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Abstracts

Conveners: Akinori Takahashi, and Kunio Takahashi (NIPR)

Diving into the world of penguins- insights from penguin-borne cameras

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Penguins are among the most charismatic species inhabiting the Southern Ocean. They often constitute valuable sentinels of environmental changes and are also important consumers contributing to ecosystem functioning. Relatively easy to study on land, their behaviour at sea has until quite recently remained poorly understood. Enabled through technological developments in both tracking devices and video cameras that can be deployed on penguins, we have been able to assess important aspects of penguin biology in relation to specific ecological contexts. I will start this talk by providing a broad overview of penguin taxonomy and ecology before detailing some of our research findings obtained through the deployment of small video cameras on penguins. This has enabled us to see how they perceive the underwater world and behave in relation to various circumstances. Among others, I will highlight observations of kleptoparasitism in Gentoo penguins where individuals steal prey from each other, both at the Falkland Islands and at sub-Antarctic Marion Island, while foraging at sea, as well as observations where prey clearly defend themselves by fighting back. At Marion Island, as is the case with many other Southern Ocean islands, marine benthic invertebrate assemblages are poorly understood, and I demonstrate how penguins are improving our understanding of the benthos around Marion Island through attached video cameras. I will furthermore show interactions of penguins in Antarctica with krill swarms and discuss this from a management perspective. I will conclude by briefly discussing a novel method, using video, accelerometer and depth data from foraging penguins to quantify prey capture rates relevant to ecosystem-based management.

Unsuccessful foragers rely on social information acquired through group departure and travel: evidence from Adélie penguins

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Colonial animals are expected to use social information to reduce uncertainty regarding food location and quality; however, empirical studies remain scarce on how they acquire and when they rely on such information. Here, we examined whether group departures from breeding colonies facilitate the transfer of social information about foraging sites and identified factors influencing its use by analyzing biologging data from Adélie penguins. We tracked 117 penguins in a small breeding colony and obtained behavioural data from 1006 foraging trips. Using these data, we tested two hypotheses regarding (1) the mechanism of social information transfer, and (2) the conditions under which they rely on such information. The first hypothesis posited that individuals acquire social information within groups of conspecifics departing the colony together, expecting that the previous trip paths of group members would influence foraging site selection. To test this, we applied integrated step selection analysis to the GPS tracking data from penguins that departed the colony together, and found that individuals adjusted their foraging sites based on the prior experiences of conspecifics beyond what would be expected by chance. The second hypothesis proposed that individuals adjust their reliance on social information based on their prior foraging success. We found that penguins with unsuccessful prior trips were more likely to follow others during subsequent trips. Foraging success was estimated using depth and video tracking data, and we examined its influence on the direction of information transfer. These findings indicate that group departure and travel promote the use of social information, particularly under unfavourable foraging conditions. Our study identifies a pathway by which sociality reduces uncertainty about the foraging environment and underscores the potential costs of population decline for species relying on social foraging.

Emergence of a prey depletion halo through penguin–krill behavioural dynamicsHina T. Watanabe^{1,2}, Junichi Takagi³ and Akinori Takahashi^{1,4}¹ *National Institute of Polar Research, Tokyo, Japan*² *Centre d'Etudes Biologiques de Chizé, UMR 7372 CNRS, Université de la Rochelle, Villiers-en-Bois, France*³ *School of Platforms (KUSP), Kyoto University, Kyoto, Japan*⁴ *Polar Science Program, Graduate Institute for Advanced Studies, SOKENDAI, Midori-cho, Tachikawa, Tokyo 190–8518, Japan*

Predators can influence prey through direct consumption and non-consumptive effects that alter prey behaviour and distribution. In colonial central-place foraging systems, such predator–prey behavioural interactions may create zones of prey depletion known as Ashmole’s halos. However, the mechanisms underlying halo formation remain unclear in marine environments, where prey are mobile and patchily distributed. Here, we investigated whether cumulative foraging activity by Adélie penguins *Pygoscelis adeliae* alters prey availability, consistent with Ashmole’s halo. Based on GPS tracking data, three-dimensional dive paths, and prey captures derived from acceleration signals, we found that penguins dived intensively near their colony, where under-ice feeding distances and dive depths were significantly greater. However, feeding rates did not vary with distance from the colony, suggesting that prey patch quality remained stable despite reduced prey accessibility near the colony. During foraging dive bouts, penguins progressively exploited more horizontally distant or deeper waters at each dive, consistent with the displacement of prey. These findings suggest that dynamic predator–prey behavioural interactions, such as prey escape and dispersal, contribute to forming prey depletion halos. Our study highlights the role of predator behaviour in shaping dynamic prey landscapes in marine environments.

Exploring narwhal surface behavior with drone in Inglefield Bredning (Kangerlussuaq), northwest Greenland

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Inglefield Bredning (Kangerlussuaq) is one of the largest summering ground for narwhals (*Monodon monoceros*) in Greenland, with approximately 3,000 individuals coming to the fjord every summer [Hansen et al., 2024]. This area is known as the only place in the world where the traditional Inuit narwhal hunt is still maintained, and narwhals are culturally and economically important to the local community. Narwhals in this area feed much less in summer than in winter [Laidre and Heide-Jørgensen, 2005], and the reasons for their summer aggregation remain unclear. Here, we conducted drone-based observations of narwhals while accompanying Inuit hunt to directly document their surface behavior. Observations were conducted over twelve days in August 2025. As the period coincided with the midnight sun, the sighting survey was undertaken continuously (24 h per day). When narwhals were sighted, a drone (DJI Mavic 3) was deployed at an altitude of > 40 meters above the sea surface to record their behavior. A total of sixty six minutes of behavior was recorded, including eighty one individuals. At least fourteen mother–calf pairs were observed (Fig. 1), with most groups consisting of mothers and calves, sometimes accompanied by young males, but rarely including adult males with large tusks. Adult males were frequently observed in male-only groups, with female seldom present (Fig. 2). Social sexual behaviors were recorded for the first time during the survey period, occurring three times over two days, with the penis visible in two of these instances. In cetaceans, differences between male and female, including energy budgets, predation risk and male harassment, drive them to segregate spatially and socially during mating [Wells et al., 1987; Galezo et al., 2018]. Moreover, individuals engaging more frequently in social sexual behaviors during the subadult stage tend to have higher reproductive success [Holmes et al., 2024]. Our observations captured behaviors suggesting that the area plays a key role in reproductive activities, including newborn nursing and mating.



Figure 1. Mother – calf pairs observed in Inglefield Bredning.

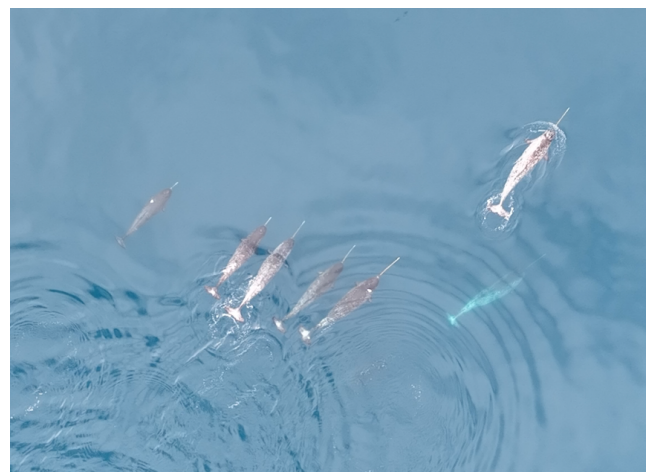


Figure 2. Adult male narwhals swimming as a group

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Seafloor video monitoring in a glacial fjord, Inglefield Bredning, Greenland

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Due to difficult access, seafloor ecosystems in Arctic glacial fjords remain understudied. At the same time, it is unclear if commonly used monitoring methods are noninvasive and suitable. As part of a long-term acoustic monitoring program for marine animals, we deployed a camera with a hydrophone on the seafloor of Inglefield Bredning, Northwest Greenland. Our goal was to document the seafloor environment and evaluate the performance of a compact mooring system, including its potential physical interaction with narwhals, which has recently been identified as a concern [Podolskiy *et al.*, 2025].

The setup included an underwater camera with a hydrophone (LoggCAM, Biologging Solutions), a sound recorder (SoundTrap ST600), an acoustic release (Ascent AR, Vemco), a buoy (Viny, 10B-8 with 10.7 kg of buoyancy), an anchor (50 kg of rocks in a net), and a Samson 3/8" line connecting all components into a chain approximately 2.5 meters long. The setup was first tested in a pool and shallow waters in Japan. On August 1, 2025, the setup was deployed in Greenland near Qeqertaq and Heilprin Glacier from a boat to a depth of around 260 meters (drop location: N 77°28.120', W 66°21.411'). On August 9, 2025, it was recovered. The camera was looking upward and recorded a 10-minute-long video (VGA, 640 x 480) with audio (96 kHz) every 20 minutes (i.e., with a 10-minute pause) for about three days. Two LED lights of the camera were at a red wavelength (650 nm). This helped avoid attracting animals and ensure the passive nature of the observations, but limited the range of observations to about a meter. The SoundTrap was continuously recording sound at a sampling rate of 96 kHz. The internal sensors of the release recorded temperature, pressure, average noise, and tilt at one-minute intervals.

