

Multi-year assessment of coastal sea-ice algae and phytoplankton in an Arctic port ecosystem, Nunavut, Canada

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Abstract

This study provides a rare multi-year assessment of sea-ice algal and phytoplankton species diversity in the coastal Canadian Arctic, across sea-ice and open-water habitats, that reflect seasonal gradients critical to ecosystem function. Samples were collected near Iqaluit, Nunavut, in 2018–2022. A total of 562 taxa were identified with *Nitzschia frigida* Grunow, 1880, unidentified flagellates, *Thalassiosira* spp. (Cleve, 1873) (20–50 µm), and *Chaetoceros* spp. (Ehrenberg, 1844) (5–10 µm) numerically dominating sea-ice, under-ice, ice-crack, and open-water surface habitat, respectively. Simpson diversity of these habitats was highest in ice-crack surface waters (0.94, July 2019), suggesting a physical concentration of cells. Variability in community composition followed Arctic phenology. Sea-ice, open-water bloom, and under-ice/transitional assemblages were differentiated by pennate diatoms (e.g., *Navicula pelagica* Cleve, 1896 and centric diatoms (e.g., *Chaetoceros* spp.), as well as Prymnesiophyceae, including *Chrysochromulina* spp. Lackey, 1939. Six potential toxin producing species were present at low frequency of occurrence (<1%–12% of sampling events). Community composition was homogenous among stations and inlets, but variability in phytoplankton bloom seasonality altered the relative abundance of the under-ice/transitional assemblage. This project provides updated records of sea-ice algae and phytoplankton diversity for the only deep-water port in the eastern Canadian Arctic, documenting seasonal and interannual community variability required to identify potential effects of climate-driven or anthropogenic events.

Key words: arctic, biodiversity, community composition, coastal ecosystem, phytoplankton, ice algae

1. Introduction

Changes in sea-ice cover are affecting marine ecosystem function throughout the Arctic (Meier et al. 2014; Niemi et al. 2024a). Coastal ecosystems, including Indigenous communities, are responding to changes in landfast and pack ice conditions and associated increases in anthropogenic activities facilitated by longer open-water periods. In the Canadian Arctic, the ice-free period has expanded by over a month in some coastal regions (Gully et al. 2023; Niemi et al. 2024b), and vessel traffic continues to increase due to industrial and community demands and ease of passage as the ice-impacted season diminishes (Arctic-Council 2009; Dawson et al. 2018). Understanding how primary producers respond to climate-driven environmental change is essential for predicting ecosystem-level effects and assessing the risks associated with coastal development.

The diversity and phenology of ice algae and phytoplankton play an integral role in all Arctic marine ecosystems, with

consumers having greater access to primary producer resources on Arctic shelves, supporting coastal food webs that include priority species for the community of Iqaluit, such as truncate softshell clams (*Mya truncata* Linnaeus, 1758) and anadromous Arctic Char (*Salvelinus alpinus* Linnaeus, 1758) that feed in marine waters. Ice algae are an early-season energy source for sympagic, pelagic, and benthic metazoan species (Gradinger and Bluhm 2010; McConnell et al. 2012; Pitusi et al. 2023). The life cycles of grazers are intended to coincide with the timing of phytoplankton blooms (Renaud et al. 2024). Both algal sources contribute significantly to the marine food web and trophic coupling that supports consumers and their predators. Ice algae and phytoplankton community composition can vary according to their habitat, with their growth constrained to the photic zone, which varies at different seasonal and spatial scales (Trudnowska et al. 2018; Benoit-Gagné et al. 2024). Ice algae grow in multiple sea ice habitats including surface melt ponds and pres-

sure ridges, interior brine channels, the bottom interstitial layer, and sub-ice water (Horner et al. 1992; Mundy and Meiners 2021). These habitats can support different species, such as *Pyramimonas* spp. Schmarda, 1849 in melt ponds where salinity is lower than in brine channels (Mundy and Meiners 2021). Arctic ice algae are largely concentrated in the bottom few centimeters of sea ice, in the interstitial or skeletal layer (Smith et al. 1990), and are usually dominated by pennate diatoms during the ice-algal bloom period (Róžańska et al. 2009; Croteau et al. 2022). Ice cracks, which are present during the seasonal breakup of first-year sea ice, can also provide a unique surface water habitat where both ice algae and phytoplankton may be present (Mundy and Meiners 2021).

