ネットワークに基づく巨大ウイルスと真核生物の関係の発見

Revealing associations between giant viruses and eukaryotes in the global ocean through community networks

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研究成果概要

Large double-stranded DNA viruses are a monophyletic group of eukaryotic viruses, corresponding to the phylum *Nucleocytoviricota*, which is highly diverse and abundant in marine environments. Giant viruses have a broad range of eukaryotic hosts, from unicellular eukaryotes to animals. However, the number of viruses isolated in the laboratory represents a small fraction of viral signals detected in the ocean. The interactions between giant viruses and eukaryotes and the drivers of interactomes remain poorly known. Thus, taking advantage of the supercomputer of ICR, we investigated the global biogeography of marine giant viruses and their associations between eukaryotes.

First, using the recently published environmental genomic databases for *Nucleocytoviricota* and eukaryotes, we built co-occurrence networks of metagenome-assembled genomes (MAGs). We then used a phylogeny-informed filtering method, Taxon Interaction Mapper (TIM), to refine the associations in networks and predict the virus-host pairs. To further validate the prediction results, we conducted a series of genome-based analyses, such as pairwise gene alignment and the Giant Endogenous Viral Elements (GEVEs) detection, using eukaryotic MAGs and isolations genomes. As a result, we observed a total of 2,083 virus-eukaryote associations in the network, involving 787 viral MAGs that are widespread in the *Nucleocytoviricota* phylogenic tree. After TIM enrichment, we found two documented virus-host pairs, *Prasinovirus* and Mamiellophyceae and *Coccolithovirus* and Haptophyta. Three other predicted hosts, *Thalassiosirales*, *Isochrysidales*, and *Chaetocerotales*, showed a large number of signals of giant viruses and virophages, the parasites of giant viruses, insertions.