The video showed numerous small particles and fibers, which we call "marine snow," constantly moving across the scene. Small animals were also occasionally seen. By manually reviewing the videos (37 hours in total), we identified several small animal species, including copepods, sea slugs, fish, shrimp, jellyfish, and others. To study marine snow dynamics, we used Particle Image Velocimetry (PIV), a common technique in fluid dynamics. It revealed changes in flow speed and direction over time, as well as turbulent vortices, highlighting highly active seafloor conditions. Narwhals produced the main biophonic sounds, although they did not appear in the camera's view. The primary geophonic sound source was the rumbling and cracking of icebergs. The boat engine was also recorded. In total, we collected 7 different streams of data, which are now being analysed. At this stage, we conclude that our setup, which fits into one Zarges box, is suitable for rapid deployments and comparative studies in various locations.

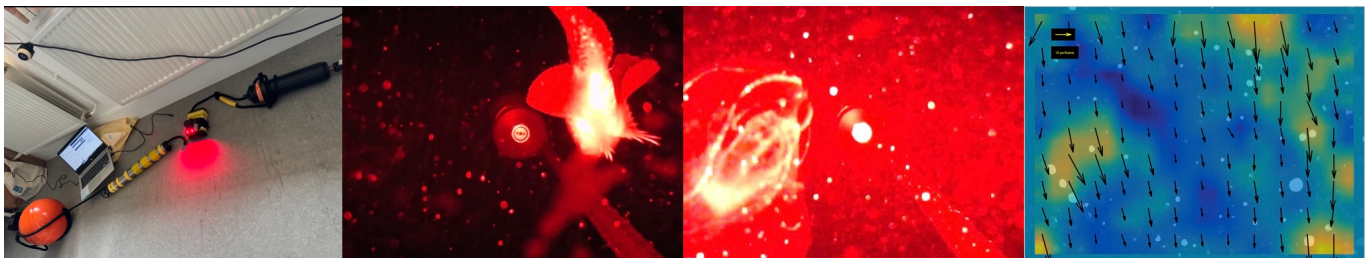


Figure 1. The setup with examples of raw and processed video data (fish, jellyfish, and PIV-derived particle speed).

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Impact of Freshwater Supply and Sea Ice Remnants on Phytoplankton in the Pacific Arctic Ocean

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In the Pacific Arctic Ocean, sea-ice melt was delayed in 2021, and substantial amounts of sea-ice remained even in the autumn (Moore et al. 2022). Such environmental changes are expected to affect phytoplankton community structure, which have short generation times and can respond rapidly. Freshwater input has also been remarkable, mainly due to the increased inflow of sea-ice meltwater and river water (McLaughlin and Carmack 2010). However, our knowledge of how changes in sea-ice and freshwater supply affect phytoplankton communities in the Pacific Arctic Ocean remains limited. This study aims to examine the phytoplankton communities during the autumn seasons of 2021, 2023, and 2024 to clarify the effects of the sea-ice melt and consequent freshwater budget on their structure.

Surveys were conducted in the Pacific Arctic Ocean from September 12 to October 1, 2021; September 7 to 30, 2023; and September 5 to 26, 2024. Water samples were collected from the surface layer and the Sub-surface Chlorophyll Maximum layer (SCM). The samples were fixed with glutaraldehyde at a final concentration of 1% and then concentrated. Diatoms, dinoflagellates, ciliates, and silicoflagellates were identified and counted under an inverted microscope. Cluster analysis was performed using the cell density data. Water temperature, salinity, Chl. *a* fluorescence, dissolved inorganic nitrogen (DIN), phosphate, silicate, fractions of river runoff (f_{tro}) and sea-ice melt water (f_{simw}), and sea-ice melt day were also obtained.

Cluster analysis based on abundance classified six groups (A-F). Group D, characterized by high cell densities, was observed around 72°N in 2021, where a large amount of sea ice remained. In the marginal ice zone, the presence of sea ice destabilizes the water column structure and alters water flow, leading to nutrient upwelling from deeper layers. Additionally, the area around 72°N is close to the continental shelf slope, where upwelling along the shelf margin has been shown in previous studies. Therefore, the formation of group D observed in 2021 was most likely caused by a combination of an improved light environment due to delayed melting of sea ice and nutrient supply from upwelling along the ice margin and shelf area, which also triggered phytoplankton blooms during the autumn season. Group E also exhibited high cell densities and was distributed in inner shelf areas around 71°N in 2024. This area receives inflows from the northern coast of Alaska, where river water is an important nutrient source in the Pacific Arctic Ocean. In this study, group E cooccurred with high f_{tro} and high nutrient concentrations, suggesting the influence of river water. Thus, the nutrient-rich environment derived from river water in the 71°N coastal area may have promoted the growth of nutrient-demanding species.

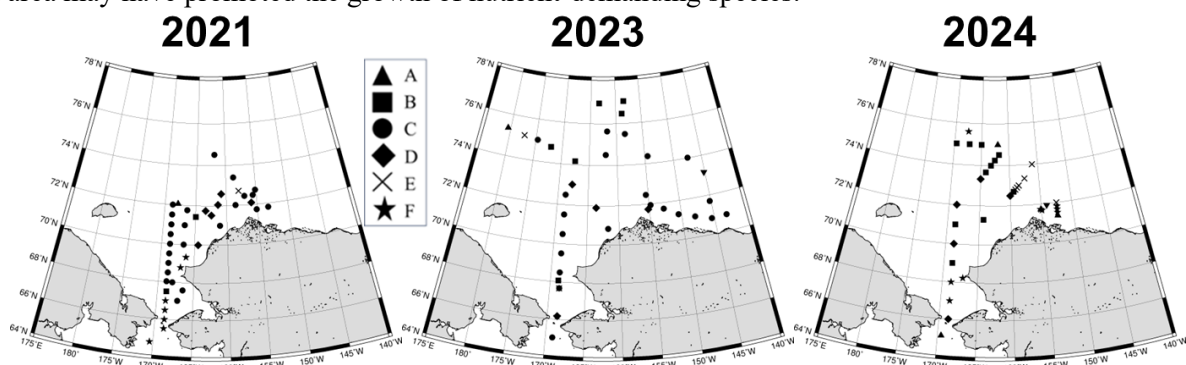


Figure 1. Distribution of phytoplankton groups in 2021, 2023 and 2024.

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Taxonomic overview of marine eukaryotic communities off Wilkes Land

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Marine ecosystems in the Southern Ocean has been impacted under climate change. Several cyclonic gyres contribute to heat transport from offshore to coastal margins off Wilkes Land, and warm Circumpolar Deep Water is attributed to melting the grounding zone of Totten Ice Shelf (Hirano et al., 2021). Because rising seawater temperature and melting ice can recently affect plankton community structure off Wilkes Land, monitoring plankton communities is needed. However, sparse dataset prevents to understand plankton communities in water column off Wilkes Land (Armbrecht et al., 2023). Matabarcoding methodologies using environmental DNA (eDNA) is helpful to support microscopic observation of organisms even though they still have biases to estimate biomass. We present the preliminary modern eukaryotic communities off Wilkes Land using 18S rRNA amplicon sequencing with aquatic DNA. Environmental DNA was filtered with 2L of seawater from 0 m to 200 m depth on the ice breaker Shirase during the 66th Japanese Antarctic Research Expedition cruise in March 2025. Sixty-two seawater samples showed Bacillariophyta, Dinoflagellata, and Arthropoda were dominant through the water column. Non-metric multidimensional scaling (nMDS) for the eDNA dataset based on Bray-curtis distances showed that molecular communities off Wilkes Land above 75 m depth clustered. Communities from deeper than 100 m depth and at lower latitudes were separated in nMDS due to a sharp decrease in relative abundance of diatom and an increase in relative abundances of arthropod and dinoflagellate.

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Isolation of β -glucan exopolysaccharide producing bacteria strains from Antarctic marine sediment

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Cold-adapted bacteria from polar habitats could be potential sources of novel biomolecules with potential beneficial applications. Under the extremes environment, microorganisms produce unique extracellular polymeric substances to protect the cells from the extreme temperatures. Some of the cold-adapted bacteria produce β -glucans the component of their extracellular polymeric substances. β -glucans have extensive applications in healthcare. It enhances immune functions with anti-infective, anti-tumour and immunomodulatory activities. β -glucan is also has promising application in dermatology which include wound care treatment. Studies have shown that β -glucans can accelerate wound healing process and inhibit the growth of pathogens. β -glucans are glucose polymers linked by 1,3; 1,4 or 1,6 β -glycosidic bonds, which differs from each other by their length and branching structures. Bacterial β -glucans have advantages compared to plant and fungi β -glucans in term of shorter production time and easier purification process. However, discovery of novel microbial β -glucans and the ability to produce the β -glucans in adequate quantity remain as a challenging research field. In this project, we aim to isolate bacteria strains from Antarctica marine sediment which could produced novel β -glucans and evaluate the wound healing properties of the β -glucans. Four β -glucans producing bacteria strains from Antarctica marine sediment were isolated on agar plates supplemented with β (1,3)-glucan binding dye. The four isolated were characterized and identified via 16s rRNA gene sequencing analysis. β -glucans produced by the isolates were extracted and its chemical properties are currently investigated.