Phytoplankton growth in open water responds rapidly to increasing seasonal irradiance, creating the spring bloom (Babin 2020). However, under-ice phytoplankton blooms have been increasingly documented in the Arctic as reduced snow cover, increased melt pond formation, and in some locations, thinner sea ice allow diverse phytoplankton communities to develop under the ice (Mundy et al. 2009; Lowry et al. 2014; Ardyna et al. 2020). The duration and magnitude of the spring bloom are largely controlled by the availability of inorganic nutrients and grazing pressure in the surface layer (Leu et al. 2011, 2015; Babin 2020), which shape the seasonal and interannual variability in phytoplankton community composition. For example, taxa such as coccolithophores and flagellates can efficiently utilize low nutrient concentrations, thereby increasing their dominance within the phytoplankton community towards the end of the bloom period in Arctic waters (Ardyna and Arrigo 2020).

The current study provides a multi-year assessment of sea-ice algal and phytoplankton species diversity in Frobisher Bay near Iqaluit, Nunavut, across sea-ice and open-water habitats that reflect seasonal gradients critical to ecosystem function, as well as environmental gradients in adjacent inlets with differing human impacts. This research was needed to improve knowledge of coastal primary producer biodiversity in the Canadian Arctic given the paucity of studies, especially those that inform both seasonal and interannual variability. In addition, this study was conducted from 2018 to 2022 during the construction of a deep-water port for the community of Iqaluit, providing a benchmark of the ice algal and phytoplankton community composition and diversity needed to assess potential impacts related to port and other coastal development. This biodiversity assessment expands our knowledge of harmful algal species, a concern for coastal communities in the Canadian Arctic (e.g., Dhifallah et al. 2022; Schiffrine et al. 2024) and supports future detection of non-indigenous harmful algae associated with shipping activity (Chan et al. 2019; Dhifallah et al. 2022). Knowledge of the spatio-temporal distribution of these taxa can help identify potential harmful effects on coastal food webs (Gao et al. 2019; Lefebvre et al. 2022; Pućko et al. 2023), including locally sourced country foods such as clams and mussels (Amiraux et al. 2021).

The specific objectives of this study are to (1) provide an up-to-date record of sea-ice algae and phytoplankton diversity for inner Frobisher Bay, and (2) assess seasonal and interannual variability in diversity and community composition in differ-

ent habitats, including adjacent inlets with different levels of human activity. We hypothesize that coastal habitats will reflect offshore diversity of sea-ice and open-water habitats, and local influences of river inflow will alter community composition near Iqaluit relative to the adjacent inlet. This study provides information on primary producer spatio-temporal variability, including harmful algal species, needed for predicting and managing anthropogenic impacts in an Arctic coastal ecosystem.

