composition and distribution of microbial communities in natural river wetlands and corresponding constructed wetlands



Qingqing Cao<sup>a</sup>, Hui Wang<sup>a</sup>, Xiaocui Chen<sup>a</sup>, Renqing Wang<sup>a,b,c</sup>, Jian Liu<sup>a,\*</sup>

<sup>a</sup> Institute of Environmental Research, Shandong University, Jinan 250100, China

<sup>b</sup> School of Life Sciences, Shandong University, Jinan 250100, China

<sup>c</sup> Shandong Provincial Engineering and Technology Research Center for Vegetation Ecology, Shandong University, Jinan 250100, China

## ARTICLE INFO

### Article history:

Received 26 January 2016

Received in revised form 6 September 2016

Accepted 11 October 2016

Available online 26 October 2016

### Keywords:

Constructed wetland

River wetland

Proteobacteria

Nitrification

Denitrification

## ABSTRACT

Microbial community plays an important role in wetland ecosystem. To explore the composition and distribution of microbial communities in different wetland types, sediments from different sites of Xinxue River (XR) and Zhaoni River (ZR), and the corresponding Xinxue River Constructed Wetland (XRCW) and Zhaoni River Constructed Wetland (ZRCW) were sampled and analyzed using high throughput sequencing. The constructed wetlands were found to have more taxa of microbes in sediments than their corresponding river wetlands. The community richness index suggests that microbial richness in XR and XRCW is higher than that in ZR and ZRCW. High potential of sulfur cycle in XRCW is suggested by the superior distribution of *Desulfobacterales*, *Syntrophobacterales* orders, and *Thiobacillus* genus of *Proteobacteria*. Moreover, ZRCW has relatively lower nitrification ability than other three wetlands according to the distribution of *Nitrospirae*, *Planctomycetes*, and *Acidobacteria* phyla. XR and XRCW show high potential of methanogenesis as the distribution of *Methanomicrobia* order in Archaea. ZRCW is suggested in a state that organic carbon mineralization exceeds aggregation, denitrification exceeds nitrification based on different distributions of the functional bacteria (such as *Nitrospirae*, *Acidobacteria*, and *Planctomycetes*). Furthermore, it indicates that ammonia removal process in ZRCW sediments is mostly limited to nitrification. This study demonstrated that wetland functions can be detected by the composition and distribution of microbial communities and influenced by the pollution status and surroundings probably. Our results are essential for understanding the interrelationship between microbial distribution and the pollution status of wetlands for the evaluation of constructed wetland.

© 2016 Elsevier B.V. All rights reserved.

## 1. Introduction

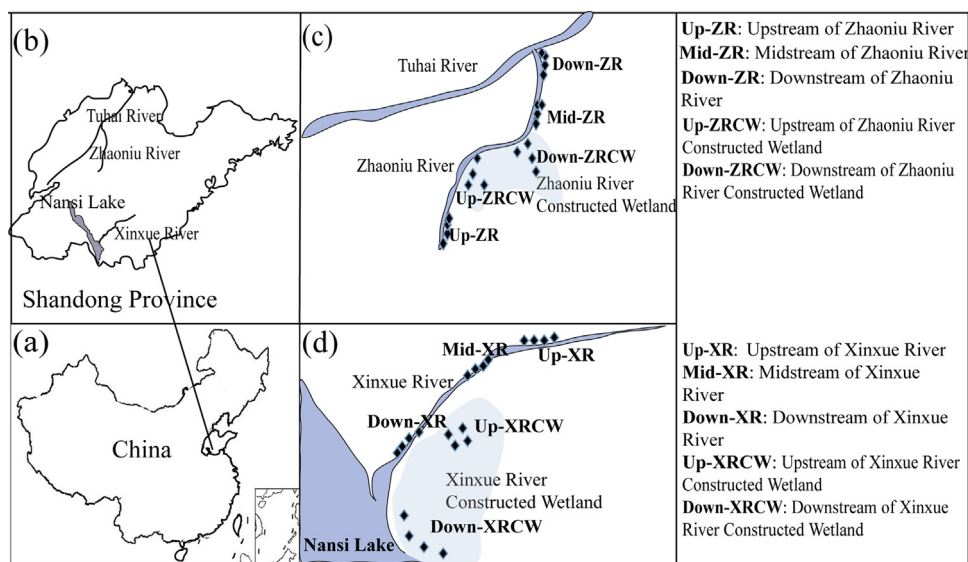
Due to their specific superiorities, different types of wetlands play various functions in ecosystems (Kansime et al., 2007; Robertson, 2004; Zhang et al., 2009). River wetlands, as one kind of natural wetlands, can purify river waters in the process of water diversion into lakes or seas (Robertson, 2004). With the discharge of domestic sewage and industrial wastewater, purification of river wetlands can hardly meet the safety standards of water quality in some regions. Based on the water purification principle of river wetlands and the aspiration to raise the purification efficiency of pollutants (Tota-Maharaj et al., 2012), many wetlands are designed and widely constructed around rivers in China, as well as worldwide (Vymazal, 2010; Zhang et al., 2009). At relatively low cost,

constructed wetlands were used to purify heavy metals, pathogenic bacteria, nitrogen and phosphorus, and other harmful organic pollutants from river waters and sediments effectively (Kadlec and Wallace, 2008; Puigagut et al., 2008). The processes of purification, such as sedimentation, decomposition, adsorption and plant uptake, mostly cannot be separated from the internal activities of microorganisms (Saeed and Sun, 2012; Samsó and García, 2013; Zhou et al., 2015).

