

浦ノ内湾におけるブルーム形成植物プランクトンとメガウイルス科の群集季節変動の解析

Linking seasonal community changes of bloom forming eukaryotic phytoplankton and
Megaviridae in Uranouchi Inlet, Japan

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研究成果概要

“Megaviridae” are a proposed family of NCLDV (nucleocytoplasmic large DNA viruses), many of these giant viruses infect single-cellular eukaryotic algae. Megaviridae were found to be both abundant and diverse in the ocean through metagenomic analysis. Hence, it was hypothesized that they contribute substantially to the dynamics of algae populations through infection and lysis.

We recently developed an analysis workflow for Megaviridae diversity in seawater samples and combined this with previously established eukaryotic diversity analysis protocols. In addition, we were able to obtain cell count data of bloom forming species and metadata (e.g. salinity, dissolved nutrients, chlorophyll concentrations and temperature) of our sampling location.

We applied metabarcoding methods on seawater samples of Uranouchi Inlet , Kochi, Japan. The inlet is home to several blooming algal species and harmful algae blooms, like the red tide, can occur spontaneously. We were able to monitor the change in algae populations through metabarcoding and cell count data, as well as in Megaviridae populations. We further observed an effect of algae blooms on the Megaviridae communities and will further investigate the conditions of bloom formation and termination.

発表論文

An optimized metabarcoding method for Mimiviridae, Prodingen et al. (in preparation)