

深海に棲息する巨大ウイルスの生態

Ecology of giant virus in deep ocean

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研究成果概要

Giant viruses (GVs) are large double-stranded DNA viruses that infect a variety of eukaryotic microorganisms. According to the large-scale metagenomic data analyses, GV s are proved to be broadly distributed at a high density and exhibit infectious activity in the ocean, potentially play critical roles in the ecological and evolutionary dynamics of eukaryotic communities.

In the marine system, knowledge about GV s is so far mainly focused on the photic zone. The investigations of GV s in the aphotic layer (at depths below 200 m) are limited because of the lower organism density and the high difficulty to conduct a large volume of sampling for extracting high-quality of DNA and RNA from eukaryotic microorganisms and viruses. So far only few studies reported focusing on conserved marker genes with low phylogenetic resolution.

In this research, we generated a metaomics dataset that includes 18S rRNA/rDNA metabarcodes, metagenomes, and eukaryotic metatranscriptomes from mesopelagic (320 m) seawater samples seasonally collected at the Kochi Prefectural Deep Seawater Laboratory in Muroto. 48 GV bins were assembled and analyzed by megahit, trinity, coverm and so on through supercomputer. Our findings highlight the presence and activity of GV s, particularly those from the Imitervirales and Algavirales orders, in the mesopelagic layer. Analyses of the seasonal variations in community compositions revealed that both GV s and microeukaryotes are more stable in the deepsea than in surface layer. Furthermore, we found that some of the identified GV s belong to a clade of GV s showing a strong habitat preference for aphotic layers of the ocean. Investigation of these mesopelagic GV s genomes is underway with the aim of understanding their ecological roles and adaptive strategy in the deep ocean.