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Microbial life in Arctic pack ice: Prospects for the *Tara Polaris Expeditions*

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Abstract

Sea ice, unlike freshwater ice, hosts abundant microbial life, thanks to the presence of liquid water inclusions encased within the ice matrix. The forthcoming Tara Polaris Expeditions (TPE), which will document drifting Arctic pack ice repeatedly over multiple years, together offer an unprecedented opportunity to advance understanding of the sea-ice microbiome — its diversity, variations, and ecological roles. In this contribution, we consider the current state of knowledge, identify key research gaps, and outline the potential for progress enabled by TPE. We envision the emergence of new insights into the seasonal evolution of microbial life, resolved at the floe (kilometric) scale, in relation to the evolution of the sea-ice environment — its morphology, light, temperature, and liquid water distribution and properties. Large potential lies in the characterization of diverse microhabitats across the central Arctic Ocean, associated with brine inclusions, pressure ridge cavities, and melt ponds. A major goal will be to document biological processes that remain poorly understood — colonization, diversity, functioning, interactions, and evolutionary dynamics — and that could benefit from the application of newly developed techniques. We argue that TPE is particularly timely, as the loss of multi-year ice may soon constrain opportunities to study life in this rapidly changing habitat.

Keywords

Arctic Ocean, sea ice, ice algae, microbial life, Tara Polar Station

Outline

This outline is here to help readers to appreciate the structure of the manuscript and facilitate browsing it. It will be removed at publication stage.

Abstract
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1. Arctic sea ice loss affects and threatens life in sea ice

Unlike freshwater ice, sea ice hosts abundant microbial life due to the presence of encased liquid water that forms various microbial habitats (Horner, 1985; Thomas and Dieckmann, 2002; Boetius et al., 2015; Campbell et al., 2022a). These habitats encompass sub-millimeter, hypersaline brine inclusions (Krembs et al., 2002), slush at the base of the overlying snow (Ewert et al., 2013; Fernández-Méndez et al., 2018), surface melt ponds (Brinkmeyer et al., 2004; Lee et al., 2012; Akino et al., 2025), and voids in pressure ridges (Salganik et al., 2023). Until the end of the 20th century, Arctic sea ice covered much of the Arctic Ocean yearlong and its peripheral seas seasonally, covering approximately 15 million km^2 in March and 7–8 million km^2 in September (Parkinson, 2014). Over the last four decades, however, the Arctic sea-ice coverage has decreased, particularly in September, by >10% per decade (Meier and Stroeve, 2022). The vast Arctic sea-ice habitat is thus in rapid decline, with large and highly uncertain implications for microbial life within the ice (Tedesco et al., 2019; Lannuzel et al., 2020; Lim et al., 2022).

Microbial life in Arctic sea ice is adapted to unique, extreme conditions (Lund-Hansen et al., 2024) with temperatures as low as –30°C, salinities from 0 g kg^{-1} in melt ponds to up to 250 g kg^{-1} in brine (Vancoppenolle et al., 2019; Zampieri et al., 2024), and large seasonal variations in light, from the dark polar night to the bright polar day (Nicolaus et al., 2010; Lebrun et al., 2023). Photosynthetic ice algae are adapted to extremely low light levels (Hoppe et al., 2024) and co-habit with other microbes. These algae thrive mostly near the ice-water interface (Arrigo, 2014; Leu et al., 2015; van Leeuwe et al., 2018; Lim et al., 2025), where temperatures and salinities are relatively mild and stable. Heterotrophic bacteria, involved in various biogeochemical cycles, and archaea of largely unknown function, along with abundant viruses, inhabit brines throughout the ice and across the seasons (Deming and Collins, 2017).

Microbial life in sea ice is deemed a key feature of the Arctic marine system from ecological and biogeochemical standpoints (Horner, 1985; Vancoppenolle et al., 2013; Mundy and Meiners, 2021). Arctic sea-ice algae produce 2.5–73 Tg organic carbon per year (Legendre et al., 1992; Lim et al., 2025), representing 0.1—21% of pelagic production in Arctic waters, depending on calculation methods and sources. Sea-ice algae can account for as much as 50% of the pelagic production in some regions and seasons (Fernández-Méndez et al., 2015). They also provide a rare carbon source during late winter and early spring (Søreide et al., 2010). Upon melting, ice algae and associated organic matter are released into the ocean, where they may seed phytoplankton communities, sustain grazers or export to the seafloor. Sea ice therefore affects underlying pelagic and benthic trophic networks that sustain fish, birds, and mammals (Post et al., 2013; Boetius et al., 2015). In this context, shifts in Arctic sea-ice microbial life could lead to significant changes in crucial ecosystem services, with cascading effects on the biodiversity of the Arctic Ocean (Post et al., 2013; Steiner et al., 2021).

The study of life in sea ice can also offer insights into the evolution of life on Earth (Trinks et al., 2005), especially during episodes of near-global ice coverage (Hoffman et al., 2017). Limited space for production, subzero temperatures and hypersalinities of brine place limits on microbial processes and rates within the ice. Yet the concentrating effect of the freezing process may have also provided unique opportunities for life, including lateral gene transfers (via viruses, other nucleic acid-containing particles or free DNA) to facilitate adaptation and evolution (Raymond and Kim, 2012). At times omnipresent across all latitudes during Earth's history, sea ice may well have been a relative hotspot for microbial evolution. Sea ice also inspires the search for microbial life on frozen planetary bodies, as many ocean worlds in our Solar System are salty and largely frozen. This abundance of extraterrestrial salty ice makes Earth's sea ice a prime habitat analog for investigating how life may have evolved beyond Earth and where it may be detectable (Deming and Eicken, 2007; Martin and McMinn, 2018; Wolfenbarger et al., 2022).

Microbial life in Arctic sea ice is thus well recognized for its exceptional value and importance. However, studying sea ice, especially its microbiology, is hampered by numerous difficulties. The Arctic is cold, remote, and costly to access, yet beyond these logistical challenges, more fundamental issues arise. Accessing the brine-filled pore spaces inhabited by microbes without altering their micrometer-scale habitat structure, or losing material, is a major sampling challenge (Junge et al., 2001; Eicken et al., 2010; Miller et al., 2015). Sea ice is very heterogeneous, and the large horizontal and vertical variations in sea-ice properties at subcentimeter-to-meter scales are amplified for biological activities (Rysgaard et al., 2001; Mikkelsen et al., 2008; Roukaerts et al., 2021), hindering efforts to characterize temporal changes and further complicating sampling. Unlike in the open ocean, ocean color remote sensing cannot detect sea-ice algae, limiting knowledge of large-scale production and variability. Under-ice optical methods provide valuable insights into sea-ice biology (Lange et al., 2017; Hill et al., 2022). Modeling offers further potential, but current efforts are at an early stage, constrained by limited knowledge (e.g., microbial diversity) and scarce observational data, which models often fail to reproduce (e.g., Castellani et al., 2025).

These difficulties help explain why many key steps and fundamental processes involved in the development of microbial life in sea ice remain poorly understood, and why most of what we do know comes from more readily accessible coastal, immobile, landfast ice. In particular, we lack the capacity to fully describe and explain the seasonal cycle, even in coastal sea ice, but especially in pack ice (i.e. ice that drifts), and from the high Arctic (e.g., Fong et al., 2024). In addition, micro-habitats within the ice and their properties are neither well characterized nor accounted for in primary production estimates (Arrigo, 2017; Campbell et al., 2022a; García et al., 2023). Adaptive strategies are well described from experimental work with cultured sea-ice microbes (Rapp et al., 2025), but less well understood at the community level in their micro-habitats. Precisely how microbes — the unicellular photosynthetic, mixotrophic and heterotrophic eukaryotes and prokaryotes, as well as their viruses — interact with each other, achieving high levels of primary production and subsequent nutrient regeneration, remains to be explored. The door to understanding evolutionary processes, in particular the role of lateral gene transfer, has been opened (Raymond and Kim, 2012; Mock et al., 2017; Zhong et al., 2020), but much remains to be learned genetically and epigenetically. Additionally, understanding the role symbioses play between sea-ice microbes is essential for understanding this unique ecosystem.

The relatively slow pace of scientific progress on sea-ice microbiology poses a significant problem in light of the rapid pace of Arctic sea-ice loss. Arctic sea-ice loss stems from anthropogenic carbon emissions, with the decline rate relating directly to cumulative carbon emissions: for each ton of CO_2 released into the atmosphere, we lose about 3 m^2 of summer sea ice (Notz and Stroeve, 2016). At current carbon emission levels, multi-year ice — the oldest type of sea ice, which is also biologically unique — is projected to disappear, resulting in a summer ice-free Arctic between 2030 and 2050 (SIMIP Community, 2020; Jahn et al., 2024; see **Figure 1**). This loss in the coming decades means that Arctic sea ice will become the first entire biome to be impacted severely by climate change, yet there is still so much to be learned about this critical environment and habitat. As other anthropogenic impacts increase, including import of atmospheric and riverine pollution, resource exploitation, and increased shipping and tourism, the pristine nature of the sea-ice habitat faces significant threats. This vulnerability is illustrated by the high concentrations of microplastics already detected in sea ice (Peeken et al., 2018) and by the release of persistent organic pollutants (POPs) and mercury (Hg) back into the atmosphere from Arctic ice and snow as a result of climate warming (Ma et al., 2011; DiMento et al., 2019). The consequences for the sea-ice microbiome and Arctic ecosystems remain largely unknown. The need for targeted and sustained research to understand what we are losing and what will remain is urgent.

