

海洋性プランクトン群の進化と生態についての研究

Research in evolution and ecology of marine planktonic communities

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研究成果概要

I have been using the super computer for four different works:

1/ to reconstruct phylogenies of DNA repair proteins encoded in the genome of Megavirales (eukaryotic viruses) and their cellular homologs. Output of this analysis was used to gain insight into the potential origin of these proteins. This work has been submitted for publication to a peer reviewed journal (Current Opinion in Microbiology) with the appropriate acknowledgement to the SuperComputer System.

2/ to align next generation sequencing data against the draft genome sequence of *Triparma laevis*, a small-sized unicellular marine phytoplankton. And to then call nucleotide variation along this genome sequence in order to get an insight into the ploidy level of this organism. This is a work done in collaboration with Dr. Akira Kuwata (Tohokku National Fisheries Research Institute, Japan).

3/ to assembled and annotate the genome sequence of two recently characterized double-stranded DNA viruses infecting *Prymnesium kappa* (Haptophyte). Genome sequences of these two giant viruses is expected to help characterized *Megaviridae*: an emerging family of eukaryotic viruses. This work is done in collaboration with Pr. Ruth-Anne Sandaa (Institute of Biology, Bergen University, Norway).

4/ to reconstruct the phylogeny of the PIP5K (Phosphoinositide Kinase) protein family in land plants. The output of this work led to the formulation of a hypothesis regarding the evolution of PIP5K3 in the model species *Arabidopsis thaliana*. Additional computational and experimental work are expected to precise its role and evolutionary history. This is a collaborative work with the laboratory of Pr. Takashi Aoyama (Institute for Chemical Research, Kyoto University, Japan).