

Bioinformatics Center – Chemical Life Science –

<https://cls.kuicr.kyoto-u.ac.jp/en/>



Prof
OGATA, Hiroyuki
(D Sc)



Assist Prof
ENDO, Hisashi
(D Environmental Science)



Assist Prof
OKAZAKI, Yusuke
(D Sc)

Proj Res

NGUYEN, Thi Tuyen

Students

NISHIYAMA, Hiroki (D3)

PRODINGER, Florian (D3)

KANEKO, Hiroto (D2)

MENG, Lingjie (D2)

XIA, Jun (D2)

BAN, Hiroki (M2)

GARCIA, Kimberly Gacayon (M1)

ZHANG, Ruixuan (M1)

HASHIMOTO, Kentaro (M1)

KIJIMA, Soichiro (M1)

FANG, Yue (RS)

YANG, Qingwei (RS)

WU, Junyi (RS)

ZHANG, Liwen (RS)

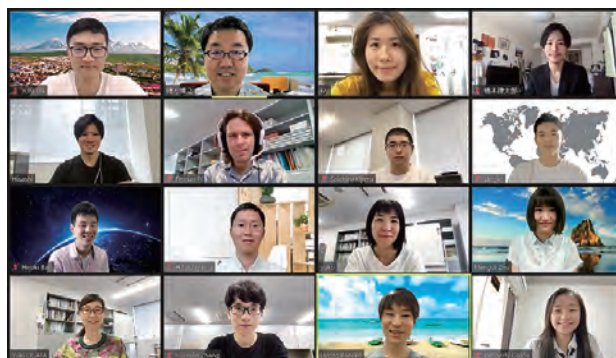
CHEN, Jingjie (RS)

Assist Techn Staff

ZHU, Mengdi

Scope of Research

We are interested in understanding the functioning and evolution of biological systems at varying scales from tiny microbes up to the Earth's environment, by leveraging rapidly accumulating big data in life science and bioinformatics approaches. We currently focus on 1) the evolution of viruses and their links to the origin of life, 2) microbial ecology in different ecosystems, and 3) the development of bioinformatics methods and biological knowledge resources for biomedical and industrial applications. To fuel these research activities, we take part in environmental sampling campaigns such as *Tara Oceans*. Our resources and developed tools are accessible through GenomeNet (www.genome.jp) to scientific communities and the public.



KEYWORDS

GenomeNet Bioinformatics Environmental Genomics Virology Molecular Evolution

Selected Publications

Endo, H.; Blanc-Mathieu, R.; Li, Y.; Salazar, G.; Henry, N.; Labadie, K.; de Vargas, C.; Sullivan, M. B.; Bowler, C.; Wincker, P.; Karp-Boss, L.; Sunagawa, S.; Ogata, H., Biogeography of Marine Giant Viruses Reveals Their Interplay with Eukaryotes and Ecological Functions, *Nat. Ecol. Evol.*, doi: 10.1038/s41559-020-01288-w (2020).

Prodinger, F.; Endo, H.; Gotoh, Y.; Li, Y.; Morimoto, D.; Omae, K.; Tominaga, K.; Blanc-Mathieu, R.; Takano, Y.; Hayashi, T.; Nagasaki, K.; Yoshida, T.; Ogata, H., An Optimized Metabarcoding Method for Mimiviridae, *Microorganisms*, **8**, E506 (2020).

Sakurai, T.; Nishiyama, H.; Nagai, T.; Goto, S.; Ogata, H.; Kudo, M., Deficiency of Gankyrin in the Small Intestine is Associated with Augmented Colitis Accompanied by Altered Bacterial Composition of Intestinal Microbiota, *BMC Gastroenterol.*, **20**, 12 (2020).

Nishiyama, H.; Endo, H.; Blanc-Mathieu, R.; Ogata, H., Ecological Structuring of Temperate Bacteriophages in the Inflammatory Bowel Disease-affected Gut, *Microorganisms*, **8**, E1663 (2020).

Sunagawa, S.; Acinas, S. G.; Bork, P.; Bowler, C.; Tara Oceans Coordinators; Eveillard, D.; Gorsky, G.; Guidi, L.; Iudicone, D.; Karsenti, E.; Lombard, F.; Ogata, H.; Pesant, S.; Sullivan, M. B.; Wincker, P.; de Vargas, C., Tara Oceans: Towards Global Ocean Ecosystems Biology, *Nat. Rev. Microbiol.*, **18**, 428-445 (2020).