Observational monitoring programs are needed to advance understanding of high-latitude marine environments (Willis et al., 2023), and particularly Arctic sea ice. In this paper, we briefly introduce how the Tara Polar Station (Babin et al., in revision), set to deploy in the fall of 2026, will provide a unique long-term platform to study life in sea ice. Over the next quarter century, Tara Polaris Expeditions (TPE) — repeated drifts of the Tara Polar Station (TPS) within the pack ice — will provide unique opportunities to investigate the high Arctic sea-ice environment. Prior drifts across the high Arctic using other platforms to study sea ice have not had biology as a top priority. Here, we review the current state of knowledge of life in Arctic sea ice, including its links to the sea-ice environment, biogeochemistry, and biodiversity, and highlight the main knowledge gaps that the Tara Polaris Expeditions can help to address. Based on considerations of the opportunities and challenges associated with the set up of the station, we make practical recommendations for sea-ice activities, with a particular focus on biological sampling.

2. Life in Arctic pack ice is microbial

Many questions about microbial life in sea ice remain open, particularly regarding how bio-physical interactions at scales ranging from the microscale to the local scale (approximately 1 km) shape sea-ice communities. How has life adapted to the physical and chemical constraints within the sea-ice microstructure? Conversely, how do microbes modify this habitat? How diverse are the strategies that enable survival and growth in this environment, and what can they teach us about evolutionary processes? How are microbial communities in sea ice structured and organized (e.g., spatial distributions, interactions), and what roles do biological interactions play in shaping them? A primary goal of research on board the TPS, closely coupled in time to shore-based analyses, is to address these questions, as discussed below.

2.1 Microbial life in Arctic Pack Ice: highly seasonal and spatially variable

Sea ice is a key component of the Arctic marine ecosystem, serving as a habitat for a diverse array of microorganisms, including bacteria, archaea, protists (notably ice algae), fungi, small invertebrates, and fish larvae. Remarkably, these communities persist despite extreme and highly variable environmental conditions — fluctuations in temperature, salinity, and pH, among others. These conditions raise an important question: where, when, and how do these microbes develop within Arctic sea ice?

For sea-ice algae, seasonality and spatial variations are closely intertwined. The Arctic is characterized by extreme seasonal variations, which drive major changes in the morphology and properties of the pack-ice habitat (Perovich et al., 2001) and impose strong constraints on primary producers. In landfast ice, algal communities are found preferentially near the ice bottom where their activity is highly seasonal (Smith et al., 1993; Leu et al., 2015; Galindo et al., 2017; Olsen et al., 2017). From the first stages of sea-ice growth, ice algae colonize the ice, providing the initial seed bank for future biomass accumulation (Mundy and Meiners, 2021). Winter is characterized by low activity or dormancy of microalgae, resulting in a net heterotrophic phase (although heterotrophic conditions can occur at all seasons and depths; Rysgaard and Glud, 2004; Søgaard et al., 2013; Campbell et al., 2022a). Photosynthetic activity begins with the return of the sun, the timing of which depends on latitude, with snow depth strongly influencing spring bloom onset (Mikkelsen et al., 2008). Ice algal blooms, dominated by a specific sub-group of ice algal taxa – the diatoms, usually develop at the ice-ocean interface, extending into the interior of the ice once permeability increases with warmer conditions. Ice algal activity slows with bottom melt onset and ceases upon complete ice decay.

For bacteria, archaea, and their viruses, spatial variability and seasonal data — especially in pack ice — remain sparse, limiting our understanding of where and when these microbes contribute to biogeochemical processes across the annual cycle (Lund-Hansen et al., 2020). Much of our knowledge on the localization and seasonality of microbes in Arctic sea ice comes from studies of immobile, landfast Arctic sea ice (Ewert et al., 2013; Leu et al., 2015). Yet, approximately 90% of Arctic sea ice is pack ice (Yu et al., 2013), which, unlike landfast ice, is mobile, drifting under the action of winds and currents (see **Figure 2** for a map of landfast and pack ice distributions and a schematic of their differences). Because pack ice drifts, it is morphologically more diverse than landfast ice, harder to access and more complex to study. Indeed, while pack ice includes a flat, level-ice component similar to that of landfast ice, it is far more heterogeneous in the horizontal dimension due to opening, fracturing, and pressure-ridge formation, processes that are associated with a non-uniform velocity field (Perovich et al., 2003; Nicolaus et al., 2022). These processes result in substantial horizontal variations in sea ice at meter scales (Thorndike et al., 1975; von Albedyll et al., 2024). Another cause of heterogeneity in the properties of pack ice, and the life it contains, is the redistribution of snow due to interacting wind and topography, with snow erosion occurring in areas of level ice and accumulation occurring near pressure ridges (Déry and Yau, 2002; Moon et al., 2019; Nandan et al., 2023).

Large horizontal variations in snow depth and ice thickness in pack ice, compared with landfast ice, have major implications for microbial life. These variations drastically affect light availability, temperature and brine physico-chemical properties, causing order-of-magnitude shifts in ice algal biomass over just a few meters of horizontal distance (Rysgaard et al., 2001). Deep snow can also foster surface infiltration communities through seawater flooding of the snow base (Horner, 1985; Fernández-Méndez et al., 2018). Thick pressure ridges trap large amounts of seawater upon formation (Leppäranta et al., 1995), contribute 30–50% of the Arctic sea-ice volume (Flato and Hibler, 1995; Mårtensson et al., 2012) and hence are biological hotspots of primary importance (Fernández-Méndez et al., 2018; Lange et al., 2024). Under-ice highly porous platelet ice, possibly more prevalent than initially expected (Katlein et al., 2020), and summer melt ponds also host distinct microbial communities (Brinkmeyer et al., 2004; Mundy et al., 2011; Lee et al., 2012), as do direct under-ice meltwater lenses in the summer (Smith et al., 2023). Overall, pack ice offers more diverse habitats than landfast ice, with poorly understood implications for primary production and for polar marine ecology.

The spatial and temporal distribution of microbial life in Arctic pack ice remains insufficiently observed, particularly its full diversity beyond ice algae, and it may differ substantially from that in landfast ice. In particular, the seasonal evolution of microbial life across micro-environments has been documented over a quasi-entire ice year only during the recent MOSAiC program (Fong et al., 2024). TPS, an observatory that can be anchored to drifting pack ice and will be deployed multiple years into the future, with a focus on the biological and physical conditions of the ice, thus appears well suited to address all phases of the seasonal cycle of pack ice, across micro-environments and across larger horizontal scales.

2.2 How the Arctic pack ice habitat constrains microbial life

Under what conditions, and at what times and locations, does the Arctic pack-ice environment support microbial life, and by what mechanisms? Observations suggest that microbial life, especially ice algal life, thrives in specific niches and at certain times of the year. As organisms respond physiologically to light, temperature, and chemical properties of the sea-ice medium (Søgaard et al., 2011; Arrigo, 2017; Lund-Hansen et al., 2020), a common perception is that seasonal and spatial variations in sea-ice conditions highly influence biological activity (Cota et al., 1991). However, Arctic pack ice remains incompletely characterized, especially as a microbial habitat. Seasonal studies are limited, rarely span an entire year, and often lack data on ecologically critical parameters.

Light availability is essential for photosynthesis, and its large temporal and spatial variations in the Arctic strongly affect sea-ice algae. The surface of Arctic pack ice undergoes extreme seasonal changes in solar radiation from polar night to polar day (Lindsay, 1998; Persson et al., 2002; Shupe et al., 2022), with effects reaching the ice base (Katlein et al., 2019; Lebrun et al., 2023). Surface conditions — particularly snow, its humidity, and the presence of melt ponds — strongly modulate surface albedo, amplifying seasonal variations in light intensity within sea ice (Perovich et al., 2002; Light et al., 2022). Light attenuates rapidly with depth in ice, and even more in snow (Untersteiner, 1961; Ehn et al., 2008; Katlein et al., 2021; Fuchs et al., 2024). Spatial variations in snow and sea-ice thickness cause strong horizontal heterogeneity in the light field within sea ice (Katlein et al., 2015; 2019; 2021; Matthes et al., 2020). Sea-ice algae are adapted to photosynthesize at very low light levels, down to 0.01 µmol photons m^{-2} s^{-1} (Hoppe et al., 2024) but can be inhibited at high light (Lund-Hansen et al., 2020). Light variations are considered to govern the growth onset (Leu et al., 2015), development (Hancke et al., 2018) and patchiness of ice algae (Rysgaard et al., 2001). Characterizing the light field remains challenging due to snow variability and the macro-porosity of pack ice (Ehn and Mundy, 2013; Matthes et al., 2019; Katlein et al., 2021), but advances during MOSAiC (Nicolaus et al., 2022) — including ROVs that document horizontal variations and autonomous sensors that resolve vertical optical structure (Katlein et al., 2021; Perron et al., 2021; Fuchs et al., 2024) — offer new opportunities.