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***Streptomyces* spp. in Antarctic Extremes: Growth Resilience and Bioactive Compound Discovery**

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The harsh and extreme environment of the Antarctic supports only highly adapted organisms, Actinobacteriota (formerly Actinobacteria) being among the most successful. *Streptomyces*, a dominant genus from this phylum, goes through evolutionary adaptations such as membrane fluidity regulation, cold-active enzyme production, cryoprotectant synthesis, spore formation, biosurfactant production, and DNA repair mechanisms, among others. These Gram-positive bacteria also produce UV-absorbing pigments to withstand intense radiation and play key ecological roles in organic matter decomposition, nutrient cycling, and microbial interactions via secondary metabolites. Furthermore, intense competition from bacteria in a specific niche has driven *Streptomyces* to evolve distinct genetic and metabolic pathways, resulting in the production of novel secondary metabolites. To explore their secondary metabolites that exhibited antimicrobial capabilities, we analysed two strains, INACH3013 and INACH3013a, isolated from Ardley Island. The 16S rDNA sequence analysis revealed that both strains are closely related to an Antarctic *Streptomyces fildesensis*. Their bioactive compounds were extracted using dichloromethane (DCM) and separated by Thin Layer Chromatography (TLC). Strain, INACH3013, showed extracellular bioactive spots at R_f 0.84 and 0.75, while INACH3013a exhibited both extracellular and intracellular bioactive spots at R_f 0.87 and 0.81. Antimicrobial assays of those compounds against Gram-positive and Gram-negative bacteria confirmed the broad-spectrum activity. These results probably explain why *Streptomyces*, in general, survives well in nutrient-deficient Antarctic environments, while also highlighting the potential of these compounds for antibiotic discovery.

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Life on Ice: Adaptation of Antarctic Yeast to Temperature Variation and Environmental Pollution

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The Antarctic environment is defined by extreme cold, prolonged darkness, and the accumulation of long-range transported contaminants such as persistent organic pollutants (POPs). Microorganisms thriving in this environment have evolved unique strategies to withstand these combined physical and chemical stressors. Antarctic yeasts, with their genetic accessibility and ecological relevance, provide an ideal eukaryotic model to investigate such adaptive mechanisms.

This study explores how Antarctic yeasts, particularly the *Glaciozyma antarctica* and *Phenoliferia glacialis* adapt to (i) extreme low temperatures and (ii) exposure to POPs, particularly polychlorinated biphenyl (PCB). The occurrence of persistent organic pollutants (POPs) in polar regions, including Antarctica, is attributed to the global distillation process, whereby these compounds undergo long-range atmospheric transport from warm, low-latitude areas to colder, high-latitude environments, a mechanism commonly referred to as the 'grasshopper effect' (Figure 1).

Yeast strains were isolated from sea ice collected near Casey Research Station, where POP deposition is significant. Using integrated omics approaches including genomics, transcriptomics and metabolomics alongside wet lab analyses, we characterized their adaptation strategies. Genomic analysis revealed expansions in genes linked to fatty acid desaturation, antifreeze proteins, antioxidant defense and xenobiotic degradation. Transcriptomic profiling at various temperatures and under POP exposure indicated a coordinated stress response, including upregulation of cold-shock proteins, molecular chaperones, glutathione-S-transferases, and multi-drug efflux transporters. Metabolomic profiling identified elevated levels of polyunsaturated fatty acids and secondary metabolites with potential protective or detoxifying properties.

Functional assays demonstrated that Antarctic yeast increased the production of polyunsaturated fatty acids (PUFAs) at lower temperatures (Table 1), leading to lipid composition adjustments that preserve membrane fluidity under cold conditions. In addition, the activity of antioxidant enzymes was upregulated to mitigate oxidative stress induced by both low-temperature conditions and exposure to POPs. Remarkably, *P. glacialis* capable of transforming or sequestering POPs, indicating potential roles in natural bioremediation. This dual adaptation strategy including the structural and metabolic adjustments for cold resilience coupled with enzymatic detoxification of pollutants underscores the evolutionary versatility of Antarctic yeasts.

These findings deepen our understanding of eukaryotic survival under multifactorial stress and have broader implications for predicting the resilience of Antarctic microbial communities in the face of climate change and increasing pollutant loads. Beyond ecological significance, this work highlights potential applications in biotechnology, from cold-active enzyme production to pollutant degradation in cold environments.

In conclusion, Antarctic yeasts offer a powerful model to dissect the interplay between physical and chemical stress adaptations. Their evolutionary innovations provide both fundamental insights into extremophile biology and practical opportunities for environmental and industrial applications.

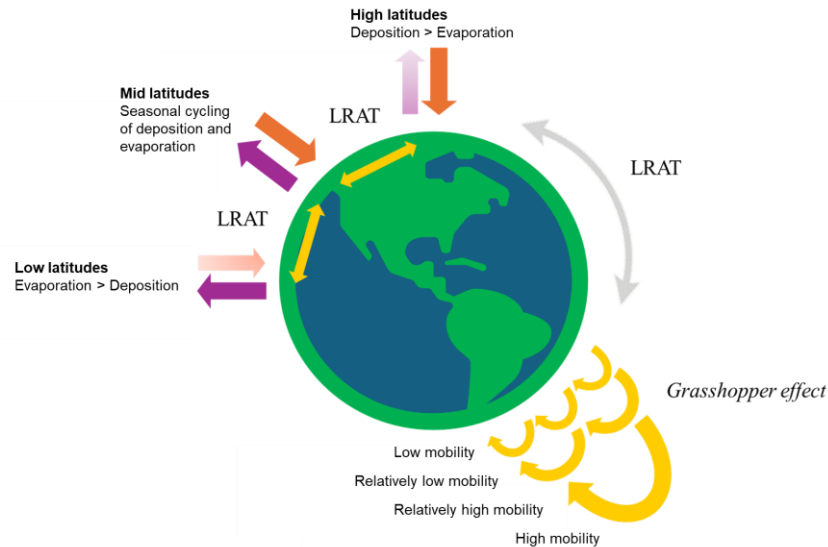


Figure 1. The movement of persistent organic pollutants (POPs) through the global distillation process, commonly referred to as the 'grasshopper effect'.

Table 1. The five most abundant fatty acids synthesized by Antarctic yeast under varying temperature conditions.

Fatty acid	15°C	4°C	-12°C
Asid palmitik (16:0)	7.50+1.17%	6.95+1.22%	6.66+1.47%
Asid stearik (C18:0)	3.81+1.47%	3.63+0.61%	3.15+1.38%
Asid oleik (C18:1N9C)	49.63+2.15%	48.97+1.14%	49.04+2.26%
Asid linoleik (C18:2N6C)	16.59+1.32%	17.78+0.77%	17.44+0.29%
Asid linolenik (C18:3N3)	16.37+3.41%	17.89+1.33%	17.25+2.01%

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7600 Years of Photosynthetic Community Transitions in a Freshwater Lake in Antarctica

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Post-glacial lakes provide a natural archive to trace ecosystem development after ice retreat (Zemp et al. 2019). However, how aquatic ecosystems emerge and develop after deglaciation remains poorly understood (Cauvy-Fraunié and Dangles 2019). Using sedimentary DNA metabarcoding (16S and 18S rRNA genes), combined with geochemical analyses and radiocarbon dating, we reconstructed 7600 years of biological community history in Lake Naga-ike (69°29'S, 39°35'E), focusing primarily on photosynthetic taxa that require light and are typically confined to the water column, so their occurrence in deep, light-limited sediments reflects ancient surface communities. Sedimentary DNA analysis also included non-photosynthetic organisms that are strictly dependent on aerobic conditions for growth.

Statistical analyses of the sediment physicochemical parameters using the CONISS algorithm were divided into five sedimentary sections that primarily reflect changes in sedimentation rate. From the deepest layers upward, sedimentation was initially rapid, slowed markedly in the middle section, and then declined gradually toward the present. Early deposits (*ca.* 7600–5000 yr BP), with high sedimentation, were dominated by 18S and 16S taxa adapted to low light, highly turbid, glacially influenced waters, including *Chlamydomonas*, *Chaetoceros*, and non-photosynthetic cyanobacteria, *Melainabacteria*. When sedimentation decreased sharply (*ca.* 5000–2000 yr BP), α -diversity increased and 18S assemblages shifted from high-turbidity specialists to taxa tolerant of moderate clarity. The increase in the abundance of genus *Navicula* indicated the development of a benthic community, which thrives in less turbid conditions. As the lake cleared, cyanobacteria shifted from ancient, water-column-derived non-photosynthetic groups to photosynthetic lineages. In the most recent sediments (2,000 yr BP onward), prolonged low sedimentation supported complex trophic structures dominated by photosynthetic Cyanobacteria (*Leptolyngbya*) and Chlorophyta (*Vitreochlamys*), which together comprised more than 90 % of the photosynthetic community. Higher-trophic microorganisms, such as tardigrades, were also detected during this period. These findings indicate that during the long-term stable phase, diminished environmental filtering and a few well-adapted taxa result in the observed decline in α -diversity.

Our 7,600-year record from Lake Naga-ike reveals a clear post-glacial succession controlled by sedimentation rate. The lake shifted from turbid, low-light communities of early phototrophs and non-photosynthetic cyanobacteria, through a more diverse benthic phase, to a stable modern assemblage

dominated by photosynthetic Cyanobacteria and *Chlorophyta*. Detection of light-dependent, water-column taxa in deep sediments confirms sedimentary DNA as a robust archive of ancient surface communities. These results show that declining glacial inputs and long-term stability ultimately reduce diversity and provide a framework for predicting the ecological development of new lakes forming under ongoing ice-sheet retreat.