2. Materials and methods

2.1. Study site

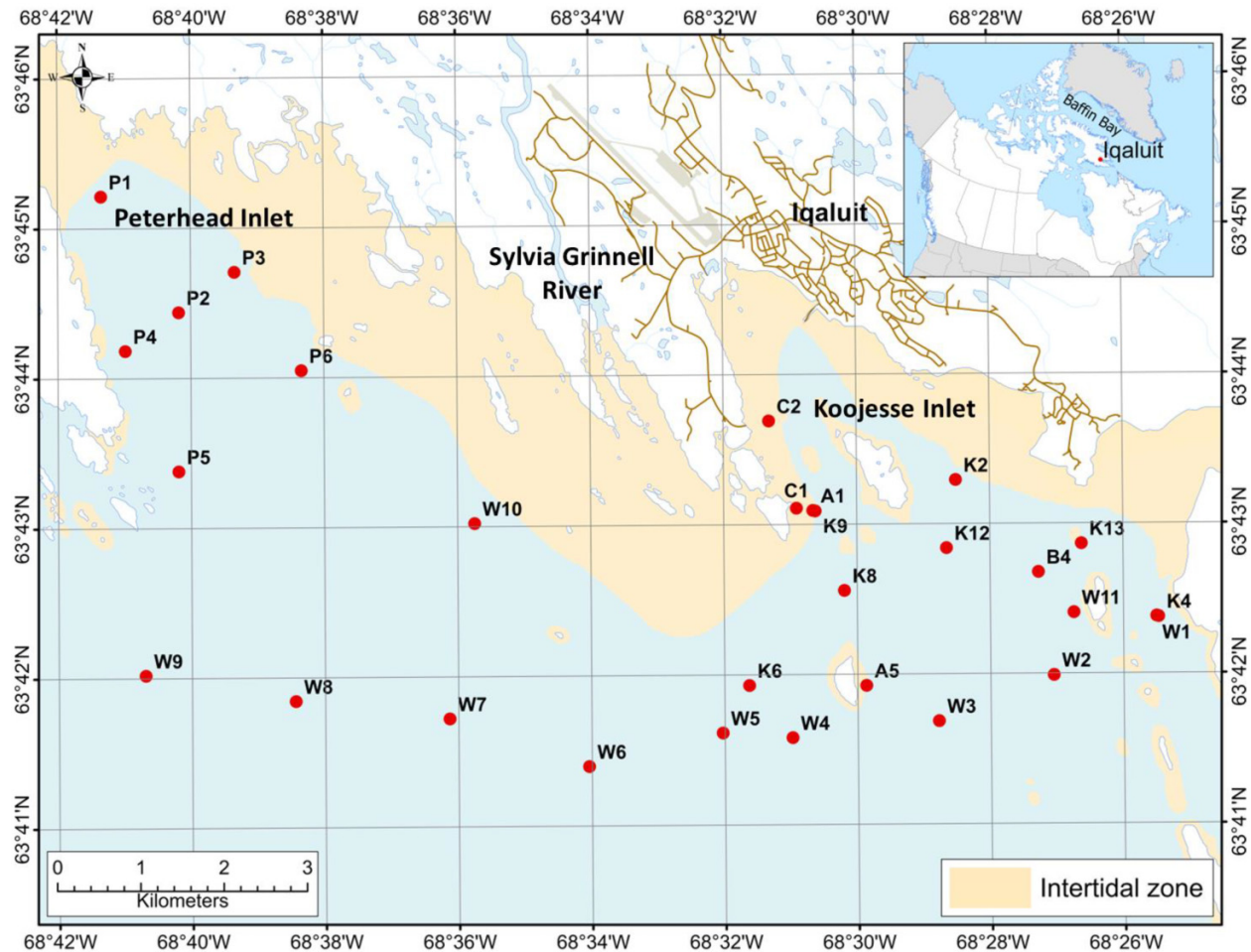
This study is part of the Iqaluit Coastal Environmental Baseline Project (Fisheries and Oceans Canada 2024) established, in part, to improve the documentation of biodiversity across trophic levels in Canadian coastal waters. Sampling was completed near the community of Iqaluit (Fig. 1), the capital of Nunavut, Canada, and home to approximately 8000 people. Iqaluit is in the eastern Canadian Arctic at the innermost part of Frobisher Bay on Baffin Island. During the study period, a deep-water port was being built to support economic development, improve marine infrastructure in the territory, and create more efficient and safe sealift/cargo operations. Frobisher Bay is typically covered with first-year ice from January to June. Transitional periods occur when the ice breaks up in late June or early July of each year and end when the bay freezes over in December or January. The inner bay also experiences extreme tides ranging from approximately 7 to 11.5 m. These large tides can move approximately 17 km³ of water in and out of the bay at an average speed of 1 m s⁻¹ (or 3.7 km h⁻¹) during one tidal cycle (Grainger 1975). All sampling sites were outside of the large intertidal zone, with an average station depth of 39 m (range 14 to 140 m) when measured at high tide.

2.2. Sampling stations

Sampling was conducted between 2018 and 2022 (Figs. 1 and S1) including ice-covered and open-water (July–October) periods. During the ice-covered period, ice core samples were collected in May 2018 and 2019 and in April 2021. The 2022 sea ice sampling extended over 15 weeks (February–June) to assess the progression of ice algal community composition at station A5 in Koojesse Inlet and station P3 in Peterhead Inlet (Fig. 1). Ice coring was accompanied by the collection of water 1 m below the sea ice. Phytoplankton from 1 m under the sea ice was also assessed during a total of 11 sampling events in 2018, 2019, and 2021. During the spring transition, narrow bands of open water are present when the ice starts to fracture. Surface water from such an ice crack was collected at two locations in June 2019.

To compare phytoplankton diversity (open-water period) between Koojesse Inlet (area of coastal development) and Peterhead Inlet (no coastal development), multiple stations, were sampled in 2019, 2020 and 2022 (Figs. 1 and S1). In Koojesse Inlet, stations A1, A5, and B4 were sampled repeatedly to provide an interannual and seasonal perspective of phytoplankton community composition. A1 (maximum depth =

Fig. 1. Map of sampling stations in Koojesse and Peterhead Inlet near Iqaluit, Nunavut, from 2018 to 2022. Basemap was created using CanVec topographic data in ArcGISPro 10.3.



43 m) was closest to the port construction, A5 (maximum depth = 46 m) was offshore from the port where the waters flow out of Koojesse Inlet, and B4 (maximum depth = 34 m) was located on the inflow side of the inlet near a community clam harvest area. Repeated sampling of stations in Peterhead Inlet occurred in 2022 only (Fig. S1).

