

論文の要約データ

Title

Molecular ecological studies on the effect of viral infection on abundant marine prokaryotes

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Summary

In the oceans, viruses infecting prokaryotes affect the marine biogeochemical cycle through host lysis. Since viral infection is believed to be dependent on host cell density, viral infection should have larger influence on the abundant prokaryotic populations. However, it was unclear whether the host frequency-dependent viral infection occurred in complex prokaryotic community because of the enormous diversity of marine viruses.

In chapter 2, I focused on the interactions between marine Bacteroidetes and their virus as a model systems of abundant prokaryotes-virus pairs. I developed efficient methods for the prediction of viruses infecting Bacteroidetes from a thousand uncultured viral genomes by using recently reported metagenome assembled genomes of marine Bacteroidetes. I successfully identified novel 81 viral species from 26 genera, including the marine dominant viral lineage Far-T4. The methods enhanced the existing knowledge on the diversity of Bacteroidetes viruses and their potential interaction with their hosts in marine environments.

In chapter 3, I applied the host prediction methods to other prokaryotic taxa. To examine whether the frequency-dependent viral infection occurred in natural community, I compared the seasonal dynamics of the abundant prokaryotes and their viruses in Osaka Bay. Increasing of viral abundance in response to their host abundance was observed between more than 6,000 of putative virus-host pairs. Further, the faster temporal change of the viral community than the prokaryotic community suggested that the viruses interacting with continuously dominant prokaryotic population might have changed temporally. These results revealed that abundant prokaryotes were infected by the viruses with frequency-dependent manner regardless of their taxa and survival strategy.

In these studies, I revealed a general trend that viral frequency-dependent infection is prevailed in abundant prokaryotes. The finding supports that frequency-dependent viral infection maintains the diversity of the prokaryotic community and the active recycling of organic matters in marine environment. Future works focusing on their co-evolutional dynamics from the observation of host and viral genome co-diversification will also help us to understand the underlying mechanism to establish the continuance interactions between abundant prokaryotes with their viruses.