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Direct video evidence of pteropod predation highlights foraging flexibility in Adélie penguins

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Understanding how climate-driven changes in the Southern Ocean may alter predator–prey interactions is essential to assess the ecosystem responses, but trophic relationships often remain poorly documented. Shelled pteropods (Thecosomata) are key members of Southern Ocean zooplankton assemblages but are highly vulnerable to ocean acidification. However, direct observations of their interactions with higher-level predators are rare. Here, we provide the first direct video evidence of pteropod predation by chick-rearing Adélie penguins *Pygoscelis adeliae*, using animal-borne video loggers at a colony near Dumont d'Urville Station, East Antarctica, during late December 2024 to early January 2025. Among eight individuals with video loggers, seven birds consumed pteropods (N = 1,424 captures), predominantly *Clio pyramidata*. For two individuals, pteropods accounted for 70% and 78% of observed prey captures. Other prey included mainly krill and fish, with occasional captures of amphipods. Pteropods were taken in both offshore areas and coastal habitats, with encounter rates varying greatly over time, suggesting that their availability is patchy and episodic. Predation on pteropods occurred at depths similar to krill, whereas fish were captured at greater depths (krill: 45.5 ± 28.5 m, pteropods: 47.7 ± 25.7 m, fish: 69 ± 9.9 m). Dives in which pteropods were captured were significantly longer than those in which krill were captured, while dives with fish captures were only slightly longer (krill: 83.2 ± 40.3 s, pteropods: 123 ± 42.1 s, fish: 132 ± 11.6 s). Krill yielded the highest capture rates per unit time (10.4 ± 9.6 krill/min), whereas both pteropods and fish were less profitable (5.0 ± 6.4 pteropods/min and 2.0 ± 2.2 fish/min). Occasionally, exceptionally high numbers of pteropod captures were observed, with a maximum of 81 in a single dive compared to 40 for krill, indicating substantial intake when dense patches were encountered. During the observation period, individuals that recorded a high proportion of pteropod captures conducted markedly shorter foraging trips (maximum foraging distance: 25.9 ± 4.1 km, duration: 21 ± 4.9 h) than those focusing on other prey (maximum foraging distance: 52.5 ± 11.6 km, duration: 25 ± 7.1 h). Although pteropods are unlikely to become a principal prey due to their presumed lower energy density compared to krill, their ease of capture and potential for high intake suggest that they can supplement penguin diets under favourable conditions. Our study underscores the importance of direct predator–prey observations in revealing previously undocumented trophic links and improving our understanding of ecosystem responses to environmental change.

Annual variations in the post-fledging movements of Adélie penguins

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In long-lived seabirds with delayed reproduction, juvenile survival influences population dynamics and the future number of breeding individuals. However, the post-fledging behavior of juveniles remains poorly understood. In penguins (Spheniscidae), although biologging has been extensively applied to study adult bird behavior, studies on the post-fledging behavior of juveniles have remained limited. In this study, we tracked fledgling Adélie penguins (*Pygoscelis adeliae*) from Torinosu Cove, Lützow-Holm Bay, East Antarctica, to examine their post-fledging movement routes. In late January 2024 and 2025, we attached satellite platform transmitter terminal (PTT) tags to 18 and 24 pre-fledging chicks, respectively. Post-fledging location data were obtained via the Argos satellite system from 15 birds in 2024 and 23 birds in 2025, and tracking durations ranged from 3 to 152 days and 7 to 144 days, respectively. In both years, fledglings left the sea-ice zone shortly after fledging and moved northward into the open ocean, followed by a westward shift around March. On the other hand, there were inter-annual differences in the northernmost latitudes reached during northward movements and in the latitudinal bands passed through during westward movements, with higher latitudes in 2025 than in 2024. Satellite imagery indicated that in 2025 a high-density pack-ice zone had been formed during the northward movement, and the movement speed of fledglings decreased when traversing this zone. The movement speed of fledglings during westward movements decreased with increasing sea-ice concentration (SIC) and increased with stronger ocean current support. In particular, fledglings in 2025 received strong current support when moving along the westward Antarctic Slope Current. Our results suggest that the northernmost latitude reached during northward movements is affected by sea-ice conditions immediately after fledging and that these conditions also affect the oceanic environments experienced by juveniles during westward movements.

Sex determination of breeding Adélie penguins (*Pygoscelis adeliae*) in Lützow-Holm Bay, East Antarctica

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Penguins are among the seabird species that exhibit weak sexual dimorphism. However, possible differences in foraging and overwintering areas between males and females may lead to sex-specific responses to environmental change. Therefore, accurate sex identification is key to understanding sex-specific behavior and distribution patterns in penguin species. Various methods have been developed for sex determination, including behavioral observation, cloacal observation, morphometric analyses, and molecular techniques using blood samples. However, many of these approaches involve invasive procedures, are time-consuming, or yield uncertain results due to regional variation in body size. This study primarily aimed to evaluate the effectiveness of molecular sexing determination using feathers, particularly focusing on the utility of back feathers. Additionally, we aimed to develop a region-specific discriminant function for morphometric sex identification relevant to the Syowa Station area. We collected back and, in some cases, chest feathers from 54 Adélie penguins during the incubation period (n=28 birds) and chick-guarding period (n=26 birds) from two colonies in Lützow-Holm Bay, in 2023-24 austral summer. Morphometric measurements were obtained from 51 birds. Using the feather samples, we successfully determined the sex of all birds through DNA extraction, PCR amplification, and analysis of electrophoretic banding patterns. Furthermore, we developed a discrimination function based on bill, head, and flipper measurements that distinguished males and females with a discriminant rate greater than 90%. These results highlight the utility of molecular sex determination using back feathers, which are often shed along with the tape strips when retrieving data loggers. This minimally invasive method allows for reliable sex identification in conjunction with behavioral data and is broadly applicable in bio-logging studies. Additionally, morphometric sex determination can provide rapid, ad-hoc sexing identification while taking into account regional variation in body size.

Foraging and Breeding of Rhinoceros Auklets on Todojima Island, under the Different Oceanic Regimes

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Long-term and short-term environmental changes in the ocean affect marine organisms. In particular, regime shifts, decadal scale marine environmental changes, induce drastic change of abundance and distribution of various species of forage fish through bottom-up effects. Seabirds, as top predators, are highly sensitive to such environmental changes and are thought to respond by adjusting their prey and foraging areas, often resulting the change of their breeding success. The warm-water living foraging fish, Japanese anchovy *Engraulis japonicus* is known to fluctuate drastically during regime shifts, become a dominant during warm regime and is critically important for breeding of the diving seabird, Rhinoceros auklets *Cerorhinca monocerata* (Watanuki et al. 2022). Previous studies suggested that availability of Japanese anchovy for auklets decreased after 2014 and increased and again from 2022 in the Northern Sea of Japan correspond with the oceanic regime shifts (Watanuki et al. 2022, Watanuki et al. In Prep., Sakai et al. 2025). In such highly fluctuation, it is intriguing to see how the Rhinoceros auklets, which are strongly rely on the Japanese anchovy, adjusts their foraging behavior and alters the reproductive success in the northern range of this forage fish species. In this study, we examined the diet, foraging area selection using bio-logging technique, and chick growth of Rhinoceros auklet in 2018 and 2019 and 2024 at Todojima Island, the northern most colony in Japan. We hypothesized that (1) the auklets used cold-water masses to feed on cold-water fish in 2018 and 2019, and shifted their foraging area to warmer southern area to feed on anchovy in 2024, and (2) chick growth would be better in years when anchovies were more available.

Most of their diet consisted of cold-water juvenile Japan sea greenlings *Pleurogrammus azonus* in 2018 (wet weight; 83.3%) and 2019 (70.2%), while anchovy dominated in 2024 (92.9%). In all years, age-1 $\geq$ sand lance *Ammodytes* spp. was the second most frequently utilized prey species, accounting for 9.3% in 2018, 23.1% in 2019, and 7.1% in 2024 (Watanuki et al. In Prep). Chick growth was higher in 2024 than in 2018–2019, when auklets mainly fed on anchovies (ANCOVA; $p < 0.05$). However, their foraging areas were consistent during all the years around Todojima Island, the Soya Strait and the coast of Sakhalin, and did not utilize southern area (UDOI = 0.71 ± 0.23 ; utilization distribution overlap index). The SSTs in the potential foraging area of the auklets during 2018, 2019 and 2024 (2018: 4.9–18.1 °C, 2019: 7.2–17.1 °C, 2024: 6.3–16.7 °C), and the SST in core area of foraging locations (UD 95%; utilization distribution) of the auklets (2018: 4.9–18.1 °C, 2019: 7.2–14.1 °C, 2024: 6.3–15.3 °C) were similar across the years. Further, the SSTs at the most frequently used location for their foraging were around 9–12 °C in 2018–2019 and around 7–8 °C in 2024.

The auklets consistently use the cold-water masses around the colony presumably because they could capture anchovies even in the cold-water (7–8 °C) below the optimum temperature of anchovy (12–15 °C, Mihara 1998). Since 2022 anchovy might expand its distribution into the cold water. In addition, the auklets breed on Todojima Island share a potential foraging range with the world's largest breeding population of the conspecifics breeding on Teuri Island, about 100 km south from Todojima Island. The auklets could avoid intra-specific competition by using northern area such as the Soya Strait and the coast of Sakhalin consistently for their foraging area. Thus, the auklets on Todojima Island might have been able to consistently feed their chicks anchovy, which might have maximized the weight of meal-loads and led to improved chick growth (Watanuki et al. 2022). Our findings may provide important insights of the foraging strategies of seabirds, and also availability and distribution of forage fishes under the highly variable marine environment.

