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メガウイルス科の DNA ポリメラーゼ遺伝子を標的とするアンプリコン解析

Amplicon analysis of Megaviridae DNA polymerase gene

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研究成果概要

To gauge the diversity of the Megaviridae family at the population level, members of the Ogata laboratory and their collaborators designed a set of 82 pairs of degenerated primers (referred to as MEGAPRIMER), targeting DNA polymerase genes (polBs) of Megaviridae. As the target regions of 82 pairs of primers on polB were not exactly the same at their extremities, their meta-barcode data were incompatible with previous meta-barcode processing pipelines. To appropriately process the meta-barcode data from MEGAPRIMER,

I designed a bioinformatics pipeline named Megaviridae Amplicon Processing System (MAPS), which was a set of scripts to automatically process meta-barcode raw reads in parallel processing. MAPS was designed to be able to trim meta-barcodes so that the user can retain only the common regions among reads that were amplified with different primers.

To conduct this research project I make use of the SuperComputer System of Institute for Chemical Research, Kyoto University. I am using the free software such as FLASH, Trimmomatic and MAFFT for developing the MAPS. PBS system on SuperComputer System was also used in the process management of MAPS.

By analyzing sequence data from environmental DNA meta-barcoding of 5 water samples from various aquatic environments with MAPS, 220-5662 non-singleton operational taxonomic units (OTUs) of Megaviridae at 97% nucleotide sequence identity were identified from individual samples. Most of reads (88.6%) were belonging to OTUs which contained reads from more than one sample. This observation suggests a relatively wide habitat and niche for individual viruses of Megaviridae and their transport between distant geographic locations.

発表論文(謝辞あり)

Li Y, Hingamp P, Watai H, Endo H, Yoshida T, Ogata H. 2018. Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters. *Viruses* 10:496

発表論文(謝辞なし)

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