

淡水細菌 SAR11 のゲノム超可変領域の単一細胞ゲノミクスによる解析

Profiling the Genomic Hypervariable Region of Freshwater SAR11 Bacteria
Through Single-Cell Genomics

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The SAR11 bacterial order consists of aquatic, free-living bacteria that are ubiquitous in freshwater and marine ecosystems. My research focuses on the characterisation a hypervariable region (HVR2) located within freshwater SAR11 genomes, which is theorised to contribute to its ecological dominance. The utilisation of single-cell genomics data added a higher level of resolution to the investigation of the HVR2 compared to metagenomics. Furthermore, freshwater SAR11 HVR2 was focused due to lesser existing studies compared to its marine counterparts. In order to understand how freshwater SAR11 HVR2 may operate across time and locations, samples were taken from 2022 and 2024 in Lakes Biwa (Japan) and Zurich (Switzerland).

My findings show that freshwater SAR11 HVR2s possess consistent average lengths and length distributions with their marine counterparts. Microdiversity is pervasive within the region, with singletons constituting at least 80% of HVR2s at 96-100% average nucleotide identity (ANI) thresholds. At the same time, there exists some level of commonality from the remaining 20%, with non-singleton clusters of up to 7 members observed. Paradoxically, nearly identical HVR2 pairs were discovered from Lakes Biwa and Zurich, with one pair retaining more than 90% amino acid identity and highly conserved synteny. When compared with marine HVR2 sequences, similar discoveries were made with at least 60% shared identity between selected pairs. Our results present the paradox that extremely diversified genomic regions can be highly conserved across continents and aquatic biomes.