

## Community and metabolic responses of marine bacteria to the dissolved organic matter derived from phytoplankton

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Dissolved organic matter (DOM) representing one of the largest reduced carbon pools in the ocean, are strongly involved in the global biogeochemical processes. It is considered that a large part of labile DOM in the marine environments is derived from the photosynthesis and cell lysis of phytoplankton. Dissolved organic matter derived from phytoplankton (DOMP) can affect the bacterial community composition and metabolisms. However, little is known about the characteristics of DOMP, and the community and metabolic response of marine bacteria to the addition of DOMP. In this study, we analyzed amino acid composition in the DOMP-lysates from two different phytoplankton cultures, the diatom *Thalassiosira oceanica* (CCMP1005) and the haptophyte *Emiliania huxleyi* (CCMP374), and examined the community and metabolism of marine bacteria in response to these DOMP-lysates using metagenomic approaches. Amino acid analyses for the DOMP-lysates from two strains showed distinctive free amino acid (FAA) compositions, but little changes in their hydrolytic amino acid (HAA) fractions. The proportions of arginine, gamma-aminobutyric acid (GABA) and serine to the total FAAs in *E. huxleyi* were relatively higher than those in *T. oceanica*. However, glutamate and ornithine were the dominant FAAs in the DOMP-lysates from *T. oceanica*. As for the HAA, glutamate and alanine were dominant HAAs in both phytoplankton cultures. In addition, we conducted incubation experiments using natural seawater amended with the lysates from both diatom and haptophyte. Analysis of 16S rRNA genes in the metagenomic sequences revealed that community shifts of marine bacteria in response to DOMP-lysate additions. Relative abundance of *Firmicutes* increased in both DOMP treatments. *Bacteroidetes* increased in response to the addition of DOMP derived from the diatom. Metagenomics analysis of functional genes showed that the genes involved in histidine-, sulfur-, lipopolysaccharide-metabolisms, and polyamine biosynthesis increased in both DOMP treatments. In contrast, the relative abundance of genes associated with glycosaminoglycan metabolism and phosphotransferase system decreased. Fluorescent DOM analysis for initial and amended seawater showed that the fluorescence intensity of a protein-like matter from *E. huxleyi* decreased during incubation. These data suggest that the DOMP-lysates derived from phytoplankton can be a primary factor to change the community composition and metabolisms of marine bacteria, and may change the DOM characteristics in the marine environments.

Keywords: Marine bacteria, phytoplankton, Dissolved organic matter, Amino acids, Metagenome