Interaction between marine bacterial community and dissolved organic matter released by pelagic phytoplankton

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Dissolved organic matter (DOM) representing one of the largest reduced carbon pools in the ocean, is strongly involved in the global biogeochemical processes. A large proportion of labile DOM in the marine environments is derived from phytoplankton. Many previous studies have shown that such DOM derived from phytoplankton (DOMP) can affect the bacterial community structure and diversity with concomitant changes in DOM characteristics in aquatic ecosystems. However, little is known about the characteristics of the DOMPs from pelagic phytoplankton, and the community response of marine bacteria to the DOMPs. In this study, we analyzed the characteristics of fluorescent DOM (FDOM) of DOMP derived from two different pelagic phytoplankton cultures, the pelagophyte *Pelagomonas calceolata* (Pelago) and cyanobacterium *Synechococcus* sp. (Synech) using excitation emission matrix fluorescence spectroscopy. To prepare the DOMPs, these phytoplankton cultures were incubated in the L1 medium. Then, the algal cells in the medium were removed by filtration (0.2 μ m pore-size Sterivex filter). In addition, we conducted incubation experiments using natural seawater amended with these DOMPs, and analyzed FDOM characteristics, and community and diversity shifts of marine bacteria using 16S rRNA gene (V4 region) tag-sequence. During incubation experiment, we collected FDOM and microbial DNA subsamples on Day 0, 1, and 5.

FDOM analysis for initial samples (Day 0) showed that the fluorescence intensity of humic-like M, C, A from DOMP_{Synech} amendments were higher than those of DOMP_{Pelago}. During incubation experiments, fluorescence intensity of protein-like B and T in the DOMP_{Pelago} decreased with time. After incubation (Day 5), decreases in humic-like M intensity were observed both in the DOMP_{Synech} and DOMP_{Pelago} treatments. The 16S rRNA gene tag-sequence revealed the relative abundance of *Oceanospirillales* and *Alteromonadales* (affiliated with Gammaproteobacteria) to total 16S rRNA sequences drastically increased in both DOMP treatments on Day 1. However, an increase in *Rhodobacterales* (affiliated with Alphaproteobacteria) was observed on Day 5. Interestingly, the proliferation of Betaproteobacteria and Deltaproteobacteria (numerically rare lineages in surface seawater) occurred in the DOMP_{Synech} and DOMP_{Synech} and DOMP_{Pelago} treatments on Day 5, respectively.

These results suggest that the DOMPs released by distinct pelagic phytoplankton can affect the bacterial community structures including numerically rare lineages, and these lineages potentially contribute to the degradation of phytoplankton-derived humic-like materials in seawater.

Keywords: Marine bacteria, Marine phytoplankton, Dissolved organic matter