Temperature has many direct and indirect effects on microbial life. Ice temperature variations thus play a key, possibly underestimated role, in shaping sea-ice microbial ecosystems. Seasonal and vertical ice temperature variations are well documented from several seasonal field programs, such as IPY-58 (Untersteiner, 1961), SHEBA (Perovich and Elder, 2001), CASES (Miller et al., 2011), TARA (Nicolaus et al., 2010), and MOSAIC (Lei et al., 2022). By contrast horizontal variations are known but remain less well characterized (Sturm et al., 2002; Zampieri et al., 2024), especially in terms of micro-environments. Temperature not only affects ice algal physiology (Arrigo et al., 1993; Mundy and Meiners, 2021), but also directly influences brine volume and chemistry, particularly salinity, liquid fraction and fluid transport, all essential to nutrient supply (Assur, 1958; Miller et al., 2015; Vancoppenolle et al., 2019). Better characterizing temperature variations is deemed a key challenge.

Liquid water within sea ice offers critical habitats for the development of life, with their size, geometry, and properties influencing which inhabitants dominate and by what biological processes, and whether microbial interactions can occur. Liquid water is typically found as inclusions within the ice and in pressure ridge voids, surface melt ponds, underlying platelet ice, and warm snow, each of which presents very different microbial habitats. Liquid inclusions within the ice, for example, shrink during winter, becoming hypersaline and losing connectivity with the ocean, yet expand and freshen in later seasons when the temperature warms, creating fluctuations in opportunities for microbial interactions and nutrient (and gene) exchanges. In this context the spatio-temporal variations of liquid water and their properties are central to biodiversity and the patchiness of microbial life in sea-ice environments. However, significant gaps remain in our understanding of the amount, geometry, and chemical properties of liquid water, not only salinity but also pH, at both the micro-scale (e.g., brine) and macro-scale (e.g., ridge voids). TPS provides a unique opportunity to make progress in characterizing the temporal-spatial fluctuations in the liquid water habitats of sea ice.

Nutrients are incorporated into Arctic sea ice during ice formation, as evidenced by many nutrients scaling to salinity. Consequently, the nutrient composition of sea ice is largely inherited from that of the underlying seawater, which in turn depends on factors such as location, water depth, and proximity to the coast or a river mouth. Fluid (brine) transport, flushing and biogeochemical transformations, also play important roles (Fripiat et al., 2017; Meiners and Michel, 2017). To sustain the biomass accumulation observed in sea ice, nutrients must be resupplied from the underlying seawater through convection and/or diffusion. These exchanges occur via natural convection during ice growth (Wells et al., 2011; Thomas et al., 2020), but also through less well-constrained mechanisms such as bottom-ice turbulent exchange (Cota et al., 1987; Dalman et al., 2019; Duarte et al., 2022). Biogeochemical processes regulating nutrient availability in sea ice are closely linked to ice algae, which actively take up and store nutrients, often maintaining intracellular concentrations well above ambient levels (Mundy et al., 2025). At the same time, nutrient regeneration within sea ice must rely on an efficient microbial loop, enabling the accumulation of remineralization products (including nutrients and dissolved inorganic carbon) near the ice algal community (Fripiat et al., 2017; Meiners and Michel, 2017; Lannuzel et al., 2020; Roukaerts et al., 2021). Significant uncertainties remain as to which nutrients (nitrogen, phosphorus, silicon, or micronutrients such as iron) constitute the principal (co-)limiting factors for primary production in sea ice, and particularly in pack ice. The Tara Polaris Expeditions, focused on the biology of mobile pack ice, present valuable opportunities to advance our understanding of nutrient dynamics in sea ice.

In summary, the sea-ice environment, especially in biologically relevant terms, remains incompletely characterized. TPS offers the means to document variations in Arctic sea ice over time and space, year after year, and to advance our understanding of how the physical sea-ice environment generates and conditions the liquid habitats for life in sea ice.

2.3 Colonizing and adapting to Arctic pack ice

We know that sea ice supports individual organisms and microbial ecosystems, and which physical-chemical parameters determine that support, even if temporal and spatial variability leaves much to be understood, but how do microorganisms initially colonize the ice? Once within the ice, and particularly within mobile Arctic pack ice, how do they adapt to the more extreme conditions encountered there? Current answers to these questions rely heavily on lab studies, yet understanding what happens in situ is the critical need. Two figures schematize current understanding of the different processes at stake, regarding colonization and adaptation to the sea ice environment (**Figure 3**), and the different microbial groups present in sea ice and their seasonal evolution (**Figure 4**), seasonally, in connection to the sea ice environment.

Colonizing sea ice in its early stages of formation may be the least understood process across the seasonal sea-ice cycle, despite its primary importance. Indeed, how microorganisms colonize sea ice remains hypothetical (Mundy and Meiners, 2021; Babin et al., 2025). The initial stage of ice formation is characterized by the supercooling of seawater which causes the nucleation of frazil ice crystals free-drifting within the water column. Observed in the upper decimeters of the water column, frazil ice crystals quickly rise (at velocities of a few cm s^{-1}) to the surface where they merge into so-called grease ice before solidifying into an ice sheet (Smedsrud and Skogseth, 2006). Microorganisms, like other particles, are easily scavenged by rising frazil crystals; they can also serve as ice nucleators, in an interactive process known as suspension freezing (D'souza et al., 2013; Ito et al., 2019; Eickhoff et al., 2023; Lund-Hansen et al. 2025).

A continuous ice cover, once formed, is subjected to under-ice ocean processes associated with currents, waves, turbulence, and eventually brine convection within bottom sea ice, fostering ice-ocean water and material exchange (Reeburgh, 1984; Cota et al., 1990; Vancoppenolle et al., 2010; Dalman et al., 2019). These processes can further enmesh algal cells within the liquid brine between ice crystals. Smaller bacteria and archaea are thought to colonize newly formed ice by attaching to algal cell surfaces and aggregates, and possibly to the ice itself. As freezing progresses, the entrained microorganisms experience a drastic phase shift from relatively well-buffered open waters to a semi- or completely enclosed ice lattice enclosing higher salinity water. Model sea-ice bacteria engage in chemohalotaxis — swimming up a thermal/saline gradient (Showalter and Deming, 2018), while sea-ice diatoms can glide along ice surfaces (Zhang et al., 2025), possibly enhancing sea-ice colonization. With sparse direct observations, however, our knowledge of physical, biological and chemical colonization mechanisms remains indirect and largely speculative. Yet, as sea ice solidifies and thickens, growing under increasingly cold atmospheric conditions, the organisms colonizing it face increasingly severe conditions, especially those that do not remain near the growing ice-water interface always moderated by the ocean below.

Adapting to sea-ice conditions thus becomes essential for microorganisms to thrive, or survive, within the ice matrix. Given the large vertical temperature and salinity variations of the brine inclusions within that matrix, microorganisms have evolved a wide range of physiological adaptations to inhabit these inclusions and sustain their cellular functions, including at the levels of membrane fluidity, enzymatic activity, and essential processes such as replication, transcription, and translation (De Maayer et al., 2014; Deming and Collins, 2017). A critical area of interest is the biogenic production of micro-habitat ice-active modifiers, like extracellular polymeric substances (EPS) and ice-binding proteins (IBPs). EPS are believed to aid in the entrapment, retention, and survival of microorganisms within the ice, including the production of biofilms (Krembs et al., 2002; Janech et al., 2006; Krembs and Deming, 2008; Ewert et al., 2013). IBPs, which may be associated with EPS, play multiple roles in cold adaptation: they help prevent freezing, provide cryoprotection, enhance ice adherence, and facilitate ice nucleation (Janesch et al., 2006; Bar Dolev et al., 2016; Białkowska et al., 2020). Furthermore, both IBPs and EPS may contribute to the structural integrity of the ice habitat by stabilizing the brine network during freezing, thereby influencing sea-ice microstructures and desalination processes (Krembs et al., 2011). Despite this general depiction, the specifics of in situ production and functionality of ice-active modifiers, which give an adaptive advantage to microorganisms entrained within sea ice, remain largely unknown.

Under favourable growing conditions, the microbial-algal biomass in sea ice can increase rapidly, as the ice environment is stable and, unlike open waters, not prone to mixing. As a result, chlorophyll-a concentrations may reach levels an order of magnitude higher than those typically found in pelagic marine ecosystems. The sea-ice biomass, however, is typically confined to the bottommost centimeters of the ice (Smith et al., 1990; Gradinger, 1999) within the tortuosity of the brine network, which represents only a small fraction of the ice volume. This high level of locally concentrated biomass, coupled with significant sub-centimeter variations in the availability of light, nutrients, organic matter, and dissolved O_2, creates microenvironments with distinct biogeochemical properties and likely different strategies for microorganisms to adapt to the ice by interacting with each other, e.g., polymicrobial biofilm, symbiosis, predation, quorum sensing, chemical and electrical signaling, horizontal gene transfer, etc. (Krembs et al., 2002; Rapp et al., 2021; Roukaerts et al., 2021). For example, anoxic microenvironments have been hypothesized in bottom Arctic sea ice, as denitrification rates — a strictly anaerobic process — along with relevant gene expressions have been measured in melted sea ice (Rysgaard et al., 2004). Traditionally, sea-ice ecological studies have relied on methods and concepts from planktonic research, which involve analyzing bulk-melted samples and thereby eliminating any spatial distribution. However, for understanding organism distribution or microhabitat specificity, fluid and solute transport, and wide-ranging microbial interactions, the seawater model may be less applicable to conceptualizing the sympagic community than models from soils or sediments. Methodological advances are necessary to account for the spatial distribution of biogeochemical properties at sub-centimeter scales in the porous sea-ice matrix, and to study the spatial configuration and related activities of the sea-ice microbiome.

