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CNRS, Nantes University, France, 22 October 2022–31 October 2022
CNRS, Nantes University, France, 14 October 2022–4 November 2022
The Czech Academy of Sciences, Czech Republic, 16 September 2022–5 October 2022

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

Tight Association Discovered between *Imitervirales* and Their Microbial Eukaryotic Host Communities in the Arctic Ocean

Imitervirales is an order belonging to phylum *Nucleocytoviricota*, or so-called giant viruses. The microbial eukaryotic community hosts various *Imitervirales*, and play an important role in marine ecosystem. To explore the association between them in the Arctic Ocean, we sampled microbial DNA from surface water of 21 stations during a cruise in the summer of 2018. Two types of water (NECS: northeastern Chukchi Sea; AS: adjacent seas) can be separated according to temperature and salinity. In AS sites, eukaryotic community was strongly correlated with physicochemical factors, while in the oligotrophic NECS sites it showed a loose association (Fig. 1). In contrast, *Imitervirales* community were consistently correlated with eukaryotic community, and correlation coefficients were rarely influenced by environmental factors in both of NECS and AS sites (Fig. 1). At the individual amplicon sequence variant (ASV) level in all sites, positive associations (above 37% eukaryotic ASVs and 25% *Imitervirales* ASVs) between *Imitervirales* and eukaryotic community were then discovered by co-occurrence analysis. These results support that *Imitervirales* community actively interacted and co-varied with eukaryotic community, even in the oligotrophic and homogeneous environment in the Arctic Ocean. This work has been published in Xia et al., *Limnol. Oceanogr.*, 2022, doi: 10.1002/lno.12086.

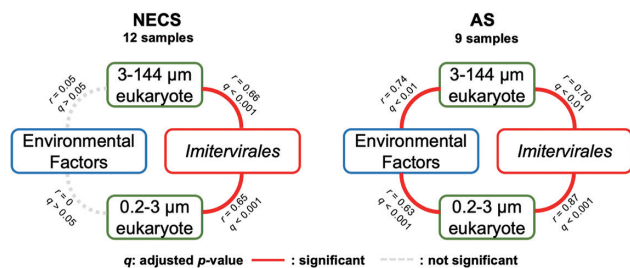


Figure 1. Mantel test result between microbial eukaryotic community, environmental factors, and *Imitervirales* community.

Recent Selected Publications

- Xia, J.; Kameyama, S.; Prodinge, F.; Yoshida, T.; Cho, K.-H.; Jung, J.; Kang, S.-H.; Yang, E.-J.; Ogata, H.; Endo, H., Tight Association between Microbial Eukaryote and Giant Virus Communities in the Arctic Ocean, *Limnol. Oceanogr.*, **67**, 1343-1356 (2022).
- Da Cunha, V.; Gaia, M.; Ogata, H.; Jaillon, O.; Delmont, T.O.; Forterre, P., Giant Viruses Encode Actin-Related Proteins, *Mol. Biol. Evol.*, **39**, msac022 (2022).
- Prodinge, F.; Endo, H.; Takano, Y.; Li, Y.; Tominaga, K.; Isozaki, T.; Blanc-Mathieu, R.; Gotoh, Y.; Hayashi, T.; Taniguchi, E.; Nagasaki, K.; Yoshida, T.; Ogata, H., Year-Round Dynamics of Amplicon Sequence Variant Communities Differ among Eukaryotes, Imitevirales, and Prokaryotes in a Coastal Ecosystem, *FEMS Microbiol. Ecol.*, **97**, fiab167 (2022).
- Zhang, R.; Endo, H.; Takemura, M.; Ogata, H., RNA Sequencing of Medusavirus Suggests Remodeling of the Host Nuclear Environment at an Early Infection Stage, *Microbiol. Spectr.*, **9**, e0006421 (2021).
- Kijima, S.; Delmont, T.O.; Miyazaki, U.; Gaia, M.; Endo, H.; Ogata, H., Discovery of Viral Myosin Genes With Complex Evolutionary History Within Plankton, *Front. Microbiol.*, **12**, 683294 (2021).

“*Mamonoviridae*”, a New Virus Family of the Phylum *Nucleocytoviricota*

Large DNA viruses of phylum *Nucleocytoviricota* are widespread in the ecosystems around the globe and show a great genetic and morphological diversity. Medusavirus is a group of viruses in this phylum, which was first represented by *Acanthamoeba castellanii* medusavirus J1 isolated from a hot spring. With the development of culture-independent techniques such as metagenomics, many related viral genomes have been identified so far. However, the current taxonomy rank of medusaviruses is not officially defined by the International Committee on Taxonomy of Viruses. The creation of new taxonomic ranks is thus warranted to capture the diversity of this group of viruses. We assessed the morphological, genomic, and gene content similarities within the two isolated medusaviruses and compared them with other large DNA viruses. Our results show that medusaviruses clearly differ from members of other families in this phylum in terms of all used metrics. We thus propose to create the family “*Mamonoviridae*” within the phylum *Nucleocytoviricota*. This work has been accepted by the journal *Archive of Virology*.

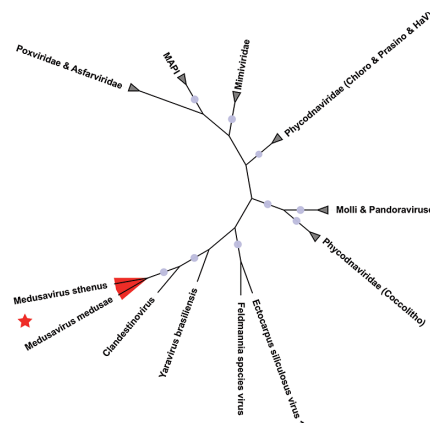


Figure 2. Phylogenetic tree based on concatenated core genes of viruses of the phylum *Nucleocytoviricota* based on a maximum-likelihood framework. Blue circles represent supports that passed confidence cutoff for branches. The red background color along branches and the star indicate medusaviruses.