

藻類発生期の自然環境における巨大ウイルス群集の継続的な遺伝的・発現的適応

Ongoing genetic and expression adaptation of giant virus community
in a natural environment during algal bloom period

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研究成果概要

This study is using the supercomputer of Institute for Chemical Research, Kyoto University, to do an analysis for exploring the phenomenon of genetic and expression adaptation of giant virus community in an enclosed bay, west Japan.

Giant viruses are very abundant and ubiquitous in the sea water and affect marine microbial community (especially for their eukaryotic hosts) by their lytic infection cycle. However, there is only a few studies about the genetic and expression adaptation of giant virus in the natural environment has been reported. Comprehensive research (especially on the virus who infect red tide forming species) is needed.

For studying giant virus and microbial eukaryotic community, we sampled surface sea water during algal-bloom period at coastal area of Japan. Then we did the sequencing both for DNA and RNA samples. Metagenomic assembled genomes (MAGs) of giant virus were generated through an updated pipeline. Genetic and expression features were then analyzed. Microbial eukaryotic community was analyzed based on meta-barcoding data. In the results we found that (1) the giant virus community was incredibly diverse, even in the enclosed area during short period; (2) Some genes were under positive selection; (3) Giant virus community was tightly associated with their eukaryotic host community in several samples; (4) Expression level of specific genes were surprisingly higher than usual. Future study will mainly focus on the more detailed analysis for exploring the reasons why giant viruses keeping adapting the environment in such a short period.