Work aboard TPS can help us to make progress on the longstanding issue of colonization: the platform will be present for witnessing and sampling the critical early stages of ice formation, and for documenting later under-ice colonization processes through its moon pool and remotely operated vehicles (ROVs). As a stable platform on the solidified ice, innovative subcellular imaging and preservation methods developed in shore-based labs can be tested and applied on the spot. TPS access to winter sea ice, over repeated annual deployments, can provide exciting opportunities to record and validate both expected and potentially unexpected microbial adaptations to the extreme conditions of temperature, salinity, light and nutrient availability.

2.4 Diversity and functioning of microbial life — the Arctic sea ice microbiome

Historically, biodiversity in sea ice was expected to be low due to extreme conditions that must be tolerated in the sea-ice habitat. Cross-study syntheses of taxa detected in sea ice (Arrigo, 2014; van Leeuwe et al., 2018) and first applications of DNA-sequencing technologies to the pack ice microbiome (Bowman et al., 2012) dispelled this perception. Piecing together available short-term studies has indicated that seasonal succession occurs within the ice, but differently in different layers and micro-habitats (van Leeuwe et al., 2018). What appears well-known in landfast ice only sometimes overlaps with drifting pack ice, leaving much to be learned, and biogeochemical and ecosystem consequences in question.

Biodiversity of microalgae in the sea-ice environment is rich, with hundreds of taxa detected (Arrigo, 2014) representing the functional groups of autotrophs, as the primary producers for the ecosystem, and mixotrophic and heterotrophic flagellates, some of which may produce climatically active gases (e.g., dimethyl sulphide). Diatoms, particularly pennate diatoms (with elongated silicate frustules), tend to dominate in bottom sea ice during springtime, while flagellates thrive in summer surface habitats (melt ponds) of Arctic sea ice. Although data are limited for comparisons, pack ice may be better characterized by mixtures of diatoms and flagellates than by dominant diatoms as in landfast ice (van Leeuwe et al., 2018). What environmental conditions, physiological adaptations, refugia from predators, and associations with ever-present bacteria may lead to mixed versus dominant microalgae is not clear. The application of DNA sequencing technologies, specifically to prokaryotic components of the sea ice microbiome, indicate surprisingly high bacterial diversity (Bowman et al., 2012; Rapp et al., 2021), which may be attributable to the ability of most seawater bacteria entrained during ice formation to persist through winter, even in coldest upper layers of the ice (Collins et al., 2010). Archaea are also entrained into newly forming sea ice and persist through winter, but as a small percentage of the sea-ice microbiome, low in taxonomic diversity and of unknown function. Currently published diversity assessments of the sea-ice microbiome are based on short-term studies that encompass widely varying methods and conditions. A more long-term approach on diversity in drifting pack ice would represent a major advance.

Succession of microalgae and bacteria in sea ice has been inferred from short-term studies, even while recognizing that data are scattered in time and space and dependent on specific conditions (van Leeuwe et al., 2018). The few studies addressing a full season indicate, for example, micro-algal succession in bottom sea ice from pennate to centric diatoms, likely linked to changes in the light field (e.g., Campbell et al., 2017). Bacterial succession, pieced together from individual studies (Deming and Collins, 2017), begins in autumn when diverse seawater bacteria, including *Pelagibacter* spp., entrain into the growing ice. Limited data on an autumn postbloom have pointed to Coscinodiscophyceae, *Amylibacter* and the SAR116 clade as predominant taxa (Wietz et al., 2021). Winter communities appear dominated by ammonia-oxidizing archaea, such as *Candidatus* Nitrosopumilus, while spring and summer transitions favor ice-adapted heterotrophic bacteria, like the gammaproteobacteria *Polaribacter*, *Colwellia*, *Formosa* and uncultured lineages, driven by fresh algal-derived carbon inputs (Rapp et al., 2021; Wietz et al., 2021; Thiele et al., 2022). Evidence exists that the abundant viruses in sea ice, most being novel compared to existing databases, may regulate seasonal microbial population dynamics and facilitate horizontal gene transfer (Zhong et al., 2020), influencing ecosystem resilience. Changing environmental conditions in the sea ice as seasons progress can thus account for differences in microbial diversity and attendant function observed in snapshot studies, yet microhabitats at different locations within Arctic pack ice change differently with the seasons, adding to the challenge of deducing microbial succession.

Our knowledge of biodiversity in Arctic sea ice is impressive given logistical constraints and snapshot sampling, but direct links between diversity, succession and environmental conditions over time are missing. The many microhabitats formed by Arctic pack ice are the least evaluated, and most threatened, of sea-ice environments. TPS offers a means to document a full annual cycle of diversity measurements in different spatial settings within Arctic pack ice, coupled to key environmental conditions. DNA sequencing technologies provide the promise of success, both for the deep information they reveal and the avoidance of complex manipulations and incubations in the field.

2.5 Microbial interactions in the sea ice

Microbial species do not live in isolation, and instead engage in a diverse suite of associations at the microscale, ranging from mutualistic to parasitic, as illustrated by cross-domain predator-prey interactions, competition, infection and symbioses between eukaryotes, bacteria, archaea and viruses. In planktonic ecosystems, microbial interactions clearly impact species evolution (Rao et al., 2025), adaptation to changing environments (Xie et al., 2013), succession (Vincent et al., 2023) and ecosystem functioning (Tschitschko et al., 2024); however, much remains to be understood in the sea-ice ecosystem. In particular, the spatial structure of pack ice coupled to seasonality creates a dynamic environment likely to impact encounter rates between species and thus frequency and type of interactions (Campbell et al., 2022b). While intra-domain microbial interactions also play an important role (diatom-diatom nutrient competition, bacteria-bacteria syntrophy), we focus below on cross-domain associations.

Food web studies examining ice-pelagic-benthic coupling and the particular role of ice algae as a critical and defining food source for the Arctic marine ecosystem are relatively common (e.g., Kohlbach et al., 2022; Amiraux et al., 2023; Koch et al., 2023). This research is typically bolstered by sea-ice biomarkers including the highly-branched isoprenoid, IP25, for which specific, but not bloom-dominating, ice algae species are the sole producers (Brown et al., 2014). However, little is known of the sea ice sub-web (Gradinger and Bluhm, 2020) and its importance to the pelagic and benthic sub-webs. Heterotrophic protists and meiofauna have been estimated to consume only 1–10% of ice algal biomass, with no substantial top-down influence on the ice algal bloom (Bluhm et al., 2018; Mundy and Meiners, 2021). However, their abundance can reach >200,000 individuals m^{-2}, concentrated towards the bottom 10 cm of the sea ice (Bluhm et al., 2018). These observations make their contribution to the pelagic sub-web a non-negligible, yet undocumented, source of cryo-pelagic coupling. Furthermore, sympagic nematodes appear to have the capacity to directly absorb dissolved organic matter in the sea-ice environment (Tchesunov and Riemann, 1995), identifying the exciting possibility of a “meiofauna loop” that redirects carbon back into the particulate food web. Little is known on trophic interactions within the sea ice, particularly for the central Arctic Ocean, or on the contribution of meiofauna to ice-pelagic coupling. TPS will provide the opportunity to observe the sea-ice food web and trophic interactions alongside the seasonal ice algal and microbial growth progressions.

Predator-prey interactions. Given the importance of food-webs for ecosystem functioning, predator-prey interactions have been relatively well studied in Arctic seas, but far less so in the sea ice itself. The constricted space of the sea-ice brine environment nevertheless provides habitat and food sources for heterotrophic protists, such as ciliates, flagellates, and amoeba, and for the meiofauna (metazoa) able to enter brine channels of the ice. These groups are often over-looked, likely due to low consumption rates of ice algae (Leasi et al., 2021). However, meiofaunal concentrations can be particularly high in the bottom decimeters of sea ice, potentially related to a lack of natural predators – the ice serves as a refuge from predation, making them an important food source for the pelagic web when the sea ice begins to melt (CAFF, 2017). As for many other ice observations, much of our knowledge of these sea-ice heterotrophs comes from shallow coastal seas and landfast ice. However, community composition in these accessible ice formations can differ greatly from that of the central Arctic, e.g., meroplankton taxa are restricted to nearshore sea ice (Bluhm et al., 2018). Furthermore, seasonality and ice thickness are strong predictors of meiofauna composition and abundance, making them particularly susceptible to climate change and thus a potentially valuable indicator of change (Bluhm et al., 2018; Leasi et al., 2021).

