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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 using short-read sequencing, here we utilized spatiotemporal samples from a deep 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), viral annotation (VirSorter/ViralRecall/genomad). As a result, we obtained hundreds of novel species of giant viruses, including the recovery of the newly discovered Mirusviruses.

Our spatiotemporal samples further enabled investigations of their habitat preferences across water depths through read mapping using mapping tools (BWA and CoverM). This finding challenges the prevailing theory that deep-water giant virus communities are merely transported from surface waters, highlighting the ecological uniqueness of deep-water habitats.

発表論文（謝辞あり）
**Zhang L.** et.al. Spatiotemporal dynamics of giant viruses within a deep freshwater lake reveal a distinct dark-water community. ISME J. 2024;18(1):wrae182.