

巨大ウイルスにおける糖関連遺伝子の進化、新規性、および活性

Glyco-genes in giant viruses evolution, novelty, and activity

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研究成果概要

Glycosylation is a fundamental biological process involved in protein stability, cell surface recognition, and pathogen–host interactions, all of which are important during viral infection. The structural diversity of glycans suggests that the genes responsible for glycosylation are also highly diverse. However, compared with cellular organisms, glycosylation and glyco-genes in viruses remain poorly understood. Giant viruses are of particular interest because previous experimental studies suggest that they may encode relatively enriched and partially autonomous glycosylation systems. Understanding the diversity and function of these genes is therefore important for clarifying giant virus adaptation and virus–host interactions in nature.

Using the supercomputer system in ICR, I conducted a systematic survey of glyco-genes in giant viruses using an ocean viral genome database in 2025. Results showed that giant viruses harbor a high abundance and broad diversity of GT families, compared to bacteriophages. Several GT families displayed clear lineage-specific distributions, indicating differential acquisition and retention across giant virus clades. Phylogenetic analyses further suggested mixed evolutionary origins of giant virus GT genes, with some viral GTs likely derived from horizontal transfer from eukaryotes, while others appear to represent ancient virus-associated lineages. I also identified multiple previously uncharacterized proteins that are consistently linked to GT-containing genomic regions. Based on synteny, orthologous group co-occurrence, and structural predictions, several of these proteins are strong candidates for novel glyco-associated factors. Importantly, metatranscriptomic data showed active expression of both canonical GTs and these newly identified glyco-associated proteins across diverse marine provinces, supporting their ecological relevance in situ.