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深い湖での最先端のロングリードシーケンシングによる巨大ウイルスの包括的な調査

Comprehensive survey of giant viruses with state-of-the-art long-read sequencing in a deep lake

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研究成果概要

To investigate giant viruses in under-investigated freshwater ecosystems and overcome previous technical limitations of using short-read sequencing, here we utilized spatiotemporal samples from a lake and MAG reconstruction enhanced by long-read metagenomics. We developed a pipeline to reconstruct giant virus metagenome-assembled genomes from environmental samples, where I mainly used tools related to contig assembly (Flye), genome binner (metabat2), and viral annotation (CAT/VirSorter/ViralRecall). This approach resulted in the recovery of hundreds of giant virus MAGs, which were the foundations of downstream analyses. We also inspected the diversity and distribution of giant viruses in this lake, revealing numerous new species of giant viruses.

Our spatio-temporal samples further enabled investigations of their habitat preferences across water depths through read mapping using mapping tools (BWA and CoverM). And we found their unique distributions in different water layer, indicating complicated life strategies employed by giant viruses.