Algal-bacterial interactions are well known in many terrestrial and marine environments, but vastly understudied in sea ice. Comprehensive reviews do not mention sea ice (e.g., (Burgunter-Delamare et al., 2024), despite algal-bacterial interactions being identified as a determinant of the sea-ice microbiome years ago (Stewart and Fritsen, 2004). Both mutualistic and antagonistic, algal-bacteria interactions are often based on exchanges of primary and secondary metabolites from one or the other partner. For instance, diatoms release extracellular polymeric substances (EPS) and DMSP that can be metabolized by bacteria which often live epiphytically on algal surfaces - such as Flavobacteria and Rhodobacterales - forming tight metabolic partnerships (Bowman, 2015; Bellas et al., 2023). As particle-associated bacteria are metabolically more active than free-living ones in winter sea ice (Junge et al., 2004), the presence of algal residues in pack ice may further influence bacterial metabolism. Interestingly, algal-bacteria interactions can also serve as a major tool for survival: some (non-Arctic) algae harbor cyanobacteria that fix nitrogen (Foster et al., 2011), a potentially crucial, but unexplored, adaptation in nutrient-limited polar environments and particularly inside the ice matrix. Another recent example reveals how the Antarctic bacterium *Marinomonas primoryensis* uses a massive adhesin protein (1.5 MDa) with multiple domains to bind specifically to ice and also to Antarctic diatoms (Guo et al., 2017). The adhesin contains regions that mediate both peptide and sugar binding, tethering bacteria to the diatom surface and enabling the bacteria to secure the algae to ice surfaces, facilitating symbiotic microbial interactions in sea-ice environments. Such a mechanism could also be at play in the Arctic pack ice, but observing it would require innovative methods, which repeated TPS deployments could facilitate.

Eukaryotic parasites in the sea ice: fungi and oomycetes. Fungal (particularly chytrid) and oomycete parasites are widespread in Arctic sea-ice microbial communities (Hassett and Gradinger, 2016; Hassett et al., 2019). While many studies in this area are based on the analysis of co-occurrence networks between putative host and parasite (Kilias et al., 2020; Dilliplaine et al., 2025) or provide limited visual evidence for infection (Ilicic et al., 2024), chytrids and oomycetes are notoriously known to infect diatoms (Garvetto et al., 2018; Danz and Quandt, 2023). In planktonic systems, such interactions exert strong influence on primary producers, seasonal microbial succession, and biogeochemical cycles as demonstrated by the “fungal shunt” (Klawonn et al., 2021). Through this process, chytrid fungal parasites infect diatoms (and other microalgae), causing host cell lysis. This releases algal organic matter directly into the environment, fueling bacterial growth and activity, rather than transferring energy up the food chain via grazers. To what extent analogies can be drawn in the winter pack ice remains unknown, but could represent a source of dissolved organic matter during an otherwise nutritiously impoverished period.

Viruses. Viruses infect virtually every living cell on Earth, with important consequences to biogeochemical cycles (Suttle, 2007); microbes in sea ice are no exception. Viruses are present in high concentrations in sea-ice brines (Collins and Deming, 2011a; Collins and Deming, 2011b), leading to high contact rates with microbial inhabitants (Wells and Deming, 2006). Multiple sequencing studies highlight the diversity of phages and potential bacterial hosts in Arctic samples (Zhong et al., 2020; Calayag et al., 2025). A recent review provides extensive coverage of what is known about phages in Arctic sea ice (Heinrichs et al., 2024). Similarly to the study of planktonic systems, research on Arctic eukaryotic viruses lags behind prokaryotic viruses, yet they may be more prevalent than previously thought (Xia et al., 2022).

Conclusion. Studying microbial interactions in the pack ice from TPS can be expected to follow a stepwise approach, akin to how interactions in planktonic systems were revealed. Moving from mapping the diversity of species to mapping the diversity of cross-domain interactions will be a first key step. As microbial interactions impact the metabolism, adaptation, and evolution of individual species, and ultimately ecosystem function, new questions can then be asked. Can bacteria help microalgae cope with sharp gradients in temperature, salinity, increasing acidification (McMinn et al., 2014) and episodes of brine flushing? Does the sea-ice microbe-concentrating effect lead to new symbiotic associations between algae and prokaryotes, potentially increasing horizontal gene transfer or kleptoplastidy and thus accelerating the rate of evolution? What is the larger biogeochemical impact of microscale interactions occurring in the sea ice?

Needs that the TPS can meet. To answer these questions, many approaches will be required, in particular in the fields of “omics” and imaging. Though mainly applied to liquid marine samples, well established technologies such as metagenomics and transcriptomics can be used, and possibly metabolomics to decipher chemical signals exchanged between species. Single-cell sequencing approaches are gaining popularity in marine microbiology, as they may reveal new host-virus pairs (Fromm et al., 2024) and plasticity of host-associated microbiomes (Priest et al., 2025). Given the spatial component of the pack ice, inspiration from other fields of molecular biology or terrestrial science may help establish spatial transcriptomics coupled to FISH technology or X-ray imaging of microbial life, thus preserving the essential dimension of species position in the ice, rather than melting of the samples. The latter, however, will require major methodological development, in particular in the area of sample preservation, with broader applications. Indeed, improved subcellular imaging techniques may provide invaluable insights into microbial interactions, but they often require tailored fixation methods, as was recently demonstrated using expansion microscopy on fixed environmental samples of diatom-bacteria interactions (Flori et al., 2025), 3D FIB-SEM to study kleptoplastidy in polar planktonic hosts (Rao et al., 2025), and activity measurements of viral infection using BONCAT-FACS (Couradeau et al., 2019) or single cell mRNA-FISH (Vincent et al., 2021). Breakthroughs in the study of such interactions often require mechanistic work in laboratory culture-based systems, but with its advanced infrastructure and molecular laboratories, the TPS represents a unique opportunity to move our understanding of microbial interactions in sea ice forward on all fronts.

2.6 Evolutionary dynamics of the Arctic sea ice microbiome

Extreme conditions presented by Arctic pack ice are understood to slow the growth rate of its inhabitants, even though photosynthesis in the ice (not necessarily coupled to growth) yields enough organic carbon to contribute substantially to the larger Arctic ecosystem. Microbial evolution through vertically inherited traits and natural selection, however, depends on organism reproduction – the passage of geological time since Earth’s first ice age has allowed for ice-adapted microbes to evolve in this way. Sea ice, by concentrating dissolved and particulate material into its pore spaces – including microbes, viruses and extracellular DNA – also offers the potential for horizontal gene transfer (HGT), which can accelerate the acquisition of ice-adapted traits. HGT in sea ice is in its infancy, as is exploration of possible epigenetic mechanisms for rapid acclimation to sea ice.

Evolution based on reproduction and natural selection can be expected to occur optimally in the springtime biofilms at the bottom of Arctic sea ice. There, conditions promote biomass production of both eukaryotic and prokaryotic microbes and thus their co-evolution. Based on what little we know about microbe-microbe interactions in sea ice, this co-evolution likely has led to mutualistic behaviors that enable current levels of biomass production and biogeochemical cycling. Understanding how these behaviors may be interrupted in the future represents a serious challenge.

Horizontal gene transfer has been hypothesized as a means to explain escalated evolutionary adaptations in cold environments (e.g., Deming, 2002), with evidence building for its occurrence in sea ice. Genomic analyses of ice-adapted model organisms have revealed HGT between bacterial orders (genes involved in compatible solute pathways for osmotolerance; Collins and Deming, 2013) and between the domains of bacteria and ice diatoms (genes for ice-binding proteins; Raymond and Kim, 2012). Viromic analyses of sea-ice brines support viruses as key agents of HGT (carrying bacterial genes for membrane fluidity; Zhong et al., 2020). Sea ice, with its freeze-concentrating effects that bring microbes, viruses and DNA into immediate and seasonally prolonged contact, may be serving as an ongoing evolutionary crucible. The potential for HGT in Arctic pack ice habitats warrants focused study.

Epigenetics can provide means to acclimate rapidly (minutes to hours) to a change in environmental conditions. Rapid changes impacting microbial life are inherent to Arctic sea-ice formation and growth (Ewert et al., 2013). Are there epigenetic mechanisms at work to enable such acclimation to sea-ice conditions, whether following initial entrainment into the ice or longer-term exposure to more severe and fluctuating conditions through winter? DNA methylation is an epigenetic mechanism well-known in model microorganisms to regulate which genes are expressed and to defend against viral infection, all on short notice. The first study of microbial methylomes of sea ice, now readily obtained using Nanopore technology, indicates that DNA methylation functions beyond traditional restriction-modification systems that protect against foreign DNA, instead favoring regulatory functions (Kanaan and Deming, 2025). Other epigenetic mechanisms remain unexplored in this ecosystem. For example, RNA modifications, of which over 100 different types have been identified across all domains of life, represent an additional unexplored layer of epigenetic regulation that could facilitate rapid microbial adaptation to sea-ice conditions.

To answer evolutionary questions about the sea-ice microbiome requires more than laboratory studies of model organisms and genomic snapshots of a selected type and season of sea ice. New, simpler and more affordable sequencing technologies with bioinformatics software have removed methodological bottlenecks of past field studies. The

TPS itself can provide the seasonal continuity needed to identify when and where Arctic sea ice may be functioning as an evolutionary hotspot.

