

Prokaryotic and eukaryotic community structures in East Antarctic coastal sediments

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The Southern Ocean plays a crucial role in the uptake and storage of carbon. Carbon uptake of the region is estimated as more than 10% of the anthropogenic carbon dioxide. The study on the Southern Ocean sea ice is essential to understand the variation of carbon uptake and biogeochemical cycle. Sea ice incorporates high levels of iron during its formation triggering phytoplankton blooms at the sea-ice edge during the melt season (Duprat et al., 2020). Recent observations reported that frazil ice could incorporate resuspended sediment through suspension freezing in a coastal polynya (Ito et al., 2019). Turbulent conditions formed a mixture of frazil/grease ice and open water in the active-frazil area (Nakata et al., 2021). These studies implied that sea ice incorporates resuspended sediment in the coastal area and releases it offshore via sea ice advection and melts. Therefore, studying the seafloor sediment is necessary to understand the Antarctic ecosystem and biogeochemical cycle. However, there are few reports on comprehensively investigating biological communities of Antarctic coastal sediments. This study aims to reveal the prokaryotic and eukaryotic communities of the East Antarctic coastal sediment that may be transferred offshore via sea ice advection.

The seafloor surface sediment samples were collected from Cape Darnley Polynya, Lützow-Holm Bay, and Langhovde Glacier by the 59th Japan Antarctic Research Expedition (Table 1). The sediment DNAs were extracted, and the 16S rRNA gene V3-V4 region and 18S rRNA gene V9 region were amplified by PCR. The PCR products were sequenced with an Illumina MiSeq sequencing system, and the sequence data were analyzed using mothur software. Sequences were classified using trainset18 for 16S rRNA genes and PR2-database for 18S rRNA genes, and those with 97% or more sequence homology were designated as one OTU (Operational Taxonomic Unit). In addition, representative sequences of OTU were identified at the species level by BLAST (Basic Local Alignment Search Tool).

Table 1. Sampling sites

Sampling sites	Abbreviations	Latitude, Longitude	Depth (m)
Cape Darnley Polynya	CDP	-67.4063, 68.5537	205
Lützow-Holm Bay	LHB	-68.5652, 39.4058	149
Langhovde Glacier 1	LG1	-69.2025, 39.8219	381
Langhovde Glacier 2	LG2	-69.1966, 39.8083	464
Langhovde Glacier 3	LG3	-69.1922, 39.8144	504
Langhovde Glacier 4	LG4	-69.1886, 39.7925	479

In prokaryotic community structures, phylum *Proteobacteria* was most frequently detected at all sites, ranging from 57 to 96%. Among this phylum, α -*Proteobacteria* and γ -*Proteobacteria* were dominant. In addition to *Proteobacteria*, phyla *Actinobacteria*, *Bacteroidetes*, *Cyanobacteria*, and *Planctomycetes* were detected relatively frequently. On the other hand, site-to-site differences were observed when comparing at lower taxonomic levels. For example, the order *Chromatiales* accounted for most of the γ -*Proteobacteria* detected in CDP and LHB, whereas it was less abundant under the ice shelf. Conversely, the order *Alteromonadales* of γ -*Proteobacteria*, detected in a high proportion under the ice shelf, especially in LG2, were rarely detected in CDP and LHB. In eukaryotic community structures, phylum *Ochrophyta* was detected at a relatively high frequency at all sites. Phylum *Dinoflagellata* and *Rhizaria* were also detected at a relatively high frequency at most sites but not in LG1 and LG2 under the ice shelf close to land. As with the prokaryotic community, the differences between the sites

become clear when comparing at lower taxonomic levels. For example, orders *Thalassiosirales*, *Dictyochales*, and *Pedinellales* were found only in CDP, whereas the genus *Fragilariopsis* was found only in LHB.

As a result of this study, it was found that there are many similarities between the community structures in the sediments in Cape Darnley Polynya and Lützow-Holm Bay. In contrast, the community structure under the Langhovde Glacier differs from other sites. These findings provide useful information for a deeper understanding of biological activities and the ecosystem dynamics affected by them in the Southern Ocean. In addition, the DNA of organisms specifically detected in sediments in specific areas may be used as tracers of sea ice formed there. However, this study uses sediments collected from only one point in each area, so it is not easy to generalize at this time. By increasing the number of sampling sites, it is thought that the characteristics of the three areas can be captured more accurately.

References

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