

Eukaryotic community structure in sea ice and sinking particles during summer off Wilkes Land, East Antarctica

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Ice edge phytoplankton blooms impact on the lower trophic level of the food web and on carbon transfer in the seasonal ice zone (SIZ) of the Southern Ocean. Sea ice melting facilitates primary production and vertical material cycling by relaxing light, nutrient (iron) limitation and releasing ice algae as a seeding population. In addition, released ice algae make an eukaryotic community structure in seawater and sinking particle dramatically variable. It is important to examine an eukaryotic community structure in various samples to understand the variations for both primary production and export flux. In this study, we compared the eukaryotic community structure in brash ice and sinking particle in the SIZ of the Southern Ocean using high-throughput DNA sequencing.

Field observations were conducted off Wilkes Land of the Indian Ocean sector. Drifting sediment traps were deployed at depths of 60 and 150 m (64°16'S, 116°58'E) from 10 December 2019 to 20 January 2020. Brash ice was sampled at the drifting array site using a stainless-steel cage. 18S rRNA gene V9 region of DNA extracted from brash ice and sinking particles was amplified. PCR products were sequenced with the Illumina Miseq system. The clustering of amplicon sequence variants (ASV) and statistical analyses were performed using QIIME2 (ver. 2022.8) and R (ver. 4.2.2.).

We totally obtained 1,409,098 reads from eight ice samples and 14 sinking particle samples. The obtained sequences were clustered 961 ASVs. Principal coordinate analysis indicated a significant difference in eukaryotic community structure between brash ice and sinking particle (PERMANOVA test, $p = 0.001$) (Fig. 1a). Ochrophyta (mainly diatom), Metazoa, and Dinoflagellata were dominant groups in brash ice samples (Fig. 1b). In contrast, Radiolaria, Metazoa, and Dinoflagellata were dominant group in sinking particle samples. These results with high-throughput DNA sequencing suggest that diatom in brash ice was seldom detected in sinking particle during sea ice melting.

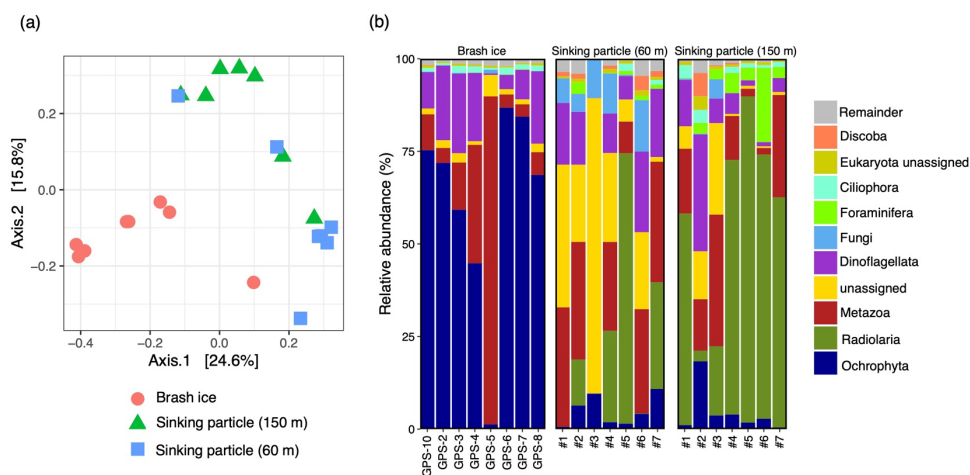


Figure 1. Differences of eukaryotic community structure in sea ice and sinking particles. (a) Principal coordinate analysis of the weighted UniFrac distances between the samples. (b) Relative abundance at taxon level 3 (phylum level).