Comparing *Mimiviridae* communities using meta-barcoding during a red tide period in an enclosed bay

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研究成果概要

This study is using the supercomputer of Institute for Chemical Research, Kyoto University, to do an analysis for comparing *Mimiviridae* communities during a red tide period in an enclosed bay, west Japan.

"*Mimiviridae*" is a proposed family of giant viruses infecting unicellular eukaryotes. They are very abundant and ubiquitous in the sea water and affect marine microbial community by their lytic infection cycle. However, only a few *Mimiviridae* members have been explored in the marine environments, and their ecological roles in marine ecosystems remains unknow.

For studying the differences of *Mimiviridae* community in two different kind of water, surface sea water samples (0.22-3 μm) were collected from an enclosed bay (Uranouchi Inret, Kochi) during a red tide period. A set of degenerated primers (called "MEGAPRIMER"), which target family B DNA polymerase genes of *Mimiviridae*, was used to assess the composition of *Mimiviridae* community. Bioinformatic analysis was applied after sequencing. As a result, hundreds of operational taxonomic units (OTUs) were identified in each sample. When we compared the *Mimiviridae* structures between within and without red-tide waters, there was a clear difference between these two samples in a community variation analysis. The difference was also visible in dominant OTU proportions between the two types of samples. Phylogenetic analysis based on a maximum-likelihood method showed that almost all of the OTUs belong to unknown *Mimiviridae* branches. Future study will mainly focus on the host-virus interactions and the relationship between viral community and environmental factors, that may reveal ecological functions of *Mimiviridae* in a coastal ecosystem.