Bioinformatics Center
– Chemical Life Science –

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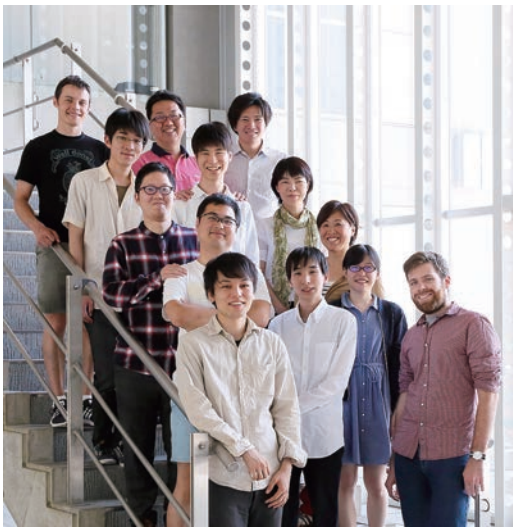
Scope of Research

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

Matsui, T.; Yoshikawa, G.; Mihara, T.; Chatchawankanphanich, O.; Kawasaki, T.; Nakano, M.; Fujie, M.; Ogata, H.; Yamada, T., Replications of Two Closely Related Groups of Jumbo Phages Show Different Level of Dependence on Host-encoded RNA Polymerase, *Front. Microbiol.*, **8,** 1010 (2017).

Nishimura, Y.; Yoshida, T.; Kuronishi, M.; Uehara, H.; Ogata, H.; Goto, S., ViPTree: the Viral Proteomic Tree Server, *Bioinformatics*, **33,** 2379-2380 (2017).

Shimizu, Y.; Ogata, H.; Goto, S., Discriminating the Reaction Types of Plant Type III Polyketide Synthases, *Bioinformatics*, **33,** 1937-1943 (2017).

Nishimura, Y.; Watai, H.; Honda, T.; Mihara, T.; Omae, K.; Roux, S.; Blanc-Mathieu, R.; Yamamoto, K.; Hingamp, P.; Sako, Y.; Sullivan, M. B.; Goto, S.; Ogata, H.; Yoshida, T., Environmental Viral Genomes Shed New Light on Virus-host Interactions in the Ocean, *mSphere*, **2,** e00459-16 (2017).

Shimizu, Y.; Ogata, H.; Goto, S., Type III Polyketide Synthases: Functional Classification and Phylogenomics, *ChemBioChem*, **18,** 50-65 (2017).

Diversity and Biogeography of Diatoms and Haptophytes in the Pacific Ocean

Diatoms and haptophytes are two major phytoplankton groups, playing pivotal roles in global biogeochemical cycles and marine ecosystems. Previous studies suggest that diatoms and haptophytes are *r*- and *K*-selected species, respectively, but precise linkages between their ecological traits and geographical distributions remain poorly understood. We recently examined the basin-scale variability of the abundance and taxonomic composition of these two phytoplankton groups across thirty-five sites in the Pacific Ocean using DNA metabarcoding targeting the 18S rRNA gene. The diatom community was generally dominated by a few genera at each sample site, whereas the haptophyte community consisted of a large number of genera in most of the sites, suggesting greater inter-genus competition among diatoms (Figure 1). Consequently, the diversity of diatoms was generally lower than that of haptophytes, with haptophyte diversity fairly stable within the study area. The diversity and composition of haptophyte community showed stronger correlations with environmental variables than diatom community, indicating that the diatom community is more affected by other factors such as physical forcing. Our data further supports that their distinct ecological strategies underlies the emergence of the contrasting diversity patterns of these phytoplankton groups in the central Pacific at a basin scale.

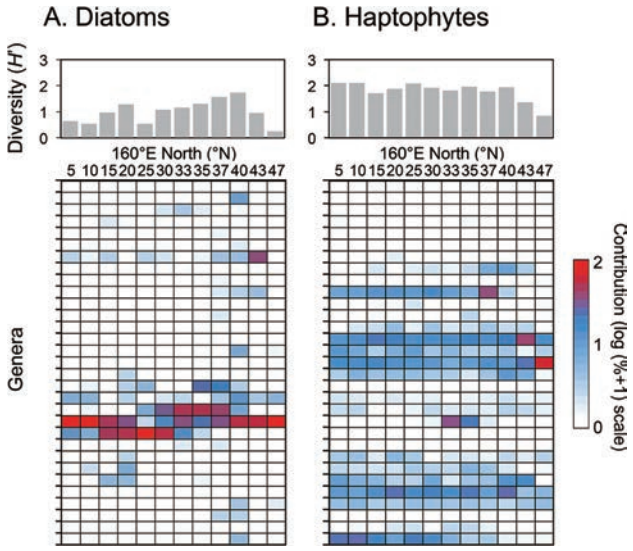


Figure 1. Genus-level diversity and distribution patterns of (A) diatoms and (B) haptophytes in the surface layer of the western North Pacific (5°N–47°N along the 160°E transect).

Two Closely Related Groups of Jumbo Phages Encoding RNA Polymerase Differ in Their Level of Dependence on Host Transcription Machinery

Ralstonia solanacearum phages ϕRP12 and ϕRP31 are jumbo phages presenting similar virion morphology, genome organization and host range. Phylogenetic and comparative analyses at both genomic and gene levels revealed ϕRP12 and ϕRP31 are closely related to previously recognized ϕKZ-related phages, and most closely related to *R. solanacearum* phages ϕRSL2 and ϕRSF1 (Figure 2). Compared with the ϕRSL2 group (ϕRSL2 and ϕRSF1), the ϕRP12 group (ϕRP12 and ϕRP31) possess larger genomes (ca. 280 kbp, 25% larger). The genomes of both groups encode many genes conserved in ϕKZ-related phages, including the β and β' subunits of the multisubunit RNA polymerase (RNAP). The replication of ϕRP12 and ϕRP31 was not affected by rifampicin treatment (20 μg/ml), suggesting that phage-encoded RNAPs function to start and complete the infection cycle of these phages without the need of host-encoded RNAPs. In contrast, ϕRSL2 and ϕRSF1 did not produce progeny phages in the presence of rifampicin (5 μg/ml). This observation suggests that some ϕRP12/ϕRP31 factors, that are absent in ϕRSL2 and ϕRSF1, are involved in their host-independent (or rifampicin-resistant) RNAP activity.

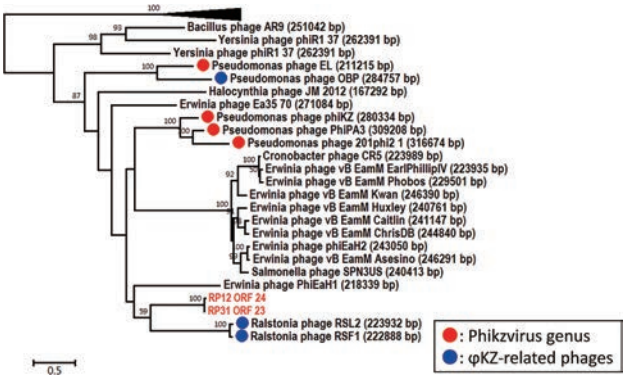


Figure 2. Maximum likelihood phylogenetic tree of the terminase proteins of ϕKZ-related phages. Bootstrap branch support is given for each branch. Number at scale bar indicates the number of substitutions per site.