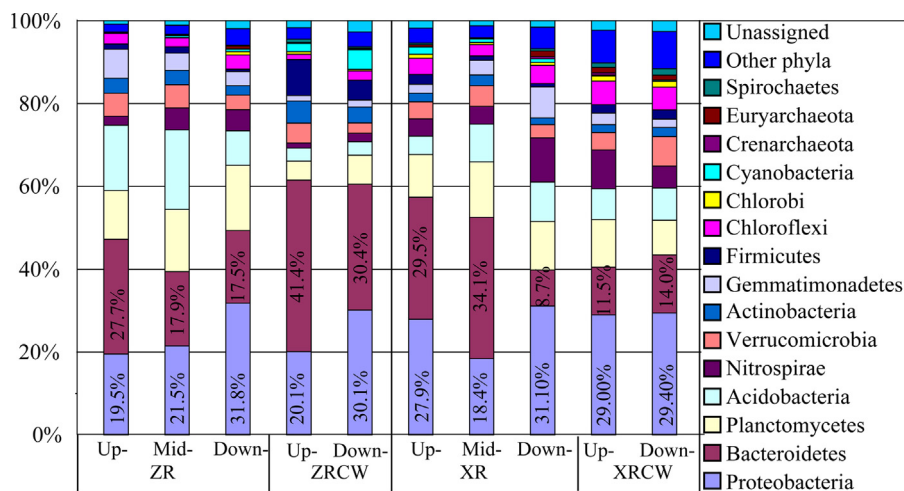
Microorganisms, including bacteria, fungi, and viruses (Schaechter, 2009), are widely in living organisms and their surroundings (Garcia et al., 2015). Microbial richness and evenness differ from their compatible environment, as microbes have their habit and features (Dheilly et al., 2015). Based on the differences of their surroundings and daily demands, microbes play different functions with daily activities (Sims et al., 2012a,b). In wetland ecosystems, plants, river waters and sediments are filled with many kinds of microbes (Tota-Maharaj et al., 2012). For example, *Proteobacteria* and *Bacteroidetes* are easily dominated

\* Corresponding author.

E-mail addresses: [ecology@sdu.edu.cn](mailto:ecology@sdu.edu.cn), [ecologyliu@qq.com](mailto:ecologyliu@qq.com) (J. Liu).



**Fig. 1.** National, regional, and local maps of the study area. Maps showing the (a) national, (b) regional, and (c and d) local geographical setting of the study area. Map (c) shows the location of the Zhaoni River (ZR) and Zhaoni River Constructed Wetland (ZRCW) and map (d) shows the location of the Xinxue River (XR) and Xinxue River Constructed Wetland (XRCW).



**Fig. 2.** Composition of different communities at phylum level in the two couples of wetlands. (Sequences that could not be classified into any known group are sorted as unassigned phylum; phyla that own few sequences are assigned as other phyla).

in wetland sediments (Ligi et al., 2014; Adrados et al., 2014). As the decomposer of the ecosystem, including the biosphere, microbial composition and function are easily interrelated with the surrounding environment (Merkley et al., 2004).

Microbes in natural wetlands have a naturally evolving relationships with their local environments (Yuan et al., 2009), whereas constructed wetlands are built and managed in order to simulate natural wetlands (Tiner, 1999; Zhang et al., 2009) for purposes that include water purification and pollution abatement (Sakadevan and Bavor, 1998). Thus, the microbial varieties and quantities, distribution and composition in natural wetland and their corresponding constructed wetland may have many differences. However, the research on microorganism by comparing constructed wetlands with the relevant river wetlands in China is sparse, or focused only on contrasting wetland types, which are not relevant (Jia et al., 2014; Rai et al., 2015).

Thus, in order to explore the differences in microbial community between relevant wetlands, two couples of natural river wetlands and corresponding constructed wetlands (Zhaoni River (ZR) and

Zhaoni River Constructed Wetland (ZRCW), Xinxue River (XR) and Xinxue River Constructed Wetland (XRCW)) of Shandong Province, China, were selected and sampled from upstream to downstream. This research is essential for understanding the processing of wetland ecosystem and for the evaluation of constructed wetland.

## 2. Materials and methods

### 2.1. Site selection and field sampling

This study was conducted at Zhaoni River Constructed Wetland (ZRCW) and Zhaoni River (ZR), Xinxue River Constructed Wetland (XRCW) and Xinxue River (XR), Shandong Province, China (Fig. 1a). ZR is a tributary of Tuhai River, which is one important river of Haihe River Basin (Fig. 1b). ZRCW was constructed in 2012 to purify the domestic sewage and industrial wastewater from cities nearby (Fig. 1c). XR is one of the principal rivers feeding Nansi Lake (Fig. 1d), one of the biggest lakes in the South-to-North Water Diversion Project. XRCW was constructed in 2007 in order to purify waters

Download English Version:

<https://daneshyari.com/en/article/5744052>

Download Persian Version:

<https://daneshyari.com/article/5744052>

[Daneshyari.com](https://daneshyari.com)