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Navigating a hazardous seascape: post-fledging movements and survival of rhinoceros auklets

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Juvenile seabirds face the challenges of developing movement and foraging skills while avoiding predation risks. This is especially true for fledgling seabirds, which must navigate from their natal colonies to suitable foraging areas on their first journey at sea. However, information on the movement and survival of fledgling seabirds has been limited due to technological challenges. In this study, we tracked fledgling rhinoceros auklets (*Cerorhinca monocerata*) from a large breeding colony on Teuri Island, Hokkaido, Japan, to examine their movement and mortality patterns during their first journey at sea. We attached small Pinpoint Argos-GPS transmitters to five and ten fledglings in late June of 2023 and 2024, respectively. Thirteen of the 15 birds transmitted GPS data (two birds transmitted no data), with tracking durations ranging from 0.3 to 15.5 days, covering distances from 3 to 485 km from the colony. The rate of transmitter signal loss was high for the first three days after fledging, indicating relatively high mortality near the breeding colony, likely due to predation. Cox proportional hazards analysis revealed that higher body mass at the time of fledging was associated with longer survival at sea. After 10 days of travel, two fledglings reached waters east of Sakhalin Island, an area frequented by post-breeding adult birds in the autumn. The travel routes of these two fledglings were highly complex, involving passages through a narrow strait to avoid landmasses, suggesting advanced navigation abilities. Our results suggest that fledgling rhinoceros auklets experience a significant survival bottleneck immediately after fledging but can navigate a complex seascape.

Multifactor Controls of Seasonal Climate–Ocean–Phytoplankton Linkages over Two Decades in the Southern Ocean

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Climate change imposes multiple interacting stressors on the ocean ecosystem, and it is important to investigate their cumulative impacts on the ocean habitats. Rising atmospheric CO₂ levels cause various environmental changes such as warming, acidification, sea-ice loss, stratification, and shifts in nutrient availability, with particularly strong impacts in the Southern Ocean. Phytoplankton play a key role in carbon uptake and as the foundation of the food web, making it crucial for us to assess CO₂ impacts for understanding various ecological consequences of climate impacts. Seasonal variability plays a central role in the Southern Ocean, where climate change exhibits distinct the effects across seasons, altering circulation, sea-ice processes, and ecosystem function. Previous observational and analytical studies have pointed to key physical and biogeochemical drivers and connected them with phytoplankton responses to describe seasonal patterns. However, previous studies have not fully captured long-term effects, broad spatial patterns, or the complexity of multiple interacting factors. In this study, by adopting a long-term, multi-factor perspective, we quantify how co-varying climate–ocean variables jointly structure phytoplankton dynamics across seasons. Building on this approach, we clarify which interactions exert the strongest influence across different seasons, and how these interactions shape phytoplankton. First, to conduct two-decadal, large-scale analyses, we utilized observational and reanalysis datasets (e.g., NSIDC, COBE-SST, MERRA-NOBM) providing monthly data on key variables and defined the Southern Ocean as the region south of the Polar Front. Second, we employed piecewise SEM (Structural Equation Modeling) and data-driven approaches for multivariable and long-term analysis. Our results show a clear signal of ocean acidification driven by increasing CO₂, and seasonal differences in both the magnitude and structure of the causal pathways, highlighting the dynamic nature of seasonal processes in the Southern Ocean. Considering the major effects on the phytoplankton dynamics we identified, our future work will focus on the dynamics of higher trophic levels, such as krill and penguins.

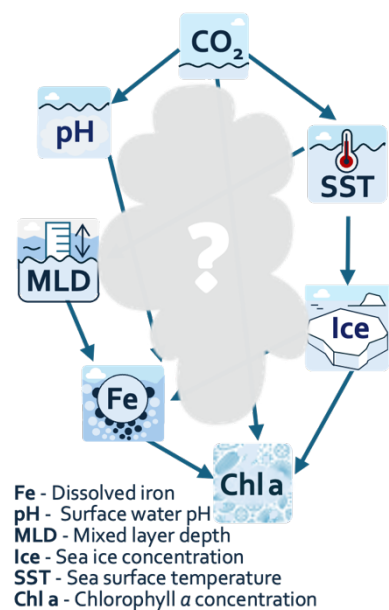


Fig. Which Linkages Dominate Across Seasons?

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Analysis of cold tolerance of the ice algal species *Fragilariopsis cylindrus* during freezing and thawing processes

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To examine the cold tolerance of the diatom *Fragilariopsis cylindrus*, an ice algal species isolated from the Southern Ocean, we investigated the characteristics of its freezing–thawing process and its growth after thawing through culture experiments. When cultured in f/2 medium at water temperatures of 5 °C and 8 °C under continuous light, *F. cylindrus* exhibited stable growth under both temperature conditions, but the culture at 5 °C showed a longer logarithmic growth phase and higher cell density.

To examine cell viability during the freezing process, cultures of *F. cylindrus* in the logarithmic growth phase were dispensed into 5 mL microtubes (5 mL each) and frozen in a -20 °C freezer. During the freezing process, unfrozen portions of the culture were collected from the tubes at 10-minute intervals, stained with Evans blue solution, and fixed with formalin to determine cell viability. The proportion of dead cells increased over time from the start of freezing, and just before complete freezing (approximately 50 minutes after being placed in the freezer), the proportion of dead cells reached about 34.1%, an increase of approximately 16% compared with the initial stage. Previous studies using freshwater green algae and diatoms reported that under similar conditions, the green alga *Closterium moniliferum* showed an increase of about 8% in the proportion of dead cells, while the diatom *Fragilaria capucina* showed a dramatic increase (about 90%) (Yoshida, 2021; Takeuchi, 2022). Compared to these results, the cold tolerance of *F. cylindrus* isolated from the Southern Ocean under low-temperature stress conditions appears to be lower than that of the freshwater green alga *C. moniliferum*.

In order to clarify the growth characteristics during the thawing process of the culture medium containing diatoms, cultures of *F. cylindrus* in the logarithmic growth phase were frozen at -20 °C for 7 days and then thawed at 0 °C, 7 °C, and 20 °C, respectively. After thawing began, samples of the thawed medium were collected every 10 minutes, stained with Evans blue, and fixed with formalin solution to determine cell viability. The results showed that although the proportion of dead cells increased by about 10% from the start of thawing to complete thawing, little difference was observed among the thawing temperatures (0 °C, 7 °C, and 20 °C), which also affected the total thawing time. These results suggest that stress during thawing is smaller compared to freezing.

Furthermore, after freezing cultures of *F. cylindrus* in the logarithmic growth phase at -20 °C for 7 days and thawing them at 0 °C, 7 °C, and 20 °C, the cultures were transferred to 5 °C under the continuous light condition. Compared to cultures grown at 5 °C without undergoing freezing and thawing, the thawed cultures showed a delay of about 22 days before reaching the logarithmic growth phase. However, the logarithmic growth phase itself was longer in the thawed cultures. These findings suggest that although *F. cylindrus* is damaged during freezing and thawing and requires time to recover, it can resume growth in a manner similar to pre-freezing conditions once recovery is complete.

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Spatial distribution of prokaryotic community structures off Totten Glacier in the Southern Ocean

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In marine ecosystems, heterotrophic prokaryotes play a crucial role in biogeochemical cycles by decomposing dissolved organic matter (DOM) and transferring it to higher trophic levels via the microbial loop (Azam et al., 1983). In the Southern Ocean, prokaryotes are known for maintaining active metabolism even at low temperatures, contributing significantly to biogeochemical cycling (Kirchman et al., 2009). Therefore, understanding their community structure and abundance is essential for comprehending the region's biogeochemical processes. Consequently, elucidating their community structure and abundance is essential for understanding biogeochemical processes in this region. Prokaryotic community structures in the Southern Ocean have been shown to vary in response to environmental factors such as SST (Surface Seawater Temperature), nutrient availability, DOM, and phytoplankton bloom (Cordone et al., 2023; Maturana-Martínez et al., 2022; Cao et al., 2019; Piontek et al., 2022; Cordone et al., 2022). However, significant differences in community structure may arise even within a single water mass where nutrient and chlorophyll a (Chl-a) concentrations exhibit little variation (Cao et al., 2019). This suggests that additional drivers shape prokaryotic community structures. Off Totten Glacier, four standing eddies forming a cyclonic eddy train have been identified (Mizobata et al., 2020), and these eddies may significantly influence surface microbial distributions. This study examined the relationship between standing eddies and prokaryotic community structures by analyzing their spatial distribution using 16S rRNA gene amplicon sequencing. Our primary objective was to test the hypothesis that microbial communities are shaped by the transport of the Antarctic coastal and pelagic water by the four standing eddies.

Surface seawater (5 m depth) was collected from 44 stations off Totten Glacier during two Antarctic cruises of the training vessel (TV) *Umitaka-maru* of the Tokyo University of Marine Science and Technology in January and February of 2023 and 2024 (Fig.1). Seawater samples were taken using a pump-underway ship intake system and subsequently filtered through 0.22 µm Sterivex filters, which were stored at -20 °C until processing. DNA was extracted from Sterivex filter samples and used as a template for PCR amplification of the prokaryotic 16S rRNA gene. Amplicons were sequenced on an Illumina MiSeq sequencing system, and raw reads were processed with QIIME2 and DADA2. Taxonomic assignments were conducted using the SILVA database (ver. 138). Subsequently, prokaryotic community structures and spatial distribution were analyzed.

