

令和 7 年度 京都大学化学研究所 スーパーコンピュータシステム 利用報告書

深湖における巨大ウイルスの生物地理学的分布の探究

Exploring the biogeography of giant viruses in deep lakes

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 化学生命科学領域 Liwen Zhang

研究成果概要

We have collected metagenomic samples from global deep lakes and using the developed pipeline to reconstruct giant virus metagenome-assembled genomes from these samples, where I mainly used tools related to contig assembly (SPAdes), genome binner (metabat2), viral annotation (VirSorter/ViralRecall/genomad/CheckV). As a result, we obtained thousands of novel giant virus species. These samples across geographic distance and water columns further enabled genome-resolved investigations of their biogeography at both vertical and horizontal dimensions through read mapping using mapping tools (BWA and CoverM). Our results show that globally distributed giant viruses nonetheless exhibit clear signatures of local diversification. Together, this study provides a fine-scale view of giant virus biogeography across water depth and geographic distance, advancing our understanding of the ecological processes shaping viral communities in freshwater systems.