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学 位 論 文 題 名/Title of Dissertation

Winter-to-spring dynamics of phytoplankton in the southern Sea of Okhotsk:
community structure, photosynthetic activity, and sinking characteristics
(オホーツク海南部における植物プランクトンの冬季から春季への動態：群集構造、
光合成活性、および沈降特性)

The southern Sea of Okhotsk (SSO) is a semi-enclosed marginal sea in the North Pacific and represents the southernmost seasonally ice-covered zone in the Northern Hemisphere. In winter, it is covered by extensive sea ice driven by the East Sakhalin Current (ESC) and northerly winds, while its spring ice melt triggers a large phytoplankton bloom that contributes significantly to annual primary production. Despite the ecological importance of phytoplankton, the winter-to-spring changes in their community structure, photosynthetic activity, and contributions to the biological carbon pump remain poorly understood.

To investigate the winter-to-spring dynamics of phytoplankton and their environmental drivers in the SSO, we applied microscopy, algal pigment signatures, and 18S rRNA gene (rDNA)-based metabarcoding to characterize predominant phytoplankton assemblages during 2022 and relate them to environmental variables. As a result, Diatoms were the dominant group in winter, leading to a phytoplankton bloom in spring. Other phytoplankton also showed relative contribution during winter and at the lower Chlorophyll (Chl) *a* stations in spring. Co-occurrence network analysis using 18S rDNA sequences showed Temperature-sensitive small-sized *Chaetoceros* and nutrient-dependent large centric diatom *Thalassiosira* had a strong coexistence relationship at coastal stations during winter, making the largest contribution to the spring bloom with higher Chl *a* concentrations. The pennate diatom *Fragilariopsis* is considered an ice-related diatom genus (e.g., Yan et al., 2022), and it existed in seawater during winter and at the lower Chl *a* stations in spring. We found that not only sea ice diatoms but also winter phytoplankton in ECS-affected coastal waters can contribute to the large spring bloom in the SSO, and that could be more prevalent in less sea ice conditions due to warming.

To investigate whether the photosynthetic activity of phytoplankton also contributes to the spring bloom, we compared the differences in the expression level of the *rbcL* gene, which encodes the large subunit of the photosynthetic carbon fixation enzyme Rubisco, among dominant diatom families in the SSO from winter to spring in 2022 and compared the results with environmental factors. Higher diatoms' *rbcL* transcription efficiency in terms of mRNA (cDNA)/DNA copy number ratio was observed in winter-coastal and spring waters than in winter under-ice waters, suggesting light availability as a key driver of their photosynthetic activity. Additionally, centric diatoms exhibited significantly higher *rbcL* transcription efficiency than pennate

diatoms throughout the study period. The transcription efficiency of three dominant diatom families- Chaetocerotaceae, Thalassiosiraceae, and Bacillariaceae showed strong positive correlations with both the maximum quantum yield of photochemistry in algal photosystem II (F_v/F_m) and Chl a concentrations. This suggests that light-harvesting capacity and carbon fixation activity (mediated by *rbcL*-encoded RuBisCO) jointly contribute to spring bloom in the SSO.

The diversity of diatoms- manifested in their morphological and physiological traits directly influences their capacity to export organic carbon to the deep ocean (Treguer et al., 2018). To investigate the sinking processes of phytoplankton before and after the ice-covered period, we deployed a sediment trap at 550 m depth on the continental slope of the SSO to collect sinking particles from December 2022 to June 2023. Using scanning electron microscopy (SEM) and molecular techniques, we analyzed changes in the flux and community composition of phytoplankton within the sinking particles. The results revealed two distinct peaks in phytoplankton flux over the sampling period: the first occurred during the early stage of ice coverage, when sea ice was transported into the study area, and the second, more pronounced peak took place during the ice melt period. The community composition analysis indicated that *Fragilariopsis cylindrus* and *Thalassiosira nordenskioeldii*, the dominant diatoms associated with sea ice (Yan et al., 2022), made the greatest contribution to the biological carbon pump during the ice-melting peak. These findings highlight the seasonal succession in phytoplankton export composition and emphasize the critical role of sea ice in driving diatom-mediated carbon flux to the deep ocean.