

Cyanobacteria And Their Phages Revealed Through Metagenomic Analysis In A Freshwater Lake

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Extended Abstract

Climate change affects aquatic environments. In Lake Biwa, the largest monomictic freshwater lake in Japan, the water temperature has slightly increased. In 2019, the water column was first not completely mixed since monitoring started in 1979 because of weaker cooling and weaker winds during the winter season [1]. These phenomena cause stronger stratification and oxygen depletion at the bottom layer, leading to the elusion of phosphorus from sediments. Moreover, nutrients (nitrogen and phosphorus) accumulated in the bottom layer will not be supplied to the surface layer during the vertically mixing period. This affects the growth and composition of cyanobacteria (including bloom-forming bacteria) in the next season [2], influencing the ecology or carbon cycling in the freshwater lakes.

In Lake Biwa, up to 70% (average 38%) of bacterial production is infected and killed by bacteriophages at the surface layer in the summer season, during which cyanobacteria are dominated [3]. However, the infection rate in the previous study was evaluated as a bulk system that did not distinguish bacterial species, and we do not know whether cyanobacteria in the summer season is suppressed by viral infection. Since cyanobacteria is a key driver of carbon cycling or may cause harmful bloom, it is crucial to clarify the interaction between cyanobacteria and their phages in the freshwater lake.

Bacterial diversity and seasonal variation have been revealed using universal primers (i.e., 16S rRNA gene) in many environments. In contrast, viral genomes lack a universal gene, and viromic study has been lagging. However, the recent metagenomic sequencing method, which is cultivation-independent, made it possible to clarify the phage diversity. Here we describe the diversity and seasonal variation of cyanophage in Lake Biwa using the metagenomic technique.

In this study, we collected lake water samples monthly from the surface euphotic layer (5m) and deep aphotic layer (60 m) for 14 months. We obtained 33 complete (circular) viral genomes and 66 viral contigs (fragments) predicted to infect cyanobacteria in Lake Biwa. Their genome or contig size was ranged from 11.0 to 355.9 kbp. Of the 99 phages, 31 were predicted as the Myoviridae family, 17 as the Podoviridae family, and 17 as the Siphoviridae family. The abundance of these 99 phages increased at the surface layer in the summer season (around July to September) when the relative abundance of cyanobacteria increased. Moreover, we identified 14 cyanophages that may infect a cyanobacterial species predominated in Lake Biwa (7% in September) using co-occurrence and association analysis. These results suggest that the activity of cyanophages in Lake Biwa is closely linked to the activity of cyanobacteria and is an essential factor in controlling the abundance of cyanobacteria.

References

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