Molecular ecological studies on effects of a marine harmful algal bloom-forming species, *Heterosigma akashiwo*, on prokaryotic community

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Summary

In the ocean, specific prokaryotic taxa drastically increase during microalgal bloom, which is local and seasonal massive growth of microalgae, affecting biogeochemical cycles. However, since microalgal blooms are often comprised of multi algal species, relationship between a specific bloom-forming alga and prokaryotic community has not been elucidated. In this study, I investigated effects of a marine harmful bloom-forming raphydophycean alga, *Heterosigma akashiwo* on prokaryotic community using microcosm experiments and microbiome data analysis.

In chapter 2, I first focused on effects of uninfected *H. aksahiwo* cells on a prokaryotic community. The exudates and cellular components (including both the membrane and intracellular components) collected from *H. akashiwo* promoted the growth of different prokaryotic species. Notably, some of cellular components-responding species also increased during a natural *H. akashiwo* bloom observed in a previous study. These results suggested that *H. akashiwo* promoted the growth of specific prokaryotic species and that my microcosm experiment could reproduce *H. akashiwo*-associated prokaryotic dynamics, at least partially.

In chapter 3, I demonstrated that effects of *H. akashiwo* and another bloom-forming species, *Chaetoceros* sp. (Diatomea), expand into the dynamics of prokaryotic viruses. The intracellular components derived from the different bloom-forming species promoted the growth of taxonomically distinct prokaryotes and viruses and increase in the viruses followed the growth of their putative host prokaryotes. These results indicated that taxonomic differences in bloom-forming species affect the dynamics of not only prokaryotes but also prokaryotic viruses.

In chapter 4, I examined effects of virus-infected *H. akashiwo* cells (virocells) on a prokaryotic community. The lysates from the virocells promoted growth of specific prokaryotes, which were different from the exudates or intracellular components of uninfected cells did. The virocell-specific prokaryotes included *Vibrio* species potentially possessing a transporter for branched-chain amino acids, which were specifically enriched compounds in the virocell lysates. These results suggested that changes in chemical properties in the *H. akashiwo* virocells enhanced growth of metabolically different prokaryotes.

Collectively, these studies unveiled that the difference in types of leakage (exudates, intracellular components, or viral lysates) from *H. akashiwo* affects the dynamics of specific prokaryotes and their viruses, which had not been revealed by analyses on only natural seawater samples. Further understanding in molecular mechanisms behind the *H. akashiwo*-prokaryotes relationship will help us to reveal biogeochemical cycles in *H. akashiwo* blooms.