3. Opportunities, challenges and recommendations

3.1 TPS provides new opportunities

Science. The Tara Polar Station (TPS) offers a unique opportunity to design innovative sampling strategies that capture the full seasonal cycle and transitions between seasons in the central Arctic Ocean. Its drifting capability enables high-resolution, long-term observations across a broad range of ice and ocean conditions — from the high Arctic near the North Pole to the subarctic boundary regions — allowing investigations of environmental gradients and temporal variability at multiple scales. TPS is particularly well-suited to studying the phenology and ecology of ice algae, enabling detailed assessments of how shifting ice regimes and environmental variability affect primary production, species composition, and ecological interactions at the base of the food web. This approach can help address key gaps in current understanding — such as the nutrient-biomass paradox (Vancoppenolle and Tedesco, 2017) and floe-scale productivity variability (Campbell et al., 2022a) — by informing process models and enabling more robust upscaling and assessment of sea-ice primary production. By integrating atmospheric and oceanic observations, and linking physical conditions with biogeochemical processes and biological responses, TPS supports a holistic understanding of feedback mechanisms in the coupled Arctic system and provides critical insight into long-term changes driven by climate forcing.

Technology. TPS work will be constrained by limited manpower but will benefit from high-bandwidth communications. In this context, autonomous measurement platforms and shore-based operations will be privileged — much like the model of space stations (Babin et al., 2025). Having a stronger focus on ecological questions, advanced molecular and genomic approaches can be coupled with shore-based analyses in real time, enabling an adaptive sampling plan to capture an ecosystem shift in progress. The privileging of autonomous platforms and shore-based operations will force the testing of innovative sampling and measurement methods that require minimal human effort. Building on the legacy of the MOSAiC expedition, environmental monitoring is likely to incorporate a range of autonomous technologies, including under-ice vehicles, drones, and stationary platforms (Nicolaus et al., 2022). High-resolution imagery above and below the sea ice, using ROVs and embedded cameras, will be employed to enhance observational capabilities and provide new knowledge on life in sea ice. Flow cytometry and emerging methods like endoscopic sampling, X-ray imaging, MR scanning and ridge sampling tools offer promising avenues for minimally invasive investigation. Moreover, progressing non-destructive techniques such as optical imaging, salinity and light harps will be developed further, enabling long-term monitoring of polar environments without disrupting fragile ecosystems.

3.2 TPS constraints provide new challenges

Sea ice presents significant challenges for sampling and measurement due to its complex, dynamic, cold and chemically specific nature. Many research programs have aimed to optimize sampling across all habitats, depths, and seasons to capture its full variability — from microscale to floe scale. However, this ideal is hindered by numerous practical constraints (reviewed by Miller et al., 2015). The number of samples that can be collected is limited by logistics, the volume required for various analyses, time-intensive processing steps (such as core extraction, melting, filtration, and subsequent analyses), and restrictions related to onboard storage and laboratory space. Moreover, sampling itself can disturb — and often destroys — the fragile sea-ice environment, with cumulative impacts over the course of a season. Measurement techniques borrowed from oceanography are often ill-suited to sea ice, where extreme cold and high brine salinity introduce additional challenges. The strong spatial heterogeneity of sea ice further complicates interpretation, often scrambling time series and reinforcing the need to capture its diverse habitats. Even within level ice, commonly used methods such as ice coring and brine sackhole sampling each come with specific advantages and limitations, underscoring the need for methodological refinement tailored to the unique conditions of the sea-ice system.

3.3 Recommendations for monitoring / sampling plan

The sampling program for the Tara Polaris Expeditions should be designed to monitor the evolution of snow and sea-ice environments over daily, weekly, seasonal, and interannual timescales by assessing their physical, chemical, and biological properties. Characterizing living conditions in sea ice — particularly for the microbial communities that inhabit the ice and its interface with the ocean — requires monitoring a broad range of physical, chemical, and biological parameters. To this end, we recommend using classical, well-established approaches for routine monitoring, while also testing new methods. The sea-ice sampling program should be closely linked to its oceanic and atmospheric counterparts (Schmale et al., 2025; Geoffroy et al., in revision), both because sea ice is strongly influenced by these media and because similar laboratory analyses will be applied to samples from different origins.

The sampling program for the Tara Polaris Expeditions should combine classical, well-established approaches for routine monitoring, while also testing new methods (see **Figure 5** for examples). Characterizing sea-ice habitats, particularly the microbial communities inhabiting the ice and its ocean interface, requires monitoring a broad range of parameters. More precisely, the physical, chemical, and biological properties of snow and sea-ice environments over daily, weekly, seasonal, and interannual timescales. The sea-ice sampling program should also be closely linked to its oceanic and atmospheric counterparts (Schmale et al., 2025; Geoffroy et al., in revision), both because sea ice is strongly influenced by these media and because similar laboratory analyses will be applied to samples from different origins.

As the targeted measurements describe the habitat quality, resource availability, and organism viability within and beneath the sea ice, the **impacts of the station** itself on the sampled sea-ice environment need to be minimized and monitored. For example, even low levels of light or nutrient pollution may affect overwintering communities in the sea ice over longer time scales (Fong et al., 2024), requiring careful selection of coring spots outside of the platform's influence despite associated logistical challenges.

Preferred sampling methods for sea-ice biological and chemical parameters are parameter-dependent, and trade between accuracy, practicality, and preservation of in situ conditions. **Ice cores** currently remain the preferred method for studies focused on physical and biogeochemical properties, as they allow for vertical resolution and budget analyses (Fripiat et al., 2017; Meiners et al., 2018). Ice core extraction, however, is a destructive technique that requires new sites to be selected each time. The process can also alter surface conditions; especially during the early melt season, it may affect the optical properties and surface meltwater drainage patterns on the ice floe. Furthermore, core extraction leads to brine loss (Notz et al., 2005), and the subsequent melting process — though necessary for most analyses — introduces biological artifacts such as osmotic shocks due to salinity changes and temperature-driven metabolic shifts which will differ strongly in intensity and impact between warmer and colder seasons. Long-term cold storage largely alters the temperature-dependent microstructure and biochemical integrity of the samples.

By contrast, for certain biological applications, especially those involving microbial or genomic analyses, brine collected from **sackholes** is often favored. This method helps preserve solute concentrations, reduces osmotic stress, and avoids the contamination risks associated with melting sea ice using external solutions that may contain DNA or viruses. Nevertheless, sackholes come with limitations: brine collection is time-consuming and limited in volume in winter ice, the depth of origin of the sampled brine is often uncertain, seawater intrusions may compromise deeper samples, and the method does not capture material embedded in the ice matrix or at the ice–ocean interface.

The **representativeness** of samples is a determining aspect on which the progress enabled by TPS operations will largely depend. Manpower, storage space and melting time, provide primary constraints on the total volume of samples that can be extracted for a given station. Trade-offs between sampling frequency, vertical resolution, and the sampling of the different ice types (multi-year ice, first-year ice) and habitats (level ice, ridges, ponds) will be necessary. We envision that sea-ice samples will provide, first, the most representative and, second, the most precise characterization of the pack-ice environment at the scale of a sea-ice floe (1 km). There will be a need to establish consensus on how best to sample complex and underexplored ice habitats such as ridges, melt ponds, or platelet ice. Finally, avoiding overload of the TPS crew is important, particularly given the concomitant goal of a sustainable long-term (20-year) program — key to bridging in-situ observations with pan-Arctic primary production estimates derived from satellite imagery and large-scale model simulations.

As we aim to resolve the seasonal cycle for an entire sea ice floe, we recommend characterizing the sea-ice environment and microbiome at the floe scale (~1 km) on daily to weekly time scales.

Physical parameters include :

- Sea ice morphology — the floe-scale distributions of ice thickness, snow depth, freeboard, fractures and ridges via images and radar scans. Morphology determines the total habitable volume, and influences light transmission, temperature, and liquid phase properties.
- Temperature field — vertical profiles and transects. Temperature influences all biological activities and, together with salinity, controls liquid phase salinity and volume fraction, and therefore habitable space.
- Light field (PAR) — vertical profiles and under-ice horizontal transects. Light controls photosynthesis and photochemistry in general.
- Liquid fraction — vertical profiles, horizontal surveys and microstructure imaging. Brine inclusions and liquid water provide habitable space for the microbiome.
- Under-ice free-floating frazil crystal abundance and distributions — ADCP and imagery. Influences harvesting of water column material and sea ice colonization.
- Ice type — first-year versus multi-year surface fraction. First-year and multi-year ice have different vertical salinity profiles, brine network characteristics and optical properties, leading to different biological communities.
- Oceanic and atmospheric properties near the sea ice as they affect air-ice and ice-ocean heat, matter and momentum exchanges.

Chemical parameters include :

- Salinity — of both sea ice and liquid water (brine, ridged ice cavities and melt ponds). Ice salinity, together with temperature, sets liquid fraction and habitable space. Salinity of the liquid can widely vary and largely influence biological processes, in particular via osmotic stress.
- Nutrient concentrations — of both sea ice and liquid water; nitrate, ammonium, nitrite, phosphate, silicate. Nutrients limit growth of primary producers.
- Organic matter concentrations — of both sea ice and liquid water, particulate and dissolved. Organic matter serves as a substrate and energy source for microbes.
- Gas concentrations — in particular oxygen, as it traces photosynthesis and respiration.

- pH, dissolved inorganic carbon and alkalinity — of both sea ice and liquid water. pH characterizes the chemistry of brine and influences biology, whereas DIC and alkalinity trace inorganic carbon cycle processes.

