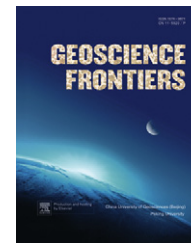


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RESEARCH PAPER

Diversity of microbial plankton across the Three Gorges Dam of the Yangtze River, China

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Abstract The Three Gorges Dam (TGD) of the Yangtze River, China, is one of the largest irrigation and hydroelectric engineering projects in the world. The effects of huge man-made projects like TGD on fauna and macrophyte are obvious, mainly through changes of water dynamics and flow pattern; however, it is less clear how microorganisms respond to such changes. This research was aimed to examine differences in microbial diversity at different seasons and locations (in front of and behind the TGD). In addition, differences between particle-attached and free-living communities were also examined. The community structures of total and potentially active microorganisms in the water columns behind and

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in front of the TGD were analyzed with the DNA- and RNA-based 16S rRNA gene phylogenetic approaches over three different seasons. Clone libraries of 16S rRNA genes were prepared after amplification from extracted DNA and, for some samples, after preparing cDNA from extracted rRNA. Differences were observed between sites at different seasons and between free-living and particle-attached communities. Both bacterial and archaeal communities were more diverse in summer than in winter, due to higher nutrient levels and warmer temperature in summer than in winter. Particle-attached microorganisms were more diverse than free-living communities, possibly because of higher nutrient levels and heterogeneous geochemical micro-environments in particles. Spatial variations in bacterial community structure were observed, i.e., the water reservoir behind the TGD (upstream) hosted more diverse bacterial populations than in front of the dam (downstream), because of diverse sources of sediments and waters from upstream to the reservoir. These results have important implications for our understanding of responses of microbial communities to environmental changes in river ecosystems affected by dam construction.

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1. Introduction

The Yangtze River is the third longest river in the world with a total length of ~ 6300 km and a drainage area of 1.8×10^6 km². The river runoff amounts to 905.1×10^9 m³/y, and sediment discharge averages 348 million t/y since the mid-1980's (Chen, 2008). For such a large river, any disturbance to the water dynamics along the water flow path is expected to cause major changes to regional climate, aquatic system health, and human activity.

The Three Gorges Dam (TGD) built in the middle reach of the Yangtze River, ~ 1800 km upstream from the Yangtze River estuary, is one of the largest irrigation and hydroelectric engineering projects in the world (Huang, 2001). The TGD is 185 m high and 2300 m long with a drainage area of 1080 km² and a total water storage capacity of 39.3 billion m³ (Jiao et al., 2007). One major consequence of the TGD is reduced sediment load from the Yangtze River to the East China Sea, from 348 million t/y for the pre-TGD period to <100 million t/y after the construction of the TGD (Chen, 2008). Such a dramatic decrease in sediment load is expected to have a large impact on water quality, photosynthetic activity, and aquatic system health (Jiao et al., 2007; Chen, 2008). One study has shown that the storage of 12.4 billion m³ of water within the first 10 days of the completion of the TGD in 2003 caused 27% reduction in flow rate and a 4-fold increase in chlorophyll-*a* production (a measure of primary production) (Jiao et al., 2007). Such an enhanced photosynthetic activity is ascribed to reduced sediment load and increased light transparency (Jiao et al., 2007). Subsequent decay of algal biomass carried to the Yangtze River estuary may enhance consumption of oxygen and results in hypoxia in the bottom layer of the estuary.

Many other studies have demonstrated the effects of habitat fragmentation of fauna and macrophyte in the Yangtze River ecosystem caused by the TGD (Lei, 1998; Wu et al., 2003; Chen and Xie, 2009; Hu et al., 2009). In contrast, only a limited number of studies have been conducted to assess the influence of the TGD on microbial ecology. Before the TGD construction, bacterial diversity was shown to gradually change from the upstream to the downstream (Sekiguchi et al., 2002a, b). After the TGD construction and water storage in June 2003, marked changes of bacterial community structure in the Yangtze River-East China Sea estuary were observed: the overall bacterial diversity became lower, the abundance of the freshwater bacteria *Betaproteobacteria* decreased and the diversity of *Alphaproteobacteria* and

Cyanobacteria increased (Jiao et al., 2007). Such observed changes were ascribed to sudden reduction of river runoff and ensuing intrusion of ocean currents (Jiao et al., 2007), little is known how the TGD construction affects the diversity of microbial communities in the immediate vicinity of the dam.

We hypothesize that (1) microbial diversity in summer is higher than in winter because of higher nutrient contents and higher temperature in warm climate; (2) differences exist in microbial diversity and community structure between water column and suspended sediment particles; (3) the TGD water reservoir traps diverse microorganisms from a variety of sediment and runoff sources from the upstream; and in contrast, the downstream river immediately below the dam would have lower microbial diversity because of reduced load and limited sources of sediments and surface runoffs. The objective of this study was therefore to test these three hypotheses by investigating microbial diversity behind (i.e., the water storage reservoir) and in front of the TGD during three different seasons in free-living and particle-attached communities.

2. Materials and methods

2.1. Field measurements and sample collections

In May, July, and December 2009, vertical profiles of water chemistry from upstream and downstream were measured near the TGD using a submersible multiple parameter probe set Horiba (U20D, Japan) on a motorized boat. The field measurements did not show any significant variations in water chemistry along the lateral (upstream and downstream by ~ 5 km) transect behind and in front of the TGD, however, important differences were detected across the dam. Therefore, for each season, one representative (in geochemical sense) sample behind the dam and one in front of the dam were analyzed for detailed water chemistry and microbiology. The locations for the July and December samples were the same, but the May sample behind the dam was further upstream (Fig. 1). At these three locations, there was no significant variation in water chemistry throughout the vertical profile of the water column. So for laboratory analyses, water samples were collected from the 5 m depth with a submersible pump. At each sampling location, river water samples were collected and preserved for dissolved organic carbon (DOC) analysis according to a previous protocol (Jiang

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