

Prokaryotic and eukaryotic community structures in surface sediments of the East Antarctic coastal region

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The annual cycle of sea ice formation and melting in the Southern Ocean significantly impacts its ecosystems. During sea ice formation in the coastal region, frazil ice incorporates particles, microorganisms, and resuspended sediments (Reimnitz et al., 1993; Sullivan et al., 1985; Ito et al., 2019). These materials are transported offshore via sea ice advection and released into the water column on melting, which occasionally triggers phytoplankton blooms (Lannuzel et al., 2013). Sea-ice algae may serve as food for heterotrophic protists, zooplankton, and juvenile fishes (McMahon et al., 2006; Gradinger, 2001). Therefore, in order to understand how sea ice influences the community composition of planktonic microorganisms in the Southern Ocean, it is necessary to understand those of the coastal sediments. In this study, we performed SSU rRNA gene amplicon analysis to characterize prokaryotic and eukaryotic community structures in surface sediments off East Antarctica.

The surface sediments were sampled from Cape Darnley Polynya, Lützow-Holm Bay, and offshore of Totten Glacier by the 61st Japan Antarctic Research Expedition from January 2019 to March 2020 (Table 1). The sediment DNAs were extracted, and the 16S rRNA gene V3-V4 region and the 18S rRNA gene V9 region were amplified. The PCR products were sequenced with an Illumina MiSeq sequencing system, and the sequence data were analyzed using QIIME2 pipeline. The obtained sequences were classified using the Silva database for the 16S rRNA gene and the PR2 database for 18S rRNA gene, respectively. In addition, representative sequences were identified at the species level by BLAST (Basic Local Alignment Search Tool).

The prokaryotic community was predominated by the phylum *Pseudomonadota* (27–68%), which was mainly composed of the cosmopolitan class *Gammaproteobacteria* (Mußmann et al., 2017) and *Alphaproteobacteria*. The exception was TG8 and TG9, where the phylum *Verrucomicrobiota* contributed 50% and 10%, respectively. It was rarely detected in other sites, hence, the phylum *Verrucomicrobiota* is considered as one of the organisms that characterize Dalton Polynya.

In the eukaryotic community, the phylum *Gyrysta* was predominant at CDP (38%), which showed two times higher contribution than the other sites. The genera *Chaetoceros* and *Porosira* contributed 43% and 41% of this phylum at this site. These diatoms are detected as dormant cells in East Antarctic coastal sediments (Armand et al., 2005; Pike et al., 2009) or as major genera in ice-edge phytoplankton bloom (Pike et al., 2009; Fukai et al., 2021). Therefore, these genera may be involved in phytoplankton blooms via annual sea ice formation and melting. On the other hand, the phylum *Dinoflagellata* was predominant at LB1 (11%), whose contribution was 1.8 times higher than other sites. Among this phylum, a single species, *Polarella glacialis* accounted for 60% at this site. The resting spores of this species are found in sediments from the Lützow-Holm Bay (Ichinomiya et al., 2008), and they form bloom in land-fast sea ice (Stoecker et al., 1998). It is considered a characteristic species of Lützow-Holm Bay.

This study revealed the community structures in surface sediments and found some taxa possibly involved in phytoplankton blooms through either sea ice melting or resting spore formation. Community compositions in offshore waters may be influenced by those in coastal sediments via sea ice formation and melting. To further understand the effect of coastal communities on offshore communities via sea ice, coastal seawater should be studied for the prokaryotic and eukaryotic communities.

Table 1. Location and characteristics of sampling sites.

Sampling sites	Abbreviations	Latitude, Longitude	Sea ice concentration (%)	Water depth (m)
Cape Darnley Polynya	CDP	-67.113, 65.825	3	644
Lützow–Holm Bay 1	LB1	-69.002, 39.611	100	34
Lützow–Holm Bay 2	LB2	-68.469, 38.478	79	310
Totten Glacier 1	TG1	-66.780, 117.108	79	410
Totten Glacier 2	TG2	-66.800, 117.237	86	870
Totten Glacier 3	TG3	-66.792, 117.356	90	670
Totten Glacier 4	TG4	-66.760, 117.753	95	710
Totten Glacier 5	TG5	-66.504, 119.577	0	696
Totten Glacier 6	TG6	-66.228, 120.62	5	487
Totten Glacier 7	TG7	-66.251, 118.751	95	830
Totten Glacier 8	TG8	-66.491, 120.821	0	304
Totten Glacier 9	TG9	-66.381, 120.679	2	434

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