Biological parameters include:

- Sea-ice algal biomass and community composition (via genomics and imaging – base of the ice-associated food web)
- Chlorophyll-a concentration (proxy for algal biomass)
- Primary production (direct measure of ecosystem functioning and carbon fixation)
- Bacterial and archaeal communities (via genomics and imaging – important for deducing biogeochemical cycling, organic matter degradation, microbial interactions)
- Gene expression (via transcriptomics and proteomics – important for identifying adaptations, functions, and microbial interactions)
- Viruses (via viromics – influence microbial dynamics, biogeochemical cycling, adaptive gene exchange)
- Zooplankton and protists (key consumers of ice algae and microbes)
- Meiofauna and the sea-ice food web (broadens the scope to higher trophic levels)

Together, these parameters can provide insights into the habitability of sea-ice environments, the functioning of microbial food webs, and the impacts of climate-driven change on sea-ice ecosystems. Effective monitoring includes combining field sampling, autonomous sensors, and remote sensing, providing links with modeling for scaling up and forecasting ecosystem responses.

4. Expected outcomes and ways forward

The TPS and its dedicated Tara Polaris Expeditions offer unique, timely and long-term opportunities to advance our understanding of Arctic sea ice, its ecosystems, and their response to rapid environmental change (Ardyna et al., in revision). Building on decades of international sea-ice research, TPS will generate an unprecedented, long-term, high-resolution dataset capturing the seasonal and spatial dynamics of the sea-ice microbiome. This effort will help close key knowledge gaps about the sea-ice ecosystem structure, function, and its role in polar biogeochemical transformations and support of the larger ecosystem. The logistical challenges of operating in the central Arctic from Tara's new drifting platform will drive innovation in autonomous observation systems, minimally invasive sampling, and remote molecular tools, enabling more sustainable and systematic sea-ice research over the 20-year mission. TPS will train a new generation of polar scientists through interdisciplinary research that bridges oceanography, microbiology, and environmental science, developing expertise essential for understanding sea ice as a dynamic habitat for life. Beyond its scientific reach, TPS will also serve as a platform for public engagement, communicating the urgency and wonder of the sea-ice environment and its inhabitants to global audiences. Through open data sharing and international collaboration, TPS will amplify the impact of sea-ice research, shaping the future of Arctic science and deepening global understanding of this fragile and rapidly transforming biome.

Contributions

Coordination and scoping of the manuscript: MV, JD, SR, FF, SA, CJM

Figure preparation: MV, FF, SA, CJM, SR.

Writing : all authors edited and wrote sections

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AI disclosure statement

ChatGPT was used to edit the style of individual sentences, in some places of the text.

Data accessibility statement

Passive microwave sea ice concentrations data used in Figure 1 are from the Sea Ice Concentration Climate Data Record Release 3.1 - Multimission https://doi.org/10.15770/EUM_SAF_OSI_0023.

CMIP6 Climate model outputs shown in Figure 1 were extracted from the IPSL ESGF node https://esgf-node.ipsl.upmc.fr/projects/cmip6-ipsl/.

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Figures

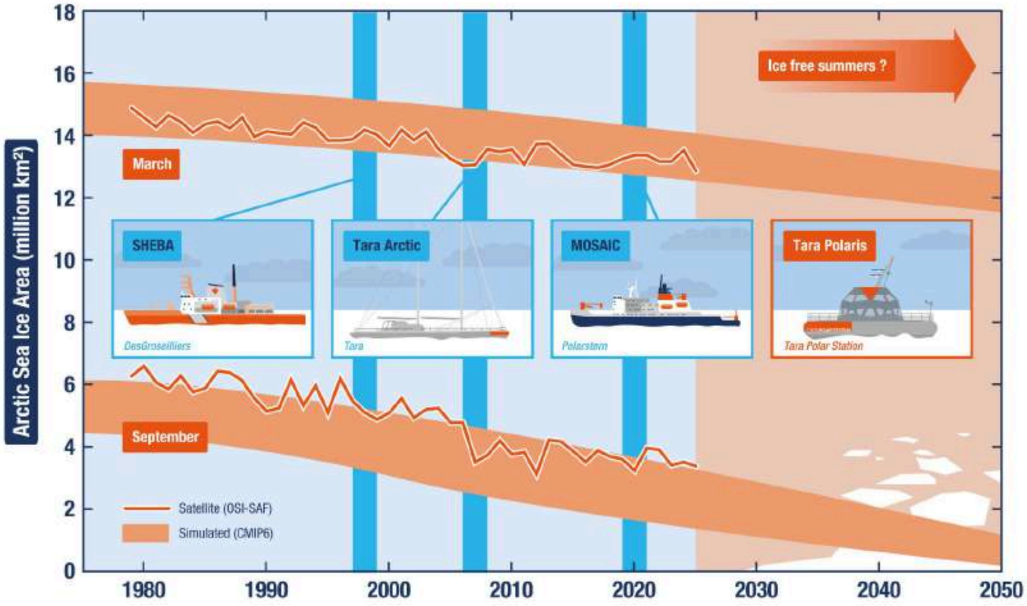

Figure 1. Tara Polaris Expeditions, contextualized with projections of Arctic sea-ice area and recent year-long observational programs. Projections of sea-ice area from satellite passive microwave data are from the OSI-450a1 / OSI-430a Climate Data Record (OSI SAF and EUMETSAT SAF On Ocean And Sea Ice, 2025), whereas model simulations are from CMIP6 historical and ssp585 simulations (Eyring et al., 2016; SIMIP Community, 2020).

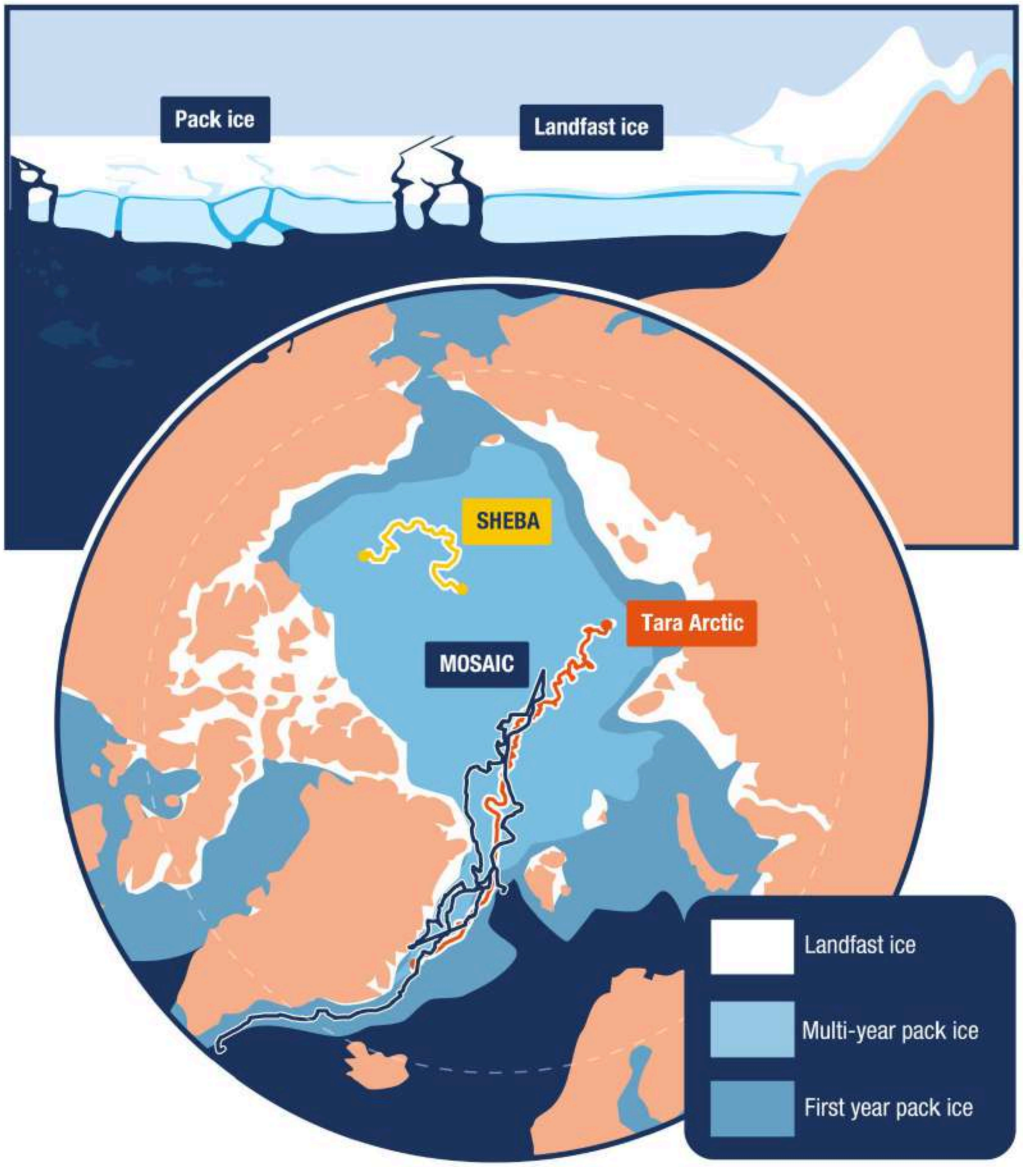

Figure 2. Different sea ice types across the Arctic. *(top)* Conceptual sketch of pack ice against landfast ice. Drifting pack ice is characterized by greater environmental diversity than landfast ice, which is immobile and typically flat. *(bottom)* Climatological map showing the distribution of landfast ice and pack ice (first-year and multi-year) along the drift trajectories of recent Arctic expeditions mentioned in the text. Landfast-ice climatology is based on National Ice Center charts (Yu et al., 2013), whereas pack ice data are derived from satellite-based passive microwave retrievals of sea ice concentration using the OSI-450a1 / OSI-430a Climate Data Record (OSI SAF and EUMETSAT SAF On Ocean And Sea Ice, 2025).