2.3. Water column sampling

A SonTek CastAway CTD and RBRconcerto³ CTD were used to obtain profiles of temperature and salinity at each station. During the ice-covered period, snow depth and ice thickness were measured at each station. A minimum of 5 replicate measurements were made for snow depth and 3 for ice thickness. Secchi disk depths were also recorded during the open-water period. Water samples were collected using Niskin bottles, and subsamples were kept for inorganic nutrients, *in vivo* chlorophyll *a* fluorescence, and phytoplankton taxonomy.

Nutrient samples were collected in duplicate in 15 mL acid-washed Falcon tubes and the samples were frozen at -80°C until analyzed. Nitrate (NO_3^-), nitrite (NO_2^-), phosphate (PO_4^{3-}), and silicic acid ($\text{Si}(\text{OH})_4$) concentrations were determined using a Seal Analytical AutoAnalyzer 3 follow-

ing Grasshoff et al. (1999). Kanto certified reference material (www.kanto.co.jp) was used, and all analyses were performed by the Water Properties Laboratory at the Institute of Ocean Sciences, Sidney, BC.

In vivo chlorophyll *a* fluorescence of well-mixed duplicate water samples kept in the dark, was measured within 6 h of collection using the BLUE module (460 nm) of the Turner Designs Trilogy Fluorometer. The fluorometer was calibrated using a two-point calibration with Rhodamine WT dye (400 ppb) and milli-Q water, and μg chlorophyll *a* L^{-1} was estimated from the Relative Fluorescence Units. Recorded *in vivo* fluorescence, an index of chlorophyll *a* concentration, allowed comparison between stations and within seasons.

2.4. Sea-ice sampling

Ice algae samples were collected using a 9 cm internal diameter Kovacs Mark II coring system. Triplicate ice cores were sampled at each station to account for spatial heterogeneity. Given the known effects of snow cover on ice algae growth (Leu et al. 2015) and community composition, a coring area with uniform snow cover was selected for each sampling event. However, environmental variability did result in variable snow cover between sampling dates. The bottom 3 to

5 cm of the three cores were cut and combined in a clean, insulated container. In the lab, 1500 mL of 0.22 μm filtered surface seawater was added to the three cores, and they were allowed to melt overnight at room temperature in the dark following established protocols to minimize cell damage during melt (Garrison and Buck 1986). A 20 mL subsample of the melted core sample was retained for taxonomic analysis, noting the dilution factor associated with the added filtered seawater.

2.5. Algal abundance and taxonomic composition

Ice algae and phytoplankton samples were preserved with Lugol's solution and stored in the dark until analysis. Ice algae and phytoplankton were identified and enumerated using an inverted microscope (Zeiss Axiovert 10) at 400 $\times$ magnification. A brief survey at 200 $\times$ magnification was also completed to ensure that larger species were not missed. Preparation and counting followed the methods of Utermöhl (1958) and Lund et al. (1958). Subsamples of 0.2, 0.5, 3, or 5 mL were sedimented in a Utermöhl counting chamber and subsequently analyzed for the ice algae samples, while subsamples of 5 or 10 mL were used for the phytoplankton samples. Phytoplankton were enumerated along transects until a minimum of 400 cells were enumerated to achieve an accuracy of $\pm 10\%$.

Specimen identification was completed to the lowest taxonomic rank as possible. Accepted names were validated against AlgaeBase (Guiry and Guiry 2025) and World Register of Marine Species (WoRMS; Ah Yong et al. 2023) using custom R functions (<https://github.com/NicoSchiff/AlgaeBaseR>) and the worrms R package (version 0.4.3; Chamberlain and Vanhoorne 2023). Unknown cells were counted and numbered sequentially, with genus noted when possible, and the cells were photographed to document their distinguishing features. To identify potentially harmful taxa, the dataset was cross-referenced with the Intergovernmental Oceanographic Commission of the United Nations Educational, Scientific and Cultural Organization (IOC-UNESCO) taxonomic reference list (Lundholm et al. 2009; last accessed: 18 February 2025; <http://www.marinespecies.org/hab/>), which was retrieved using custom R functions (<https://github.com/NicoSchiff/AlgaeBaseR>). To further refine our list of potentially harmful species, taxa from Bates et al. (2019, 2020) were incorporated, notably including the ciliate *Mesodinium rubrum* Lohmann, 1908, which was retained due to its significant ecological role (Olsen et al. 2019; McKenzie et al. 2021). However, the dinoflagellate *Protoperidinium crassipes* (Kofoid) Balech, 1974 from Bates et al. (2020) was excluded, as this heterotrophic species functions more as a toxin vector than a direct toxin producer (e.g., Tillmann et al. 2009).

