

# Study on the Mechanism of Microbial Communities in Bottom Sediments Driving Algae Bloom by Phosphorus Oxygen Cycle

**Yemei Kong<sup>\*</sup>**

College of Resources and Environment, Southwest University, Chongqing, China

## Email address:

1599588931@qq.com (Yemei Kong)

<sup>\*</sup>Corresponding author

## Abstract

In order to reveal the ecological mechanism of the regulation of algal blooms by the functional network of sediment microorganisms, this study conducted an outdoor water ecosystem space experiment on high-temperature sterilization of sediment in the Three Gorges Reservoir area, Pengxi River Bay, from April 30 to May 19, 2023. The experimental group S (sterilized sediment+river water in Pengxi River) and the control group C (sediment+river water in Pengxi River) were set up. Combined with high-throughput sequencing of 16S/18S rRNA genes, monitoring of water phosphorus and oxygen parameters, and analysis of algal biomass, the regulatory effects of microbial community structure on phosphorus cycling, dissolved oxygen dynamics, and competition between blue-green algae and dinoflagellates were systematically analyzed. The results showed that on April 30th (day 0), functional bacterial groups such as *Sphingomonas* (8.17%), *Micrococcaceae* (9.35%), and *Acanthodiatomus* (14.01%) were the dominant groups in Group C; After high-temperature sterilization, the sensitive bacterial community (such as *Alkandiges*) disappeared in Group S, and the heat-resistant bacteria *Exiguobacterium* (27.35%) and the native organism *Cercomonas* became the dominant groups. (2) On May 19th (the 20th day), Group C formed a stable microbial network (26.87% of *Micrococcus* and 36.43% of *Daphnia*), while Group S experienced a significant increase in dissolved total phosphorus (DTP) release by 37% (up to 0.039 mg L<sup>-1</sup>) due to excessive proliferation of eukaryotic phosphate solubilizing bacteria (*Acinetobacter*, 7.88%) and feeding inhibition of planktonic animals, with a peak biomass of 95.0 mg · L<sup>-1</sup> for dinoflagellates. (3) Correlation analysis showed that the heterotrophic respiration of group S dinoflagellates intensified the depletion of dissolved oxygen (DO) (12.44 → 7.18 mg · L<sup>-1</sup>), driving the enrichment of low oxygen tolerant heterotrophic bacteria (such as *Lysobacter*,  $r=0.743^{**}$ ); At the same time, the absence of *Novosphingobium* weakens the phosphorus retention capacity of sediment, promoting a shift in chlorophyll sources from live cyanobacteria to dinoflagellate residues ( $r=-0.452$ ). In summary, sediment microorganisms suppress dinoflagellate blooms by maintaining a dynamic balance of phosphorus and oxygen, while the collapse of sediment microbial communities caused by high-temperature sterilization leads to phosphorus competition imbalance and low oxygen environment, driving dinoflagellates to become dominant species. The research results provide a theoretical basis for maintaining the steady-state of sediment microorganisms in the restoration of eutrophic water bodies, and provide scientific references for monitoring and management of water ecological protection and restoration in the Three Gorges Reservoir area.

## **Keywords**

Mesocosm, Sterilization of Sediment, Microbial Functional Network, Phosphorus Oxygen Cycle, Dinoflagellate Bloom, Pengxi River, Gene Sequencing