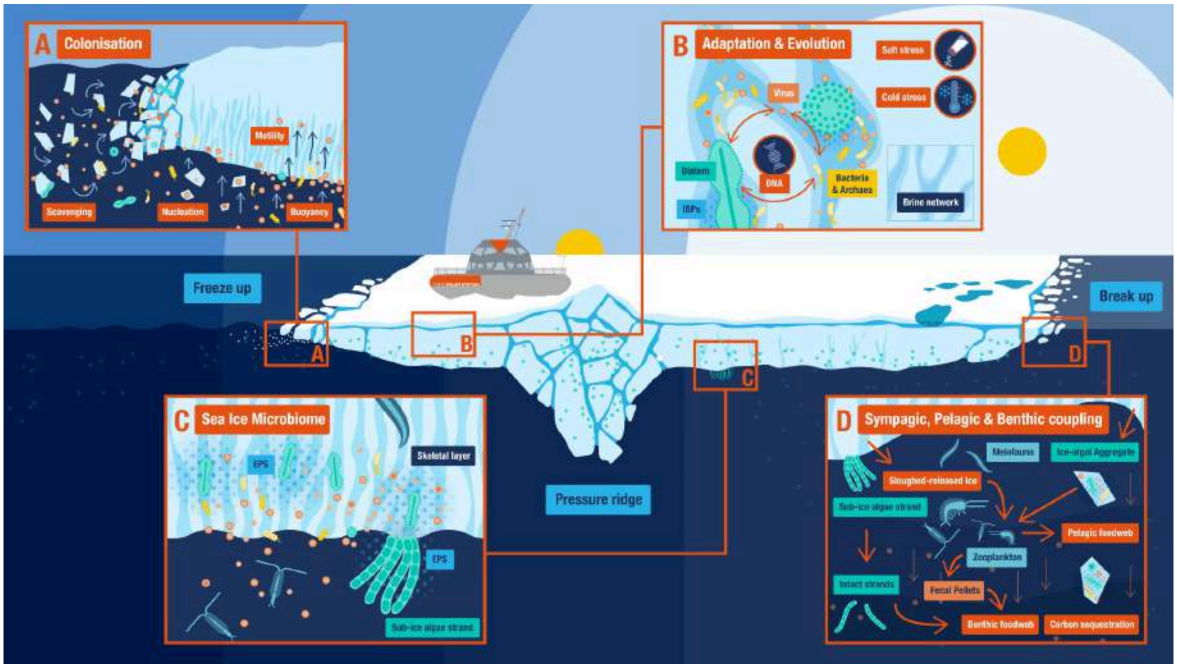

Figure 3. Microbial life processes. The sea ice environment and its connection to the processes involved in the development of sea ice microbial life (see Section 2 for details).

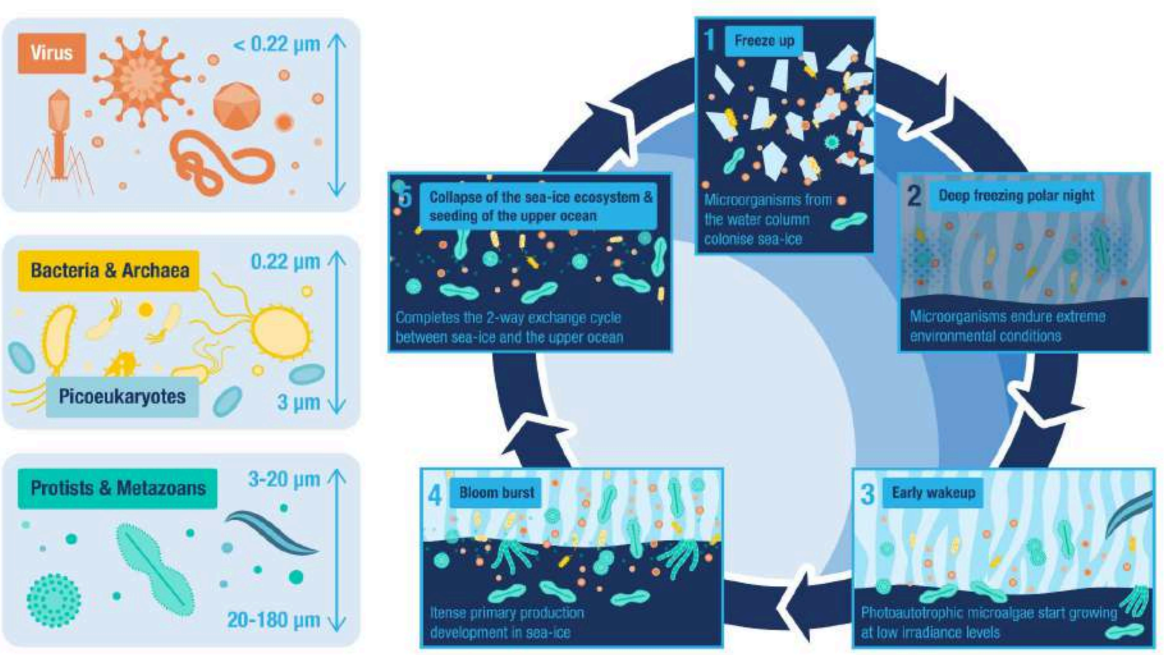

Figure 4. Microbial targets and processes for "omics" sampling of sea ice and under-ice waters. Size fractionation (left panel) enables both specific group analyses and an integrated view, from viruses to protists and (not shown) metazoans. Different points in the sea-ice cycle (right panel), fully and repeatedly sampled by the Tara Polaris Expeditions, allow investigations to address both longstanding and emerging questions about the sea-ice microbiome.

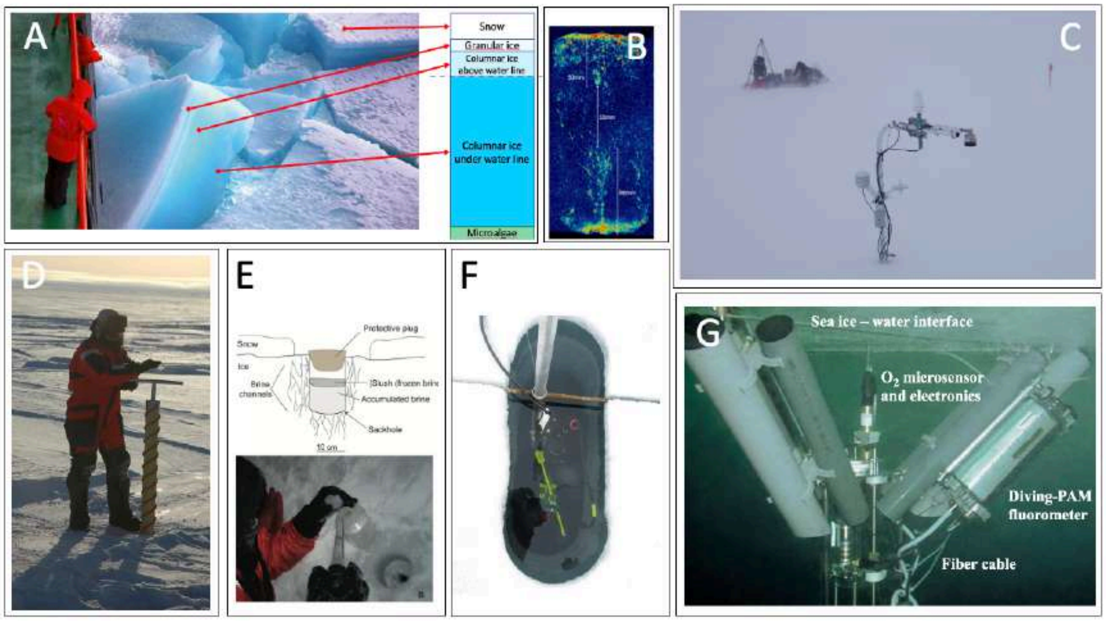

Figure 5. Examples of observing and sampling sea ice for various physical, chemical and biological measurements. (A) Sea ice breaking up and revealing its structurally different layers. (B) The microbially inhabited brine network within sea ice (image from Galley et al., 2015). (C) Deploying a weather station and thermistor string. (D) Sea-ice coring. (E) Sackhole sampling. (F) Measuring oxygen fluxes at the ice–ocean interface with an eddy covariance instrument. (G) Microsensor profiling and pulse-amplified modulation (PAM) in the sea-ice algal bottom layer (image from Rysgaard et al., 2001).