

全球海洋メタゲノム解析を通じた巨大ウイルスの多様性と進化の解明

Unveiling the Global Diversity and Evolution of Giant Viruses Through Ocean Metagenomics

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研究成果概要

Giant viruses are a group of eukaryote-infecting double-stranded DNA viruses that possess large functional repertoires. So far, all known giant viruses belong to the phylum *Nucleocytoviricota*. By infecting a wide variety of eukaryotes, giant viruses are abundant and widespread in the ocean, from the Arctic Ocean to the Southern Ocean. Despite their importance in the marine ecosystems, our knowledge of marine giant viral ecology and evolution remains largely limited as the scarcity of isolated virus-host pairs. Compared to fastidious isolation approaches, *in silico* analyses hold the promise of bridging knowledge gaps, to reveal the enigmatic world of marine giant viruses. Thus, taking advantage of the supercomputer of ICR, we investigated the diversity and evolution of marine giant viruses at a global scale.

Taking advantage of the recent large-scale marine metagenomics census, we explored the ecology and evolution of marine giant viruses using global ocean data (i.e., the *Tara* Oceans). Four major findings are organized into separate chapters in this dissertation as outlined below. 1) The global distribution of marine giant viruses showed various latitudinal diversity gradient patterns along size fractions and lineages, suggesting they have a diverse host range. 2) A distinct boundary between giant viral communities in polar and nonpolar environments was identified. Further, results supported the hypothesis that recurrent evolutionary adaptations across the boundary are likely driven by alterations of viral gene repertoire. 3) '*Mirusviricota*', a group of plankton-infecting DNA giant viruses with remarkable chimeric attributes, was discovered prevalent in the ocean, providing missing links in the evolution of both herpesviruses and giant viruses.

発表論文(謝辞あり)

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