

Genome-Resolved Dynamics of Giant Virus Communities and HaV Populations During a Short-Term Harmful Algal Bloom in Japan

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研究成果概要

This study is using the supercomputer of Institute for Chemical Research, Kyoto University, to do an analysis for giant virus community and HaV population during the short bloom period in an enclosed bay of Japan.

We explored the dynamics of giant viruses during a natural harmful algal bloom in Uranouchi Inlet, Japan. By integrating high-frequency sampling with metagenomic, metatranscriptomic, and metabarcoding approaches, we reconstructed hundreds of giant virus metagenome-assembled genomes (GV-MAGs), including a near-complete environmental genome of *Heterosigma akashiwo* virus (HaV). The project required large-scale co-assembly of time-series metagenomes, genome binning, dereplication, phylogenomic reconstruction, and genome refinement. These analyses enabled us to trace fine-scale temporal shifts in viral population structure, microdiversity, and gene expression during bloom progression, revealing rapid diversification dynamics and signatures of host-driven selection acting on standing genetic variation.

Rapid shifts in HaV population structure over short time scales, accompanied by dynamic changes in nucleotide diversity and allele frequencies, were observed. These patterns suggest that viral populations respond quickly to fluctuations in host abundance and environmental conditions. Selection analyses revealed that most viral genes were under purifying selection, while a limited subset showed signatures of positive selection, indicating adaptive fine-tuning during host-virus interactions. In particular, certain highly expressed viral genes maintained low nucleotide diversity, implying functional conservation and potential ecological importance during bloom development. These findings provide genome-resolved evidence that giant viruses exhibit rapid diversification and adaptive dynamics *in situ*.

発表論文(謝辞あり)

Xia J., Meng L., Fang Y., Ban H., Okazaki Y., Yoshida T., Endo H., Nagasaki K., Ogata H. (2026) Rapid diversification of a natural *Heterosigma akashiwo* virus population during a host bloom. *bioRxiv*. doi: <https://doi.org/10.64898/2026.02.06.704369>.