

ゲノム解析を通じた巨大ウイルスの種内多様性

Genome-resolved year-round dynamics reveal a broad range of giant virus microdiversity

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研究成果概要

Giant viruses are a diverse and abundant group of double-stranded DNA viruses infecting marine microeukaryotes. They significantly influence marine ecosystem dynamics by regulating host populations, accelerating carbon and nutrient cycles, and driving host evolution through co-evolutionary processes. Despite their recognized ecological roles, the genetic mechanisms underlying observed seasonal fluctuations in giant virus abundance remain poorly understood.

Leveraging supercomputing resources, we analyzed time-series metagenomic data from coastal seawater samples over 20 months, generating 1,065 high-quality genomes from six giant virus lineages. Our analyses revealed consistent year-round recovery of viral communities, with distinct dynamics categorized as persistent, seasonal, sporadic, or others. Importantly, year-round recovery was evident not only at the community level but also within individual viral populations, particularly those classified as persistent or seasonal. Further investigation revealed a significant relationship between niche breadth and microdiversity, with viruses occupying broader ecological niches exhibiting higher levels of genetic diversity. This increased microdiversity likely facilitates enhanced adaptability, improving virus survival during prolonged interactions with hosts.

発表論文(謝辞あり)

1. Fang Yue†, **Lingjie Meng**†, Jun Xia, Yasushiro Gotoh, Tetsuya Hayashi, Keizo Nagasaki, Hisashi Endo, Yusuke Okazaki, and Hiroyuki Ogata. (2024). Genome-resolved year-round dynamics reveal a broad range of giant virus microdiversity. *mSystems*, e0116824 (2024).