

Seasonal dynamics of phytoplankton and bacteria community in Sendai Bay

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Phytoplankton and bacteria play ecologically and biogeochemically significant roles in marine ecosystem as a primary producer and as an interface of dissolved organic materials into marine food web. Recently, study about marine microbial diversity has been accelerated using molecular techniques, but basic information of those diverse types of microbes and seasonal dynamics are still limited because of insufficient reference sequence data in public database and of the difficulty of constant monitoring in short term interval. In this study, monthly level monitoring survey was continued for more than two years in 1–3 months interval in the Sendai Bay. Seawater samples were collected for analyzing phytoplankton abundance, diversity and environmental parameters. The abundance of picophytoplankton (pico-sized eukaryotes and cyanobacteria) was counted by flow cytometry, and diatoms and dinoflagellates were counted under microscopy. Size fluctuated seawater was used for phytoplankton composition analysis using both microscopy and molecular techniques (Shotgun metagenome sequencing), and was also used for bacterial 16S rDNA amplicon analysis. Furthermore, frozen preservation technique combined with flow-cytometry was applied to sort specifically the pico-/nano-size phytoplankton followed by metagenome analysis of 18S rDNA amplicon. The higher phytoplankton biomass, which was examined by chlorophyll *a* concentration, was observed from winter to spring in the Sendai Bay during the monitoring. Diatom was dominated throughout year, while small phytoplankton and dinoflagellates were abundant from summer to fall. Pico-eukaryotic phytoplankton was dominated ca. 50% of the small phytoplankton cells throughout year but in summer period when cyanobacteria prominently dominated them. In the Sendai Bay, massive diatom bloom was observed in spring, and the dominant diatom changed from genus *Chaetoceros* to *Skeletonema costatum*, *Leptocylindrus danicus* and *Thalassiosira* cf. *mala* according to the seasonal succession. For the small eukaryotic phytoplankton, taxonomic analysis showed that 19 operational taxonomic units (OTUs) were frequently distributed in all seasons. Composition analysis showed that the OTUs had characteristic patterns and were divided into four main groups. Two groups reflected the low-saline water and winter season, with the characteristic OTUs belonging to diatoms; to note, *Chaetoceros* and *Leptocylindrus* were characteristic of low saline water, and two diatom genera (*Minidiscus* and *Minutocellus*) and Cryptomonadales-related OTUs were prevalent in the winter. Bacteria in the 0.2–0.8 μ m size fraction showed that the most frequent and abundant OTUs belonged to oceanic clade of SAR11, indicating inflowing oceanic water into the bay. Moreover, according to phytoplankton bloom state, a Rhodobacteraceae related OTU and cyanobacteria related OTUs increased in bloom formation period (January–April) and in high temperature period after the bloom was decayed (June–September), respectively. Those results indicated that the microbial community including phytoplankton and bacteria dynamically changed in the Sendai Bay.

Keywords: Microbial community, Phytoplankton, Bacteria, Sendai Bay, Metagenome analysis