Prokaryotic community structures were compared among four standing eddies (Vincennes Eddy, Poinsett Eddy, West Sabrina Eddy, and East Sabrina Eddy) and the Southern Boundary (SB) of the Antarctic Circumpolar Current (ACC). Across all samples, the predominant orders were *Flavobacteriales* (34%), *Rhodobacterales* (21%), *Oceanospirillales* (15%), and “*Pelagibacterales*” (13%). At the genus level, *Polaribacter* and SAR11 clade Ia were consistently abundant. Spatially, *Polaribacter* was more abundant in bloom regions where Chl-a concentrations exceeded 1 µg L⁻¹ (bloom mean: 34%; non-bloom mean: 12%), while SAR11 clade Ia was more abundant in non-bloom waters (bloom mean: 6%; non-bloom mean: 14%). These findings align with previous studies linking these taxa to Chl-a concentrations (Piontek et al., 2022; Cordone et al., 2022). Nonmetric multidimensional scaling (nMDS) analysis indicated that samples from the Poinsett Eddy and SB clustered tightly, suggesting community homogeneity within these regions (Fig.2). In contrast, in other eddies, prokaryotic community structures differed among stations, even within the same eddy. This heterogeneity is likely due to partial mixing of Antarctic Circumpolar Current waters with resident eddy waters, which alters the water mass distribution and shapes the prokaryotic community structures within individual eddies. These results support our hypothesis that the eddies influence microbial communities by transporting different water masses.

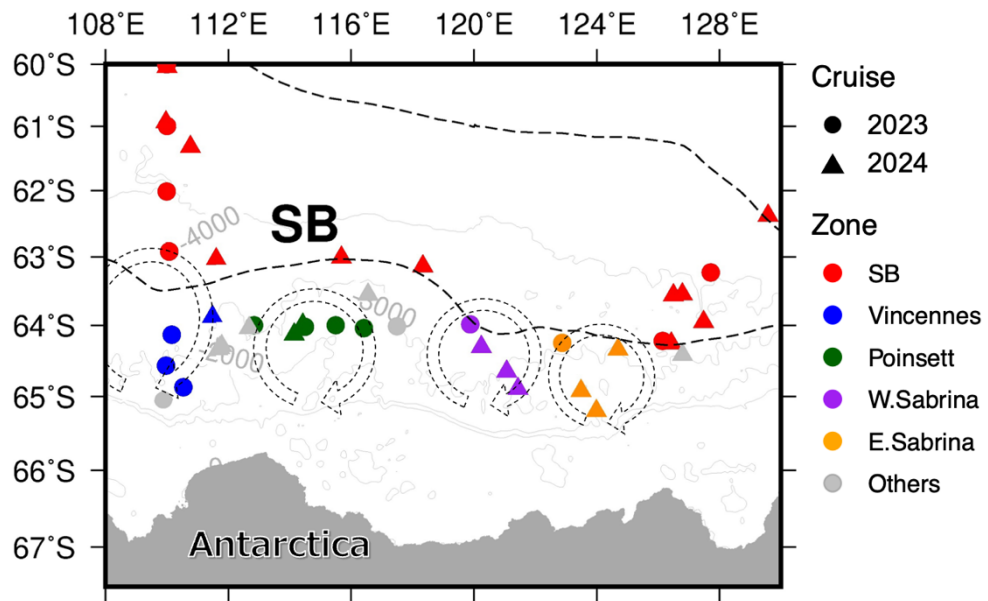


Fig.1. Sampling stations off Totten Glacier during the 2023 and 2024 cruises. Symbol color indicates zones (SB, Vincennes, Poinsett, W. Sabrina, E. Sabrina, Others), and symbol shape indicates cruise year.

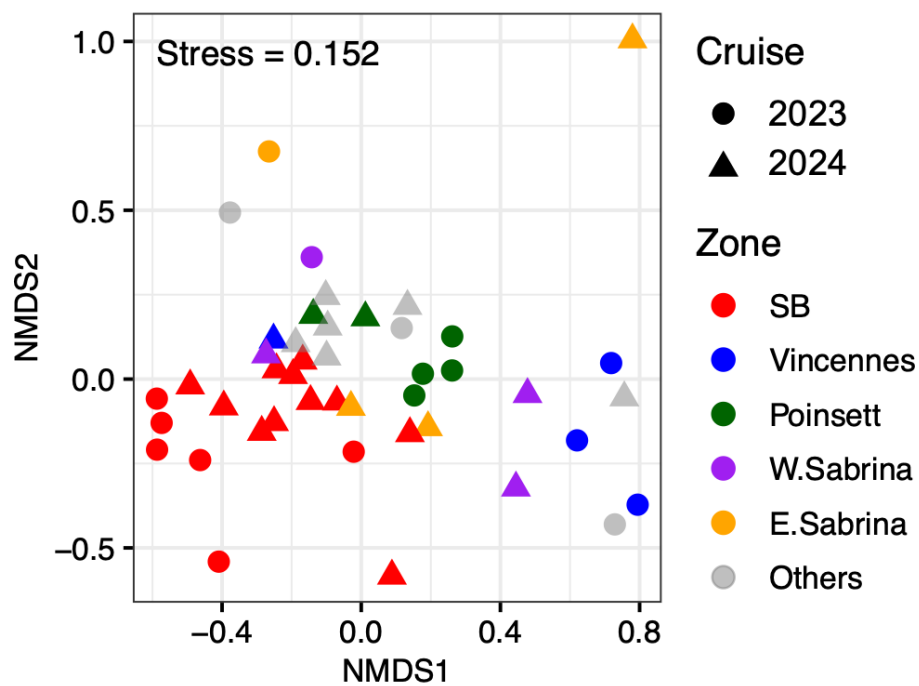


Fig.2. Non-metric multidimensional scaling ordination representing Bray-Curtis dissimilarities among samples. Symbol color and shape indicate sampling zone and cruise year, respectively.

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Summer Distribution Patterns of Zooplankton in the Surface Layer of the Southern Ocean

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The ocean plays a central role in the global uptake of carbon dioxide, and the biological pump—which transports and sequesters carbon fixed at the surface into the deep ocean—is one of its principal mechanisms. Because the magnitude and efficiency of the biological pump depend on food-web structure, a quantitative understanding of zooplankton communities is essential for accurately characterizing the carbon cycle. The Southern Ocean is a key region that accounts for roughly 40% of anthropogenic CO₂ uptake (Khatiwala et al., 2009), and multiple oceanic fronts there function as biogeographic boundaries (Hunt & Hosie, 2005). However, many previous studies have used nets with mesh sizes around 200 µm, which have low retention efficiency for small zooplankton; this has limited quantitative assessments such as numerical density (Gallienne and Robins, 2001). To elucidate the distributional characteristics of zooplankton communities including small-bodied taxa, we conducted multi-year sampling across a broad region from the subtropics to the seasonal ice zone using a 20 µm-mesh net capable of quantitatively retaining small taxa.

Field observations were conducted during Southern Ocean cruises aboard the Training Vessel Umitakamaru (Tokyo University of Marine Science and Technology, TUMSAT). Surveys followed a southbound transect along 110°E from 35°S to 65°S during January campaigns in 2014, 2016–2019, 2023, and 2024. Zooplankton were collected by concentrating continuously pumped seawater from the ship's keel for ~1 h through a 20-µm hand net. Front positions were determined from sea surface height (SSH) using the SSH–front correspondences defined by Sokolov and Rintoul (2007). For each observation year, SSH was obtained by adding the January-mean sea level anomaly (SLA) reanalysis from the Copernicus Marine Environment Monitoring Service to the mean surface dynamic height climatology referenced to 2500 dbar (Olbers et al., 1992). The study area was partitioned into the Subantarctic Zone (SAZ; north of the Polar Front-N, PF-N), the Polar Frontal Zone (PFZ; between PF-N and the northern branch of the Southern ACC Front, SACCF-N), and the Seasonal Ice Zone (SIZ; south of SACCF-N).

Zooplankton numerical densities spanned 1–106,181 ind. m⁻³. By hydrographic zone, mean densities were highest in the PFZ (SAZ: 9,897 ind. m⁻³; PFZ: 35,142 ind. m⁻³; SIZ: 12,182 ind. m⁻³), with consistently elevated values in the PFZ across all survey years. Our estimates were 1–2 orders of magnitude higher than those from a January 2015 survey in the same region using a Continuous Plankton Recorder with 270-µm mesh (Takahashi et al., 2021), most likely reflecting the greater retention of small zooplankton by the 20-µm net. Averaged across stations, copepod nauplii (72%) and the small cyclopoid *Oithona similis* (18%) strongly dominated, together accounting for ~90% of all individuals. While previous studies targeting medium- to large-bodied taxa have reported oceanic fronts acting as biogeographic boundaries (Hunt & Hosie, 2005), our cluster analysis identified both water-mass-specific clusters (e.g., characteristic of the SAZ and SIZ) and clusters ubiquitous across all water masses. Although broad community differences among water masses were evident, we did not detect a consistent front-aligned biogeographic break common to all years. This pattern likely reflects the pervasive dominance of the cosmopolitan *O. similis* throughout the domain and, additionally, the lack of finer taxonomic resolution within the abundant copepod nauplii.

