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Cyanobacterial Abundance and Diversity During Algal Blooms in a Korean Large Reservoir

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Blooms of the cyanobacteria such as *Microcystis*, *Anabaena* and *Oscillatoria* are ubiquitous phenomena in eutrophic lakes and reservoirs in many countries of the world. Many strains of bloom-forming cyanobacteria are known to produce cyanobacterial hepatotoxins called microcystins. These toxins are soluble peptides and are lethal to many kinds of aquatic organisms. Therefore, cyanobacterial bloom is an important issue in the management of water quality.

Daechung Reservoir is located on the upper part of the Geum River in the central region of South Korea (36° 50' N; 127 ° 50' E) and is a large branch-type, dimictic, and temperate lake. It was constructed in 1980 to conserve water resources. Since the end of the 1980's, the reservoir has shown some signs of eutrophication, such as cyanobacterial blooms in the summer and a deterioration in water quality. The quantitative expression of bloom formation has been done using chlorophyll-*a* data traditionally. However, chlorophyll-*a* could not represent the degree of cyanobacterial blooms satisfactorily because chlorophyll-*a* also increases during the dominance of diatoms in autumn. Under these conditions, new indicators other than chlorophyll-*a* and nutrient concentrations are required to monitor bloom formation, particularly cyanobacterial blooms.

Cyanobacterial diversity and abundance can be determined based on the data of the identification and cell counting under the light microscope. In the identification of cyanobacterial species, we usually have some difficulties such as the following: the identification should be carried out by the algal taxonomist, the picocyanobacteria which are so tiny to be observed under the microscope become more important in the aquatic environment, etc. Therefore, we tried to use the molecular techniques to identify and quantify the cyanobacteria in water and to compare the results by the molecular methods with those by the traditional methods.

1. Phytoplankton community in Daechung Reservoir

The physicochemical and biological water qualities were investigated from spring to autumn in 1999 in the Daechung Reservoir, Korea. The dominant species in the cyanobacterial blooming season

was *Microcystis*. The microcystin concentration was highly correlated with the phytoplankton number ($r = 0.650$; $P < 0.01$) and chlorophyll-*a* concentration ($r = 0.591$; $P < 0.01$). Therefore, it seems that the microcystin concentration in water can be estimated and indirectly monitored by analyzing the following: the phytoplankton number and chlorophyll-*a* concentration, the ratio of particulate to the dissolved form of N and P, and the particulate N:P ratio when the dominant species is toxigenic *Microcystis*.

The phytoplankton community and environmental factors were investigated from July to October in 2001 and 2003 on Dam site in Daechung Reservoir. The maximum chlorophyll-*a* concentration was observed higher at 131.5 $\mu\text{g/L}$ in 2003 than at 45.4 $\mu\text{g/L}$ in 2001. The cyanobacterial number in 2001 was counted up to over 200,000 cells/ml, which was much higher than the maximum number of 49,000 cells/ml in 2003. The relative abundance of cyanobacteria in the phytoplankton community was about 97% in 2001 and 74% in 2003. *Microcystis* spp. were absolutely dominant species in 2001, while a couple of cyanobacteria such as *Oscillatoria* spp., *Phormidium* spp. *Chroococcus* spp. and *Microcystis* spp. were dominant species in 2003.

2. Analysis of microbial communities by using DGGE

The change of bacterial communities during cyanobacterial bloom was analyzed by denaturing gradient gel electrophoresis (DGGE) in Daechung Reservoir from July to October in 2003. The traditional morphological analysis showed that the genera of *Microcystis*, *Chroococcus*, *Oscillatoria*, and *Phormidium* were dominated. The most frequent band in the DGGE profile by 16S rDNA sequence analysis was identified to *Microcystis flos-aquae* and the cyanobacterial bloom was peaked on September 2. *Oscillatoria* spp. were also identified and *Aphanizomenon flos-aquae* dominated in the middle of August. Judging from the analysis of the digitalized DGGE profiles using the cluster analysis technique, the microbial community on September 2 was considerably different. Consequently, it seems that the gene fingerprinting method can give not only the similar results to the traditional morphological method but also additional information on the bacterial species and similarity among the examined microbial communities.

3. Cyanobacterial abundance and diversity based on *cpcBA* sequences

Diversity of cyanobacteria and their community dynamics during cyanobacterial bloom were studied in Daechung Reservoir, Korea, based on analysis of *cpcBA*. For amplification of *cpcBA* from environmental samples, polymerase chain reaction (PCR) primers were developed based on known *cpcBA* sequences. From samples around the peak of bloom (Sept 2, 2003), we found seven groups of *cpcBA* sequences. Except *Microcystis*-like group, *Aphanizomenon*-like group, and *Pseudanabaena*-like group, other 4 groups of *cpcBA* sequences were distantly related to previously reported sequences

(about < 85% similarity in *cpcB* sequence to closest relatives). A dynamic change of cyanobacterial community during the bloom was observed.

References

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