

水圏ウイルスおよび原生生物の分子生物学的研究
Molecular biology of aquatic viruses, and protists

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研究成果概要

Viruses infecting marine prokaryotes have a large impact on the diversity and dynamics of their hosts. Model systems suggest that viral infection is frequency dependent and constrained by the virus-host encounter rate. However, it is unclear whether frequency-dependent infection is pervasive among the abundant prokaryotic populations with different temporal dynamics. To address this question, we performed a comparison of prokaryotic and viral communities using 16S rRNA amplicon and virome sequencing based on samples collected monthly for 2 years at a Japanese coastal site, Osaka Bay. Concurrent seasonal shifts observed in prokaryotic and viral community dynamics indicated that the abundance of viruses correlated with that of their predicted host phyla (or classes). Cooccurrence network analysis between prokaryotes and viruses revealed 6,423 cooccurring pairs, suggesting a tight coupling of host and viral abundances and their “one-to-many” correspondence. Although stable dominant species showed few cooccurring viruses, a fast succession of their viruses suggests that viruses infecting these populations changed continuously. Our results suggest that frequency-dependent viral infection prevails in coastal marine prokaryotes regardless of host taxa and temporal dynamics.

Viral infection of marine microalgae alters organic matter composition of the algae, which should affect prokaryotic dynamics. We investigated the effects of viral infection of the red tide alga *Heterosigma akashiwo* on prokaryotic communities. Cell lysate of *H. akashiwo* infected by a virus was abundant in branched-chain amino acids, and enhanced growth of different prokaryotes including *Vibrio* compared to cell extracts from non-infected *H. akashiwo*. It suggested that *Vibrio*, which utilize branched-chain amino acids, respond to the lysate of virus-infected cells.

Microcystis aeruginosa is predicted to interact and coexist with broad- and narrow-host-range viruses within a bloom; however, little is known about their effects on *Microcystis* population dynamics. Here, we developed a real-time PCR assay to quantify these viruses with broad- and narrow-host-range and monitored these viruses in an environment with host *Microcystis* population dynamics. In the sampling period, total *Microcystis* abundance showed two peaks in May and August with a temporary decrease in June. The abundances of the broad-host-range virus increased from April to May and from July to October with a temporary

decrease in June, in which its dynamics were in proportion to the increase of total *Microcystis* abundances regardless of changes in host population composition. The narrow-host-range viruses were considerably less abundant than the broad-host-range virus and generally did not fluctuate in the environment. Considering that *M. aeruginosa* increased the abundance and sustain the bloom under the prevalence of the broad-host-range virus, host abundant and diverse antiviral mechanisms might contribute to coexistence with its viruses.

Viral infection dynamics of marine cyanobacteria affects nutrient cycles, however, the number of infection pairs of cyanobacteria and viruses, and the daily dynamics of each pair remain unsolved. Therefore, we performed time-course metagenomic and metatranscriptomic analyses of seawater of Osaka Bay. We found 169 viruses closely related to viruses which infect *Synechococcus*. The transcript abundance of these viruses and *Synechococcus* peaked at the same time, suggesting that different viruses infect simultaneously.

The growth of marine microalgae is influenced by coexisting prokaryotes. The haptophyte *Pavlova* *ranunculiformis* is globally distributed, but ecological knowledge is scarce. Therefore, we investigated the effect of coexisting prokaryotic communities on the growth of *P. ranunculiformis*. In the absence of prokaryotes, the loss of the cells of *P. ranunculiformis* was faster after the late log phase than in the presence of prokaryotes, suggesting that prokaryotes affect the survival of this alga. Prokaryotic community structure analysis suggested that bacteria of the families Rhodobacteraceae and Flavobacteriaceae were dominant during the logarithmic and stationary phases, respectively, and that they affected the survival of this alga.

発表論文(謝辞あり)

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学会発表(謝辞あり)

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- ハプト藻類 *Pavlova ranunculiformis* NIES-3900 株における共存原核生物群集との相互作用
- 海洋性真核微細藻類に対するウイルス感染が原核生物群集構造に及ぼす影響

- ・大阪湾における優占シアノバクテリア感染性ウイルスの日周感染動態の解明
- 令和4年度日本水産学会近畿支部後期例会
- ・大阪湾における優占シアノバクテリア感染性ウイルスの日周感染動態の解明