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Seasonal variation in abundance and vertical distribution of the *Parmales* community in the Oyashio region, western North Pacific

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Parmales, a sister group of diatoms, is siliceous pico-eukaryotic marine phytoplankton and abundant in polar and sub-polar waters. Seasonal variation in abundance and vertical distribution of the *Parmales* community was investigated in the Oyashio region surrounded by the cold Oyashio Current, the western North Pacific. In May the *Parmales* abundance was high with the maximum of 1.0×10^5 cells L^{-1} at 30 m depth (Fig. 1). *Parmales* was absent at 0-10 m depth where water temperature was sufficiently below $10^\circ C$ and NO_3-N concentration was not depleted ($>3 \mu M$). Hydrographic condition was suitable for the *Parmales* growth and did not cause absence of the population at the surface. In July and October, the *Parmales* community showed the subsurface distribution, making peaks at 50 m depth. The population survived under the pycnocline when water temperature was high over $15^\circ C$ in the surface layer. In January the *Parmales* widely distributed at 0-100 m depth with high abundance over 2.0×10^5 cells L^{-1} . The *Parmales* community grew in the surface layer before becoming evenly distributed with depth. In May many fecal pellets including empty walls and/or plates of the *Parmales* cells were observed (Fig. 2). Size of the fecal pellets was generally 5-20 μm , indicating that the main grazers for the *Parmales* are microzooplankton. This suggests that grazing by microzooplankton is an important factor to decrease the *Parmales* population from May to July.

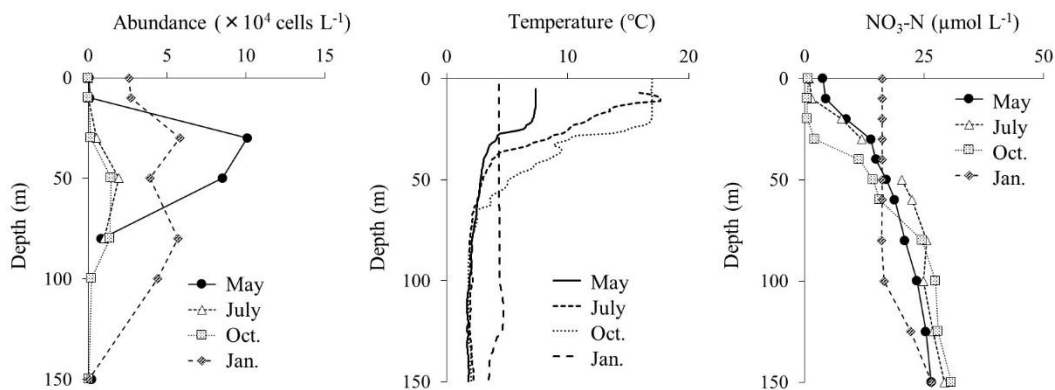


Fig.1. Seasonal change of the *Parmales* abundance, water temperature and NO_3-N concentration in the Oyashio region.

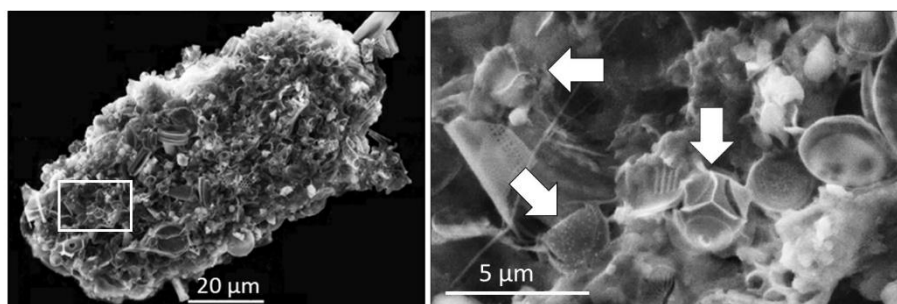


Fig. 2. Light micrographs of a fecal pellet comprises *Parmales* cells (allows).

Analyses of heterocyclic compounds degradation by Antarctic soil bacterium strain BS19

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The release and accumulation of chemical substances in the environment can have adverse effects on humans and ecosystems. Petroleum is composed mainly of hydrocarbons and consists of a variety of compounds. Among these, carbazole(CAR) is a heterocyclic compound because it contains heteroatoms other than carbon and hydrogen in the atoms that form the ring. Heterocyclic compounds are structurally stable and have toxicity and resistance to decomposition. In addition, they are suspected of having mutagenic properties, and has potential adverse effects on humans and ecosystems. Petroleum-derived pollutants have been detected around Antarctic research stations, raising concerns about their impact on the polar environment. As a method for removing these environmental pollutants, bioremediation approaches utilizing the metabolism of microorganisms are being explored. In polar regions like Antarctica, it is essential to select removal methods with minimal environmental impact. In Antarctic bioremediation, the design of an optimal bioreactor requires consideration of the characteristics of the contaminated site, the properties of the microorganisms used, and accumulated knowledge from previous studies.

Previously studies have isolated a bacterium strain BS19 with CAR degradation ability was isolated from Antarctic soil. Whole genome sequencing was performed on this strain BS19, and the existence of genes related to CAR degradation was confirmed. However, it is still unclear whether this gene are active when strain BS19 metabolizes CAR. Therefore, in this study, we used the CAR-degrading bacterium strain BS19 to confirm the expression of CAR-degrading-related genes and quantitatively analyze the expression levels of degradation-related genes under different culture conditions, with the aim of evaluating the applicability of this strain for bioremediation in polar environments.

Primers corresponding to the degradation-related genes *carAa* and *carBa* were designed, and gene expression was confirmed by RT-PCR. Furthermore, strain BS19 was cultured using CAR, dibenzothiophene (DBT), dibenzofuran (DBF), and biphenyl as carbon sources, and cDNA was synthesized by RNA extraction and reverse transcription. The expression levels of *carAa* and *carBa* were quantitatively analyzed by qPCR. Additionally, the amount of carbazole degradation in the culture medium was measured by GC-FID as needed, and the correlation with degradation activity was evaluated.

This study revealed that strain BS19 possesses degradation-related genes and expresses *carAa* and *carBa* during the degradation of CAR. Furthermore, it was suggested that the presence of CAR induces the expression of *carAa* and *carBa*.

Going forward, it is necessary to evaluate the quantitative expression of degradation-related genes and their correlation with degradation activity under different cultivation periods and temperatures to collect data that can contribute to bioremediation.

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Microbial diversity of the Arklio Glacier in the Canadian High Arctic

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The High Arctic is characterized by extremely harsh environments with low air temperature and small amount of precipitation. The Arklio Glacier (80°50'N 82°50'W), located in the northwest part of the Queen Elizabeth Islands in the Canadian High Arctic, is characterized by well-developed glacial moraines that record multiple developmental periods since the Last Glacial (King, 1981; Okitsu et al., 2004).

While the geomorphological and botanical features of the Arklio Glacier foreland have been studied in some detail, little is known about the microbial diversity associated with this glacier. In particular, the composition and distribution of bacteria and fungi across the glacier surface and its deglaciated forefield remain unexplored. To address this gap, we investigated the microbial diversity of seven sites spanning the glacier ice and forefield, with a focus on both bacterial and fungal communities.

Environmental DNA was extracted from 50 mg of each sample using the DNeasy PowerSoil Pro Kit (Qiagen). The extracted DNA was amplified targeting the V3–V4 region of the 16S rRNA gene for bacteria and the ITS1 region for fungi. The amplicons were sequenced on an illumina MiSeq using MiSeq reagent kit v3. Sequencing reads were processed in QIIME2 version 2025.5. For bacteria, primer and adapter sequences were trimmed using cutadapt and denoised with DADA2 (Callahan et al., 2016). The denoised sequence data were used to generate ASVs via Dada2. ASVs classification was performed using the Silva 138.2 database. For fungi, sequence data were trimmed using ITSXPRESS to extract sequences from the ITS1 region. Subsequently, OTUs were generated using VSEARCH. OTU classification was performed using UNITE ver10.0.

As a result, we found that both bacterial and fungal communities differed greatly between the glacier surface and the glacier foreland. Furthermore, since most of the microbial communities on the glacier surface and at the foreland were not shared, they formed independently microbial ecosystems at the glacier surface and the foreland.

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Characterization of Ring-cleavage Dioxygenase for Carbazole Metabolism from Antractic Bacterium Strain BS19

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Heterocyclic compounds, including carbazoles and polycyclic aromatic hydrocarbons (PAHs), represent a major group of environmental pollutants. They are found in petroleum, tar, and crude oil, and are also used in rubber, plasticizers, and plastic colorants. Consequently, these compounds can easily enter the environment through human activities, leading to contamination of soil and marine ecosystems. Moreover, their chemical structures, which contain multiple benzene rings, confer high toxicity, including carcinogenicity and resistance to degradation, making their environmental persistence a serious concern. Therefore, both the removal and continuous monitoring of these compounds are crucial for environmental protection.

Bioremediation is an environmentally friendly approach and is considered a promising method for environmental cleanup even in extreme regions such as Antarctica, where the introduction of new plants and animals is strictly restricted. To implement bioremediation effectively, research has focused on bacterial strains capable of degrading heterocyclic compounds and PAHs.

Sphingobium sp. strain BS19, was the first bacterium reported to degrade carbazole and PAHs isolated from Antarctic soil (Sato et al., 2023). Whole-genome analysis of strain BS19 identified genes for enzyme CarBaBb, a ring-cleavage dioxygenase involved in carbazole degradation pathway. Ring-cleavage dioxygenases catalyze the oxidative cleavage of aromatic rings and often produce colored metabolites, making them useful not only for biodegradation but also for potential environmental monitoring applications. While most ring-cleavage dioxygenases involved in heterocyclic compound degradation are homomeric, CarBaBb is a rare heteromultimeric enzyme, highlighting its uniqueness and scientific interest. Therefore, this study aims to characterize CarBaBb and evaluate the applicability of strain BS19 derived enzymes, with the goal of bioremediation and environmental monitoring of recalcitrant heterocyclic pollutants.

