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海洋巨大ウイルス宿主同定に関する研究
Study on the host identification of giant viruses

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 Lingjie Meng

研究成果概要

Megaviridae, also termed as the Giant virus, is a family of viruses proposed to infect mainly protists. Large genomes (280kb-1.51Mb) and particles (140nm-1 μ m) make them unique in nature. The evolutionary origin and the ecological function of Megaviridae are attractive but mysterious. With the development of sequencing and omics, it has been demonstrated Megaviridae is abundant and diverse in the oceans, the diversity of which is three orders magnitude greater than the number of their hosts to date. “What do they infect?” is a challenge faced with us.

In regard to hosts identification of giant viruses, I make use of the SuperComputer System of Institute for Chemical Research, Kyoto University. Mainly, I focus on the Megaviridae, as well as other NCLDV and their eukaryotic host candidates from TARA oceans data *in silico*. In this project, I need to use various software and packages to do deal with short reads sequences, to alignment the different sequences and reconstruct phylogenetic trees, and to conduct the co-occurrence analyses.

発表論文(謝辞あり)

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