

A Holistic View of Microbial Community Dynamics during a Toxic Harmful Algal Bloom

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Abstract : The relationship between microbial diversity and algal bloom has received considerable attention for decades. Microbes undoubtedly affect annual bloom events and impact the physiology of both partners, as well as shape ecosystem diversity. However, knowledge about interactions and network correlations among broader-spectrum microbes that lead to the dynamics in a complete bloom cycle are limited. In this study, pyrosequencing and network approaches simultaneously assessed the associate patterns among bacteria, archaea, and microeukaryotes in surface water and sediments in response to a natural dinoflagellate (*Alexandrium* sp.) bloom. In surface water, among the bacterial community, Gamma-Proteobacteria and Bacteroidetes dominated in the initial bloom stage, while Alpha-Proteobacteria, Cyanobacteria, and Actinobacteria become the most abundant taxa during the post-stage. In the archaea biosphere, it clustered predominantly with Methanogenic members in the early pre-bloom period while the majority of species identified in the later-bloom stage were ammonia-oxidizing archaea and Halobacteriales. In eukaryotes, dinoflagellate (*Alexandrium* sp.) was dominated in the onset stage, whereas multiply species (such as microzooplankton, diatom, green algae, and rotifera) coexistence in bloom collapse stag. In sediments, the microbial species biomass and richness are much higher than the water body. Only Flavobacteriales and Rhodobacteriales showed a slight response to bloom stages. Unlike the bacteria, there are small fluctuations of archaeal and eukaryotic structure in the sediment. The network analyses among the inter-specific associations show that bacteria (Alteromonadaceae, Oceanospirillaceae, Cryomorphaceae, and Piscirickettsiaceae) and some zooplankton (Mediophyceae, Mamiellophyceae, Dictyochophyceae and Trebouxiophyceae) have a stronger impact on the structuring of phytoplankton communities than archaeal effects. The changes in population were also significantly shaped by water temperature and substrate availability (N & P resources). The results suggest that clades are specialized at different time-periods and that the pre-bloom succession was mainly a bottom-up controlled, and late-bloom period was controlled by top-down patterns. Additionally, phytoplankton and prokaryotic communities correlated better with each other, which indicate interactions among microorganisms are critical in controlling plankton dynamics and fates. Our results supplied a wider view (temporal and spatial scales) to understand the microbial ecological responses and their network association during algal blooming. It gives us a potential multidisciplinary explanation for algal-microbe interaction and helps us beyond the traditional view linked to patterns of algal bloom initiation, development, decline, and biogeochemistry.

Keywords : microbial community, harmful algal bloom, ecological process, network

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