

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 is 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 is so far mainly focused on the photic zone. The investigations of GV 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, by sampling at different layer in the East Indian Ocean, enough DNA were extracted for sequencing. 18S v4 region were ampliconed and sequenced by next generation sequencing. Eukaryotes community structures were figured out by using Qiime in supercomputer, a pipeline for analyzing 18S barcoding sequencing results. The result showed that community composition of eukaryotic microorganisms, which served as host of GV, changed greatly between different ocean layers. That indicate GV communities may also evolve a correspond strategy to adapt to such change of their host and a rush environment condition in deep sea layer. Further research will focus on the genetic composition and infectious activity of the GV and probe the interactions between the GV and eukaryotic microbes in the aphotic layer.