

巨大ウイルスの進化過程に関する研究

Analysis of the evolution of giant viruses

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研究成果概要

To understand the whole picture of evolution history of giant viruses, this study investigated their on-going evolution first. This study starts with investigating the true diversity of giant viruses in a freshwater lake. I used the metagenomic data from Biwa Lake. Spatiotemporal sampling from two water layers enabled us to investigate their different adaptive strategies in hypolimnion and epilimnion respectively.

I mainly used tools related to contig assembly (SPAdes), genome binning (metabat2), and viral annotation (CAT/VirSorter/ViralRecall). As a result, I got hundreds of metagenomes assembled NCLDV genomes for downstream analysis. Then I analyzed the community genome dynamics across the whole sampling year and found NCLDVs are showing different consistency in two water layers. I also used mapping tools to evaluate the coverage of contigs and MAGs (BWA/minimap2/samtools/CoverM/Bowtie2). I removed low-coverage MAGs from downstream analysis.

For further analysis, I would analyze the tandem repeats found in NCLDV MAGs are family-specific or prevalent in all NCLDV genomes.