

Abstract

# Ubiquity, Diversity, and Genomic Complexity of Cyanophages in Freshwater Environments <sup>†</sup>

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**Abstract:** Cyanophages are viruses that infect cyanobacteria (also known as blue-green algae) and are ubiquitous in marine and freshwater environments. In recent years, freshwater cyanophages have attracted more attention because they can affect global freshwater ecosystems. The spatial distribution and morphological diversity of cyanophage populations were examined in Lake Donghu with three trophic regions: hypertrophic, eutrophic, and mesotrophic regions. The surprisingly high viral abundance (ranging from  $10^8$  to  $10^9$  phage  $\text{mL}^{-1}$ ) and morphological diversity were detected. Most of them have tails and belong to the families *Siphoviridae*, *Myoviridae*, and *Podoviridae*. Various morphotypes were observed, such as prolate-headed virus-like particles and lemon-shaped virus-like particles. In addition, some cyanophages were studied by virological experiments and whole-genome analyses, combined with morphological observation. For example, three cyanophages were isolated and their whole genomes were sequenced. Contractile tail myonophage MaMV-DC infects bloom-forming cyanobacterium *Microcystis aeruginosa*. Tailless cyanophage *Planktothrix agardhii* virus isolated from Lake Donghu (PaV-LD) infects filamentous cyanobacterium. Short-tail podovirus A-4L can infect the model cyanobacterium *Anabaena* sp. strain PCC 7120. The MaMV-DC genome contains 169,223 bp encoding 170 putative open reading frames (ORFs). The PaV-LD genome possesses 95,299 bp encoding 142 putative ORFs. The genome of short-tail podovirus A-4L has 41,750 bp encoding 38 putative ORFs. There are significant differences in their genomic size and encoded tail proteins, but all three cyanophages contain genes that are not commonly found in phages. By studying the vast biodiversity of viruses in freshwater environments, these novel findings of cyanophages broaden our insights, and allow us to gain more useful knowledge about the global impact of these viruses in freshwater ecosystems.

**Keywords:** cyanophages; genomic complexity; freshwater environment

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