

Title: 16S rRNA based bioassessment of water quality impacted by 5th WWTP effluent in Ba River

Members' names

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1. Aim: The objective of the present study was to evaluate the effects of WWTP effluent on the structure of microbial community.

2. Procedure

2.2 Sampling sites

Water samples were collected from the Ba River that includes an outfall of the 5th municipal wastewater treatment plant (WWTP; Fig. 1). Three sampling sites were selected including a site located up-stream (U) from the WWTP outfall, a mid-stream site (M) located near the outfall of WWTP, and a site located down-stream (D) from the WWTP discharges. Here, sharpbelly collected from up-, mid- and down-stream of Ba River that were designed to be interpreted as control, high, and low treatment groups, respectively. Four water samples were collected from each fishing spot for determination of the physico-chemical parameters (ammonium nitrogen, chemical oxygen demand (COD), conductivity, dissolved oxygen, pH, redox potential, and temperature).

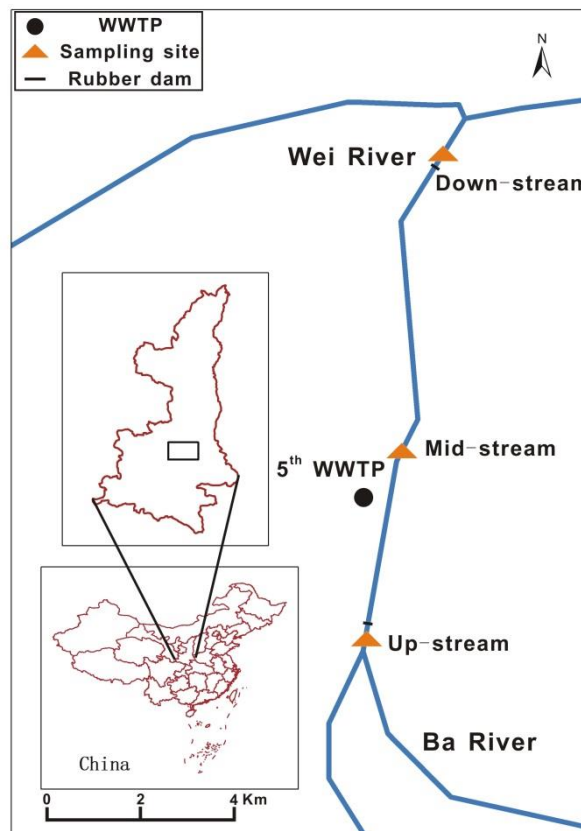


Fig. 1. Map of the study area and the sampled site location. The study design incorporated three sampling sites, including a site located up-stream from the WWTP outfall, a mid-stream site located near the outfall of WWTP, and a site located down-stream from the WWTP discharges.

2.3 Illumina PE250 sequencing and Bioinformatics analysis

Biodiversity of microbial communities in each sample was analyzed by Biozeron biotechnology company (Shanghai, China) following the standard 16s rRNA procedures.

3. Result

We have obtained the 16s rRNA sequencing results but it still takes time to analyze in depth. Some key findings are illustrated in the figures below.

