

真核生物のゲノムデータを用いた内在性ミルスウイルスの解析
Investigation of endogenous mirusvirus from eukaryotic genomic data

京都大学化学研究所バイオインフォマティクスセンター化学生命科学研究領域 趙宏達

研究成果概要

A recent marine metagenomic study uncovered a novel group of viruses called mirusviruses, proposed to bridge the evolutionary gap between two realms of double-stranded DNA viruses, Varidnaviria and Duplodnaviria. Metagenomic data suggest that mirusviruses infect microeukaryotes in the ocean's photic layer, though their full host range remains largely unknown.

In this study, we screened 1,901 publicly available eukaryotic genome assemblies, primarily from unicellular eukaryotes, for mirusvirus marker genes to identify potential hosts. Marker sequences were detected in 915 assemblies spanning 227 genera across eight eukaryotic supergroups. These putative hosts inhabit not only marine environments but also a variety of other ecosystems.

Among the major capsid protein (MCP) signals found in the genome assemblies, 85 sequences exhibited strong sequence and structural similarities to reference mirusvirus MCPs. Phylogenetic analysis revealed their distant evolutionary relationships with the seven previously reported mirusvirus clades. Most scaffolds containing these MCP sequences also encoded multiple mirusvirus homologs, suggesting that mirusviral infection influences host genome evolution.

Additionally, we identified three circular mirusviral genomes within the genomic data of the oil-producing thraustochytrid *Schizochytrium* sp. and the endolithic green alga *Ostreobium quekettii*. These findings indicate that mirusviruses likely infect a broad range of eukaryotes and exhibit greater diversity than previously recognized.

発表論文(謝辞あり)

Eukaryotic genomic data uncover an extensive host range of mirusviruses