## Sea ice melt affects algal photosynthesis and growth: A laboratory study on an ice algal community from the Sea of Okhotsk

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Algae colonizing sea ice are important primary producers in ice-covered regions. As sea ice forms, highly saline water expelled during freezing is partly entrapped into brine channels and pockets, which provides microhabitats for ice algae (Horner, 1985). Ice algae have to cope with not only the low metabolic rate caused by the low temperature, but also the stress caused by the high brine salinities. In early spring, increased porosity of sea ice promotes release of ice algae into the water column. Some released ice algae can continue to grow in seawater and seed phytoplankton blooms after ice retreat. Others may die due to the rapid changes in the conditions of surrounding waters or sink out from the water column over time (Szymanski and Gradinger, 2016; Kauko et al., 2018). The Sea of Okhotsk is a marginal sea of the Northwest Pacific and has the largest subarctic extent of sea ice (Kaartokallio et al., 2017). The melt of the Okhotsk sea ice may significantly contribute to the phytoplankton growth in early spring (Kanna et al., 2018). Survival and growth of ice algae during ice formation and melt would be important factors determining the algal community dynamics in the water column. The growth of algae is particularly related to their photosynthetic performances. Therefore, we investigated the changes in the photophysiology and community composition of an Okhotsk ice algal community in a 6-day incubation experiment that simulated the ice melt condition using a sea ice core collected from the southwestern part of the Sea of Okhotsk in the field campaign of the icebreaker Patrol Vessel (P/V) Soya in Feb 2019. The bottom 5 cm of the ice core with dense ice algal cells was cut down and melted in 2 L glass beakers that contained 1.7 L autoclaved in situ seawater. The temperature was controled at around 0 °C and the irradiance level was set at 50  $\mu$ mol photons m<sup>-2</sup> s<sup>-1</sup> with a 12L/12D cycle. Water samples of algal cells were taken during and after complete ice melt from the beaker. Centric diatoms overwhelmingly dominated the ice algal community, contributing to >85 % of the total cell abundance. Both light microscopy and the diatom 18S rRNA gene sequence data showed that Thalassiosira and its morphologically similar species were the most abundant among the centric diatoms. Centric diatoms showed significant growth only after complete ice melt, while pennate diatoms showed little growth with relatively high mortality during the ice melt. Cellular pigment content showed a decreasing trend until the minimum was reached after the melt of 10 h and then increased until the end of the incubation. The maximum photochemical efficiency of Photosystem II  $(F_{\nu}/F_m)$  was lowest at the beginning of the ice melt and gradually recovered with time. While the transcription levels of the *rbcL* gene was three times higher during ice melt than that after complete ice melt, indicating an urgent need for running the Calvin Cycle irrespective of the high energy cost to run it. The results suggest that while the photophysiology of algal cells was affected immediately by the ice melt, effective physiological acclimation strategies in some strong algal taxa allow them to bloom even at low temperatures after all the ice has melted out.

## References

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