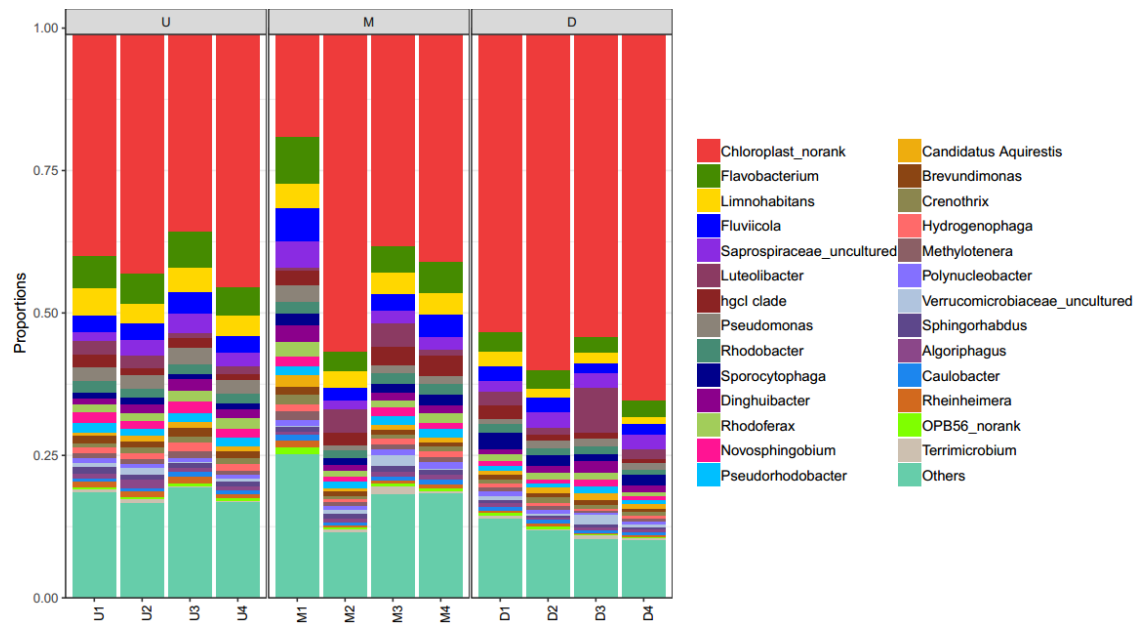


Fig.2 Genus-level microbial community barplot of water samples collected from each sites.

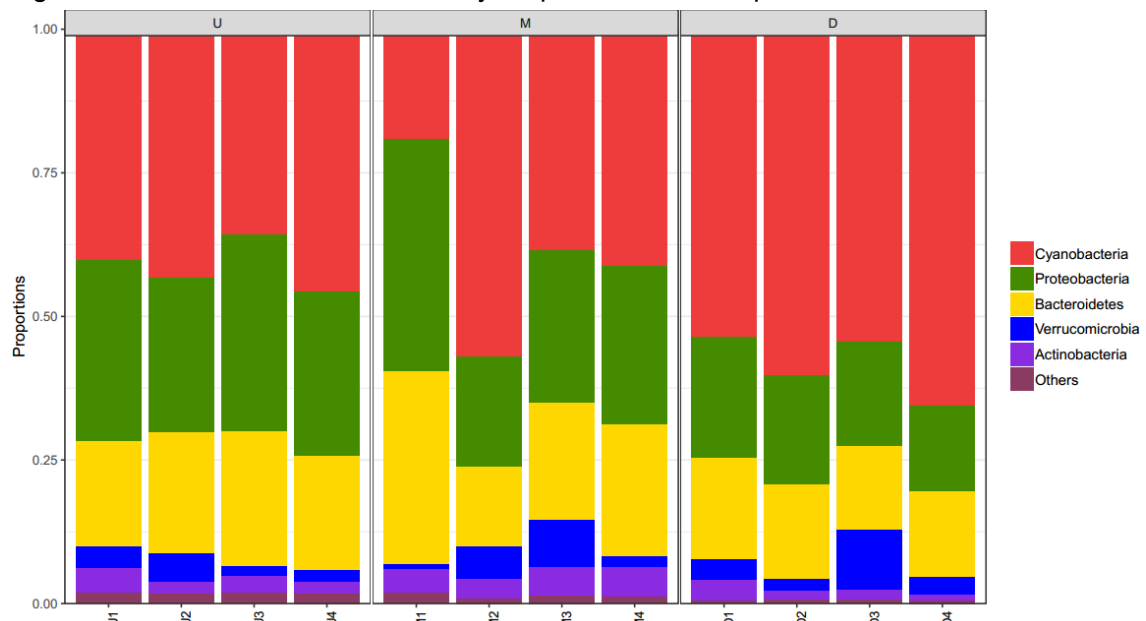


Fig.3 Phylum-level microbial community barplot of water samples collected from each sites.

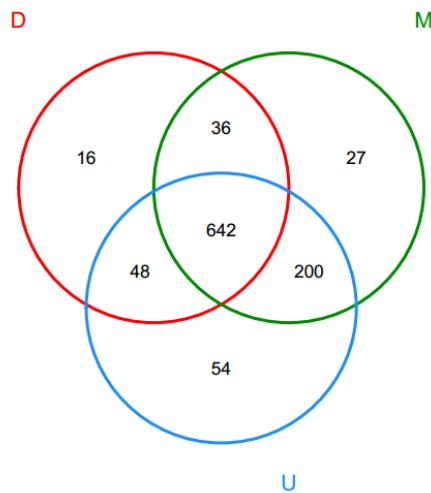


Fig.4 Venn diagram of operational taxonomic unit (OUT) in water samples collected from three sites.

4. Publication/conference presentation,

This work has not been published/ presented in any conference.

5. Perspectives in future

16s rRNA is a cheap technique to investigate the structure of microbial community compared to metagenome (environmental DNA), so 16s rRNA is valuable for preliminary checking prior to performing metagenome and chemical analyses. As indicated in figures 2&3, it seems that the structures of microbial community have not been significantly affected by WWTP effluent. As this may be due to the flow of river, we may consider to move to sediment study, which characterize the effects of WWTP effluent on the structure of microbial community in sediment. Similarly, preliminary check using 16s rRNA will be initially conducted.