

海洋巨大ウイルスとその宿主の多様性解析について

Diversity analysis of giant marine viruses and their hosts.

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研究成果概要

My research focuses around diversity analysis of megaviridae in sea water samples of Osaka and Uranouchi bay. Usually, the diversity analysis of megaviridae involves metagenomics[1]–[3], however recently a primer base method was published with promising results[4]. I have been improving the referenced method and generated datasets using the so called MEGAPRIMERS, a set of 82 primers which target the megaviridae polymerase B gene. The generated data is stored on the supercomputer. Additionally, I use the supercomputer to analyze MEGAPRIMER sequencing datasets using MAPS[4] and 18S rRNA sequencing data with qiime2[5] and I utilize python 3 and R scripts for data manipulation and plotting.

References

- [1] W. H. Wilson *et al*, “Genomic exploration of individual giant ocean viruses,” *ISME J*, vol. 11, no. 8, pp. 1736–1745, 2017.
- [2] T. Mihara, H. Koyano, P. Hingamp, N. Grimsley, S. Goto, and H. Ogata, “Taxon Richness of ‘Megaviridae’ Exceeds those of Bacteria and Archaea in the Ocean,” *ISME J*, vol. 33, no. 2, pp. 162–171, 2018.
- [3] P. Hingamp *et al*, “Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes,” *ISME J*, vol. 7, no. 9, pp. 1678–1695, Sep. 2013.
- [4] Y. Li *et al*, “Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters,” *ISME J*, vol. 10, no. 9, p. 496, Sep. 2018.
- [5] J. G. Caporaso *et al*, “QIIME allows analysis of high-throughput community sequencing data,” *Nature Methods*, vol. 7, no. 5, p. 335, May 2010.