

湖沼で優占する細菌の難培養性の背景にある適応進化の解明

Resolving the adaptive evolution behind the uncultivability of dominant freshwater bacteria

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研究成果概要

This server usage supported the project “Resolving the adaptive evolution behind the uncultivability of dominant freshwater bacteria,” which aims to identify genomic and evolutionary features associated with the uncultivability of dominant freshwater bacterial lineage, *Nanopelagicales* of *Actinobacteria*.

Freshwater metagenomic datasets from multiple lakes in Japan were processed on the server. Metagenome assembly was performed using SPAdes, generating contigs that were used to reconstruct 50,332 metagenome-assembled genomes (MAGs). In parallel, flow cytometry-based single-cell processing produced 2,764 single-cell amplified genomes (SAGs), and the resulting genome sequence datasets were also handled and analyzed on the server.

For taxonomic classification of the full genome collection (53,096 genomes), GTDB-Tk was executed on the server. The classification results indicated 3,355 MAGs and 751 SAGs as belonging to *Nanopelagicales*. Genomes assigned to *Nanopelagicales* were then extracted, and a phylogenetic tree was constructed using RAxML based on alignments of the conserved single-copy gene set generated by GTDB-Tk.

For the next step, genomes belonging to the genus *Nanopelagicus* will be selected for comparative genomics against other related groups. Planned server-based analyses include (i) genome annotation using Prokka and/or DRAM, (ii) ortholog identification and pangenome analysis using OrthoFinder and/or Panaroo, and (iii) functional profiling using eggNOG-mapper and/or KEGG tools (e.g., KofamScan).