

Title	Research in evolution and ecology of marine planktonic communities
Author(s)	Blanc-Mathieu, Romain
Citation	京都大学化学研究所スーパーコンピュータシステム研究成果報告書 (2019), 2018: 25-25
Issue Date	2019-03
URL	<a href="http://hdl.handle.net/2433/241153">http://hdl.handle.net/2433/241153</a>
Right	
Type	Article
Textversion	publisher

平成 30 年度 京都大学化学研究所 スーパーコンピュータシステム 利用報告書

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

Chemical Life Science Laboratory, Institute for Chemical Research, Kyoto University  
Blanc-Mathieu Romain

研究成果概要

My current projects are as follow:

1. Assessing the diversity and deciphering the roles of marine eukaryotic viruses in epipelagic oceans using environmental genomics and contextual data.
2. Understanding the evolutionary history of large nucleocytoplasmic DNA viruses via genomic analysis of in-lab isolated viruses.
3. Study of standing genomic variation in the phytoplankton *ri ar a la vi* : what mechanisms shape this variation and how this variation channels future evolutionary changes?
4. Understand the processes that led to functional diversification of their phosphatidylinositol phosphate 5-kinases in core eudicotyledons.

To conduct these research projects I make use of the SuperComputer System of Institute for Chemical Research, Kyoto University. I am using various software to reconstruct phylogenies (phylobayes, RaXML, ete3 package), to assemble genomes (Spades and ABySS), to trim and map short read sequences (trimmomatic, bowtie, bwa), to perform sequence alignment and manipulation (Diamonds, Blast, Seqtk, Emboss) and to run my own scripts for parsing and downstream analysis.

発表論文(謝辞あり)

Yoshikawa G., Blanc-Mathieu R., Song C., Kayama Y., Mochizuki T., Murata K., Ogata H., Takemura M. Medusavirus, a novel large DNA virus discovered from hot spring water. *J. Virol.* doi: 10.1128/JVI.02130-18. (2019).

Yoshikawa G, Askora A, Blanc-Mathieu R, Kawasaki T, Li Y, Nakano M, Ogata H, and Yamada T. Xanthomonas citri jumbo phage XacN1 exhibits a wide host range and high complement of tRNA genes. *Sci. Rep.* **8**, 4486 (2018)