Improving a Metabarcoding Method for *Mimiviridae* Ecological Analysis

Mimiviridae is a group of mostly eukaryotic phytoplankton infecting viruses with big virions and long genomes. The relevance of *Mimiviridae* in the ecology of marine environments has been increasingly recognized by metagenomics based studies. We previously proposed a meta-barcoding approach based on 82 degenerate primer pairs (MEGAPRIMER) targeting the DNA polymerase gene of *Mimiviridae* to enable ecological profiling of *Mimiviridae*. Even though this method detected many operational taxonomic units (OTUs), it required large quantities of DNA and was laborious. Recently, we examined coastal seawater samples using varying PCR conditions and purification protocols to streamline the MEGAPRIMER method. The biggest advantage of our newly conceptualized methods are “primer cocktails”. We mixed several different primer pairs before PCR amplification and thereby reduced the required amount of environmental DNA by up to 90%, while reproducing the results of the original protocol. We compared and critically assessed the outcome of the different meta-barcoding approaches with quantifications using qPCR for selected OTUs. The quality control of MEGAPRIMER amplicon sequencing performed in this study solidified the MEGAPRIMER method as a new tool for ecological analysis of giant marine viruses. These newly developed MEGAPRIMER protocols will be especially useful for ecological analysis of a larger set of environmental samples.

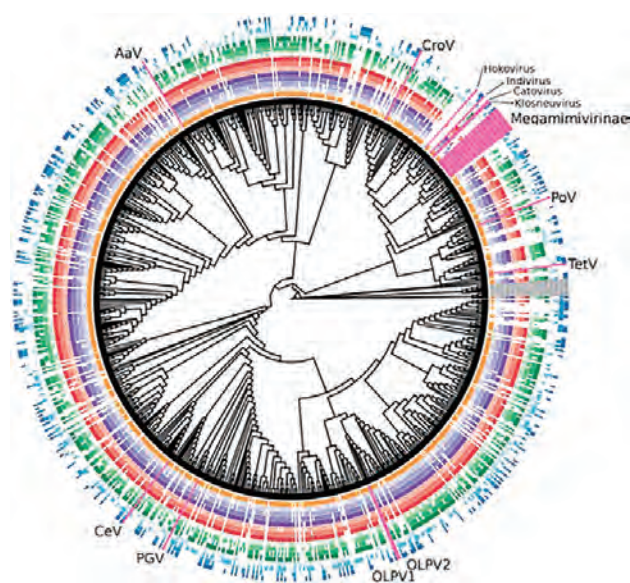


Figure 1. Phylogenetic tree of *Mimiviridae* OTUs found in different samples. Several OTUs that were closely related to isolated *Mimiviridae* were found.

Biogeography of Giant Viruses in the Global Ocean

Nucleocytoplasmic large DNA viruses (NCLDV, so called “giant viruses”) are thought to be ubiquitous in marine environments and infect diverse eukaryotes. However, their biogeography and ecology have yet to be explored at a global scale. By leveraging the *Tara* Oceans pole-to-pole metagenomic data, we investigated the distribution of NCLDV across size fractions, depths and biomes, as well as their associations with eukaryotic communities. Our analyses revealed a heterogeneous distribution of NCLDV across oceans, with an elevated uniqueness in polar biomes. Community structures of individual NCLDV families were found to be correlated with those of specific eukaryotic lineages such as chlorophytes, haptophytes, and choanoflagellates, suggesting clade specific geographical associations between NCLDV and host lineages (Figure 2). NCLDV communities were generally distinct between surface and mesopelagic zones, but exhibited a high similarity between the two depths at some locations. This vertical connectivity was correlated to surface phytoplankton biomass but not to physical mixing processes, suggesting the potential role of vertical export in structuring mesopelagic NCLDV communities. These results underscore the importance of the coupling between NCLDV and eukaryotes in biogeochemical processes in the ocean.

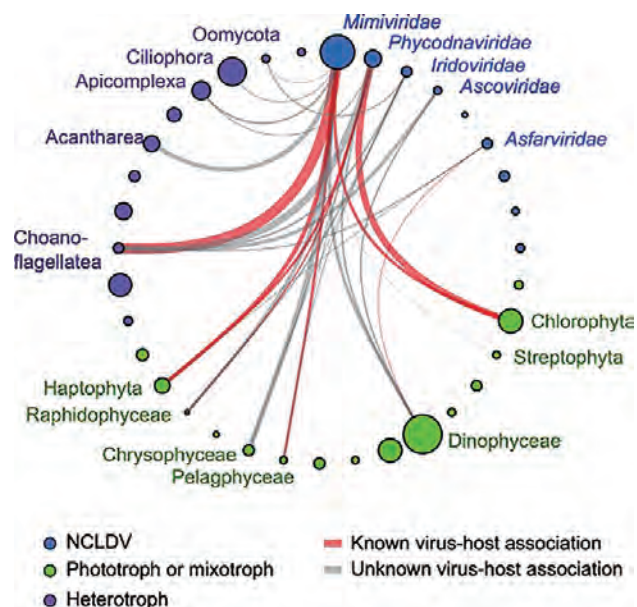


Figure 2. Associations between NCLDV and eukaryotic lineages as estimated by their distributions.