In this study, the *carBa* and *carBb* genes from BS19 were cloned and overexpressed in *Escherichia coli* to evaluate their degradation activity and substrate specificity. Resting cell reaction revealed that 4-methylcatechol was degraded by approximately 80% within 2 hours, although substrate inhibition at higher concentration was observed. Among the tested substrates—including 4-methylcatechol, 4-tert-butylpyrocatechol, and 4-(2-aminoethyl)pyrocatechol hydrochloride—activity was observed for all except 4-tert-butylpyrocatechol, indicating selective substrate specificity.

Future work will involve purification of the CarBaBb enzyme, comparative analysis with other ring-cleavage dioxygenases, and computational approaches such as molecular docking to evaluate substrate diversity and better understand the enzyme's catalytic mechanism.

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First report of *Pythium monospermum* in Spitsbergen Island

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The oomycete *Pythium monospermum* Pringsh., the type species of the genus *Pythium*, has been reported from mid- to high-latitude regions (van der Plaats-Niterink, 1981), but has not previously been documented in polar environments, with the exception of Greenland (Höhnk, 1960). In July 2022, a *P. monospermum*-like strain was isolated from a living *Ulva* sp. in Ny-Ålesund, Spitsbergen Island, Norway, and was identified as *P. monospermum* based on morphological characteristics and sequence analyses of rDNA-ITS, *COX1*, *COX2*, and *rps10* genes. To the best of our knowledge, this study represents the first record of *P. monospermum* on Spitsbergen Island and the second record in polar environments. We previously isolated a species of *Globisporangium*, a genus closely related to *Pythium*, from decayed *Ulva* sp. in Ny-Ålesund (Saga et al., 2024). Similarly, Herrero et al. (2020) isolated *Pythium* spp. from *Ulva* sp. in an intertidal zone of the Oslo Fjord, Norway. These previous studies suggest that *Pythium* and *Globisporangium* can colonize living or decaying *Ulva* spp. in coastal areas of Norway. *Ulva* spp. are cosmopolitan seaweeds capable of floating on the sea surface and dispersing along coastal areas worldwide (Salomonsen et al., 1999). The isolation of the present strain from a living *Ulva* sp. suggests that *P. monospermum* can infect *Ulva* under the polar environmental conditions of Ny-Ålesund. Taken together with previous findings, our results suggest that *P. monospermum* associated with *Ulva* spp. may have expanded its distribution into polar regions through dispersal via floating *Ulva* fragments.

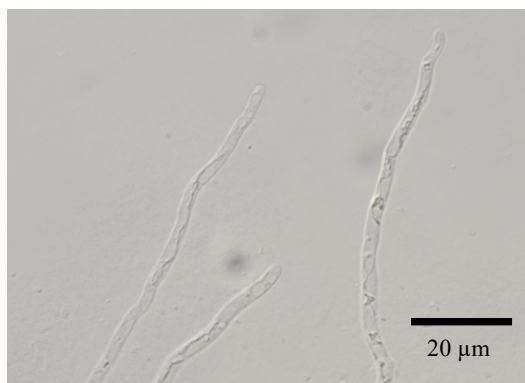


Figure 1. Hyphal tips of *Pythium monospermum* isolated from *Ulva* sp. collected in Ny-Ålesund, Spitsbergen Island, Norway.

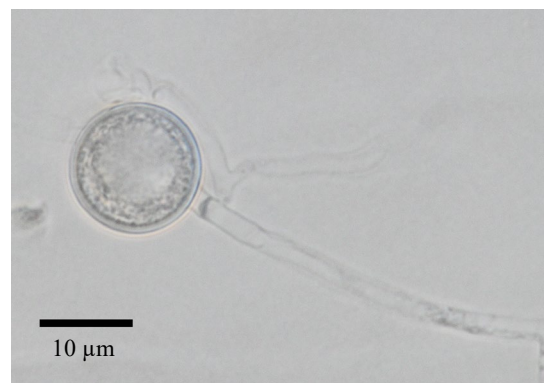


Figure 2. An intercalary oogonium and an oospore with a monoclinous antheridium of *Pythium monospermum* isolated from *Ulva* sp. collected in Ny-Ålesund, Spitsbergen Island, Norway.

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Triggers of Rapid CO₂ Flux from Ground Surface at Sub-Zero Temperatures

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Rain-on-snow (ROS) events have been widely observed in snow-covered areas, including the Arctic. These events are projected to become more frequent under ongoing climate change (e.g. López-Moreno et al. 2021; Serreze et al. 2021). Recent field observations have shown a rapid increase in ground-level CO₂ concentrations during ROS events. However, the underlying mechanisms driving this increase remain poorly understood. In this study, we conducted controlled laboratory experiments to evaluate the effect of water addition and temperature changes on CO₂ emissions using Arctic soils.

Organic and mineral soil samples were collected from Ny-Ålesund, Svalbard, Norway, and transported to a laboratory in Japan, where they were incubated at sub-zero temperature conditions. The samples were subjected to two treatments: water addition and temperature elevation. The CO₂ concentration in the laboratory was measured using a methodology based on the flow-through-chamber technique (Yonemura et al. 2019).

It has been observed that a sharp increase in the CO₂ emission rate following water addition alone. On the other hand, we also observed an increase in CO₂ emissions when soil temperatures were raised from subfreezing levels. These findings suggest that the presence of liquid water, together with temperature increases associated with ROS events, may play a critical role in stimulating CO₂ release from the ground surface.

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Chemical changes in decomposing leaves and stems of *Salix arctica* as elucidated with ATR-FTIR

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Attenuated total reflection Fourier transform infrared (ATR-FTIR) is a useful tool for the study of plant litter decomposition, and recently Osono et al. [1] demonstrated that it is useful for characterizing and discriminating tundra plant leaves in different growth forms. However, the applicability of ATR-FTIR has rarely been explored in documenting the chemical changes in decomposing plant litter in high-arctic tundra. In the present study, we investigated the chemical changes in decomposing leaves and stems of *Salix arctica* collected in Ellesmere Island, high Arctic Canada using ATR-FTIR. The ATR-FTIR spectra in the fingerprint region (wavenumbers of 1800–800 cm⁻¹) of leaves and stems in different decay classes showed an overall similarity between the organs and between the decay classes. At least 11 major peaks were noticeable in the spectra and are attributed to chemical features of lignin, cellulose, and/or hemicellulose. One-way permutational multivariate analysis of variance showed that the overall spectra in the fingerprint region were significantly different between the decay classes of leaves and stems, indicating that ATR-FTIR spectroscopy is applicable to discriminating dead plant organs in different degrees of decomposition. Principal component analyses showed the separation of the spectra between the decay classes of leaves and stems and indicated that the patterns of chemical change were characterized by the loss of cellulose and the decrease of cellulose crystallinity. These results demonstrated that ATR-FTIR spectroscopy is useful in documenting the chemical changes during decomposition in arctic tundra and suggest future applicability to the study of decomposition of tundra plants of other growth forms including mosses.

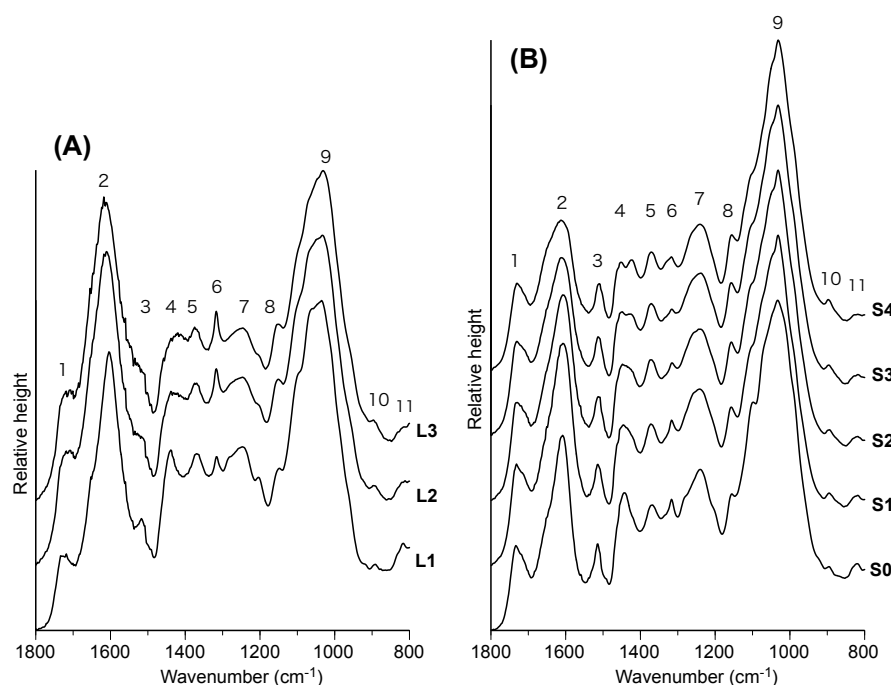


Figure 1. The ATR-FTIR spectra of *Salix arctica* leaves in decay classes L1 to L3 (A) and stems in decay classes S0 to S4 (B). Values of relative heights are averaged for each decay class. Numbers indicate the 11 major peaks.

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