

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) of the phyla *Nucleocytoviricota* and *Mirusviricota* are large double-stranded DNA viruses that infect a variety of eukaryotic microorganisms. Large-scale metagenomic analyses have shown that GVs are broadly distributed and exhibit infectious activity on Earth. In marine systems, knowledge of the diversity and ecological roles of GVs in the photic zone has been well studied. However, less is known about their activity, population dynamics, and adaptive strategies in the aphotic layer (at depths below 200 m) due to lower organismal densities and the difficulty of collecting large volumes of seawater to extract high-quality DNA and RNA from eukaryotic microorganisms and viruses.

In this research, we conducted eight seasonal time-series samplings of the surface and mesopelagic layers at a coastal site in Muroto, Japan, and generated a multi-omics dataset that includes 18S rRNA/rDNA metabarcodes, metagenomes, and eukaryotic metatranscriptomes to investigate mesopelagic GV and their potential hosts. The analysis identified 48 GV genomes, including six that were exclusively detected in the mesopelagic layer and showed persistent activity across seasons. To further investigate the global distribution of GV across broader depths, a global GV MAG dataset (named the GVGR database) was compiled from publicly available data. Using the GVGR database, we performed a systematic analysis of 1,890 public marine metagenomes to identify deep-sea-specific GV. This analysis revealed 101 deep-sea-specific GV distributed across the GV phylogenetic tree, indicating that adaptation to deep-sea environments has occurred in multiple lineages. Seventy-six KEGG orthologs and 74 Pfam domains were specifically enriched in deep-sea-specific GV, encompassing functions related to energy metabolism, nitrogen acquisition, and the ubiquitin system. These findings support the idea that distinct GV lineages have adapted to hosts in deep-sea environments by altering their gene repertoire to thrive in this unique habitat.

発表論文(謝辞あり)

Liu W, Nagasaka K, Wu J, Ban H, Mimick E, Meng L, Neches RY, Moniruzzaman M, Yoshida T, Nishimura Y, Endo H, Okazaki Y, Ogata H. Giant viruses specific to deep oceans show persistent presence and activity. *mSystems*, 10:e00932-25 (2025).