Differences in diversity and photoprotection capability between Ice algae and under-ice phytoplankton in Saroma-Ko Lagoon, Japan: a comparative taxonomic diatom analysis with microscopy and DNA barcoding

Kazuhiro Yoshida^{1,2,3}, Hiroshi Hattori⁴, Takenobu Toyota⁵, Andrew McMinn² and Koji Suzuki¹

¹Faculty of Environmental Earth Science, Hokkaido University
²Institute for Marine and Antarctic Studies
³Graduate School of Agriculture, Saga University
⁴Department of Marine Biology and Sciences, Tokai University
⁵Institute of Low Temperature Science, Hokkaido University

Sea ice algae are the main primary producers in polar ecosystems (Arrigo, 2017). Bottom communities are particularly composed of diatoms with the highest biomass (Horner, 1985; van Leeuwe et al., 2018). Ice algae are unique and diverse communities. Although young ice communities usually reflect the composition of the underlying seawater when ice forms, species selection in sea ice over time can change the community composition of ice algae from that of under-ice phytoplankton. However, less attention has been paid on the difference or similarity in community composition between sea ice and under-ice. The taxonomy of sea ice communities has been traditionally investigated with light microscopy. Recently, molecular techniques, including pigment analysis, have provided new insights into the diversity and physiology of sea-ice communities (Hardge et al. 2017; Yoshida et al., 2020). However, no comparative taxonomic survey has been conducted for ice algae thus far. Here, we investigated differences and similarities in (1) the diversity and (2) the photosynthetic strategies of diatom communities in sea ice and the underlying seawater of Saroma-Ko Lagoon, Hokkaido, Japan, using algal pigment signatures determined by ultrahigh performance liquid chromatography (Suzuki et al., 2015), light and scanning electron microscopy (hereafter LM and SEM, respectively, Nosaka et al., 2017; Roukaerts et al., 2018) and Ion Torrent next-generation sequencing (NGS) techniques targeting the 18S rRNA gene (i.e., DNA barcoding) (Endo et al., 2018; Yoshida et al., 2018). Ice algae typically possessed greater biomass (> 20-fold) and chlorophyll (chl) a breakdown products than under-ice phytoplankton, suggesting that the ice algae formed blooms, and cell senescence and disruption could be significant mitigating factors. LM and SEM showed a good agreement for the ice algal community compositon. However, LM overlooked small species of under-ice seawater. Although the results of NGS were neither consistent with those of LM nor SEM, this method successfully identified some easily-misidentified species by microscopy. We concluded that SEM would be the most reliable method to identify ice algae and under-ice phytoplankton. Although NGS cannot be used for sea ice taxonomy work at this stage, NGS can provide useful auxiliary information on their identification. Further molecular investigations of ice algae, including the expansion of nucleotide databases, are needed (Rimet et al., 2019). The diversity of diatoms in sea ice was higher than in under-ice seawater, although the evenness was comparable or lower in ice algae than in under-ice phytoplankton (Fig. 1). Ice algae had a larger xanthophyll pool size and a higher ratio of photoprotective to photosynthetic pigments (11-fold and 4.5-fold higher, respectively) than under-ice phytoplankton. The results indicated that ice algae were well adapted to changes in the light regime, which could partly support their survival capability and high taxonomic diversity.

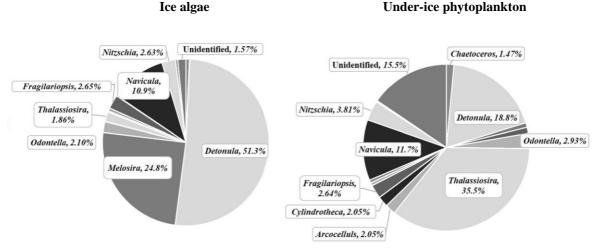


Figure 1. Diatom community composition in sea ice and under-ice seawater determined by scanning electron microscopy (SEM). The left and right panels show the taxonomic results of ice algae and under-ice phytoplankton, respectively.

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