

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 evolution history of giant virus, we should investigate its ecological function first. Since there are studies looking into the diversity of giant viruses in marine system, my study starts with investigating what kind of giant viruses are there in fresh water.

I used the metagenomic data from Biwa Lake. on the one hand, we want to investigate from the aspect of MAG (metagenomic assembled genomes). Firstly, SPAdes Genome assembler is used to assemble the short reads into longer contigs. Secondly, contigs are binned into MAG using metabat. Also, to annotate the contigs and bins we got, viralrecall, virsorter, and CAT are used to recognize bacterial and viral contigs, which helped the downstream decontamination. This whole process is not finished yet.

On the other hand, we detect single copy gene—polB from contig level. We considered one polB as one individual giant virus present in the environment. We can quantitate giant viruses from different families and look into the reason behind this ecological diversity pattern.