

論文の要約データ

Title

Comprehensive studies on transcriptional dynamics of cyanoviruses infecting a bloom-forming cyanobacterium *Microcystis aeruginosa*

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Summary

Toxic bloom-forming cyanobacterium *Microcystis aeruginosa*, which has the highest number of putative antiviral defense genes, interacts with diverse viruses in the environment, resulting in the diversification of their population. Despite such potential importance of cyanoviruses in *Microcystis* blooms, little is known about even the whole host transcriptional responses and infection process of a sole *Microcystis* virus Ma-LMM01.

In chapter 2, I first performed a transcriptome analysis to investigate infection process of Ma-LMM01 and assess host transcriptional responses to infection in a culture experiment with a Ma-LMM01 infection. Interestingly, almost all of the host genes did not show a significant change in expression, whereas transcriptional program of Ma-LMM01 showed the distinct three temporal expression classes of early, middle, and late, like other lytic ds DNA viruses. In addition, cyanobacterial primary σ factor SigA recognition-like sequences were found in the upstream region of each viral class genes. These findings suggested that Ma-LMM01 achieves three gene expression patterns without affecting the host physiology to escape the highly abundant host defense systems by exploiting SigA for its transcription.

In chapter 3, I further examined the genomic information and transcriptional dynamics of *Microcystis* viruses in the environment using cross-omics analysis. As a result, virome approach revealed that three novel phylogenetic viral groups: Group I (including Ma-LMM01), Group II (high abundance and transcriptional activity) and III (new lineages). Of these, Group II viruses interacted with all three phylogenetically distinct types of host populations whereas other two group viruses interacted with only the one or two types of host populations. All these viruses showed transcriptional peak levels at daytime, indicating that they actively infect its host in the environment.

These studies expand our knowledge about infection profiles, host responses, the genomic features of other *Microcystis* viruses. Future work on the seasonal dynamics of each viral group and their hosts will also help us to further understand the viral impact on *Microcystis* blooms as well as the isolation and characterization of them.