Abundance and diversity of sulfate-reducing bacteria in the sediment of the Zhou Cun drinking water reservoir in Eastern China

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ABSTRACT. Sulfate-reducing bacteria (SRB) play an important role in the sediments of bay areas, estuaries, and lakes. However, information regarding the genetic diversity of SRB in the sediments of drinking water reservoirs is scarce. In this study, we collected sediment samples from different sites in the Zhou Cun drinking water reservoir between April and June 2012. To explore the genetic diversity of SRB, we used the most-probable-number (MPN) method, polymerase chain reaction denaturing gradient gel electrophoresis (PCR-DGGE), and a cloning approach. The average content of acid-volatile sulfide at the deepest sampling site was 205.87 μg/g sediment. This result is often associated with a large abundance of SRB in the associated sediment. The highest MPN estimate (1.15×10^5 cells/g sediment) was detected in May at the deepest sampling site. The PCR-DGGE fingerprints of SRB based on the dissimilatory sulfite reductase beta subunit (*dsrB*) gene varied according to the different sampling sites and dates. The highest abundance of SRB in the sediments was predominantly found at the deepest sampling sites,

as expected from the acid-volatile sulfide content. The dominant species were *Desulfobulbus* sp, *Desulfobacterium* sp, and uncultured sulfate-reducing bacteria. Redundancy analysis revealed that organic matter and the concentrations of nitrogen and phosphorus in the sediments were significantly correlated with the diversity of SRB communities present. The results of this study provide a better understanding of the sulfate-reducing microbial species in the sediments of the Zhou Cun drinking water reservoir.

Key words: Drinking water reservoir; Sulfate-reducing bacteria; Dissimilatory sulfite reductase beta subunit gene