2.6. Statistical analyses

The similarities in phytoplankton community structure were assessed with the Bray–Curtis similarity index. Non-metric multidimensional scaling (nMDS) on a Bray–Curtis similarity matrix was used to visualize and identify possible clusters. Abundances of 17 taxonomic groups were in-

cluded in the analysis (Table S1): Bacillariophyta (including both centric and pennate diatoms), Dinophyceae (including both naked and thecate dinoflagellates), Chlorophyceae, Chrysophyceae, Cryptophyceae, Dictyochophyceae, Euglenophyceae, Prasinophyceae, Prymnesiophyceae, Raphidophyceae, unidentified flagellates, Cyanophyceae, heterotrophic protist group, Choanoflagellidea, and ciliates. Hellinger transformation was used to normalize the abundance data, enhancing compatibility with multivariate statistical analyses. A group-average cluster analysis was performed on the nMDS results to group stations with similar taxonomic composition. A similarity percentage (SIMPER) analysis was conducted on the transformed data to identify key taxonomic groups contributing to dissimilarities among clusters. Simpson diversity indices were calculated to assess species richness and evenness among stations. Species accumulation curves (SACs) were generated for each sample type to characterize whether sampling was sufficient to estimate the biodiversity of these areas (Fig. S2). The Michaelis–Menten model was fitted to the SACs to estimate asymptotic species richness, which provides insight into the completeness of species detection. This model was chosen for its ability to capture the asymptotic nature of species accumulation, offering a biologically meaningful upper limit that aligns with real-world sampling patterns better than linear models or non-parametric estimators.

Kruskal–Wallis tests were used to compare diversity indices among habitats, repeated stations, years, and inlets due to the non-parametric sampling design. If the number of groups was greater than two, pairwise comparisons were then made using Dunn's post-hoc test with Bonferroni correction to determine which pairs of groups differed significantly. All analyses and visualizations were performed in R (R version 4.4.2; R Development Core Team 2019) using the *vegan* (version: 2.0.0; Oksanen et al. 2020) and *ggplot2* (version: 3.5.1; Wickham 2016) packages.

3. Results

3.1. Ice and ocean conditions

Ice thickness at the time of sampling averaged 131 cm in 2018, 132 cm in 2019, 109 cm in 2021, and 118 cm in 2022 (Fig. S1). Snow cover varied among years and sampling dates, with the highest accumulation of snow at a sampling site occurring in 2018 (max 34.5 cm). Variability in Koojesse and Peterhead Inlet water masses during the open-water period (10 August to 1 September) in 2019, 2020 and 2022 is shown in Fig. S3. Variable conditions include freshening at stations A1, A5, and B4 in 2022 (Fig. 1), but not in Peterhead Inlet. Freshened surface waters were also evident at station A5 in September 2019 and 2022, with variable surface conditions occurring seasonally and interannually (Fig. S4).

Average open-water conditions for Koojesse Inlet (A1, A5, and B4) and Peterhead Inlet (P1–P6) stations are summarized in Table 1. During the study period, the warmest surface water occurred in Peterhead Inlet in 2022. In 2020, Secchi depth was on average 6 m deeper in Peterhead Inlet than Koojesse Inlet. In addition, the depth of maximum chlorophyll *a* flu-

Table 1. Average ($\pm$ standard error) open water ocean conditions at Peterhead Inlet (P1 to P6) stations and Koojesse Inlet (A1, A5, and B4) repeated stations in 2018–2022.

Year	T_{surf} ($^{\circ}\text{C}$)	S_{surf} (psu)	T_{mean} ($^{\circ}\text{C}$)	S_{mean} (psu)	Z_{sd} (m)	$Z_{\text{Chl Fluor max}}$ (m)	$\text{Chl}^{\text{Fluo}}_{\text{surf}}$ ($\mu\text{g L}^{-1}$)
P1 to P6							
2019	4.81 ± 0.37 ($n = 6$)	30.25 ± 0.47 ($n = 6$)	0.91 ± 0.34 ($n = 6$)	31.67 ± 0.08 ($n = 6$)	6.1 ± 0.33 ($n = 5$)	13.81 ± 3.21 ($n = 6$)	3.8 ± 0.84 ($n = 6$)
2020	3.46 ± 0.72 ($n = 6$)	30.67 ± 0.76 ($n = 6$)	1.35 ± 0.10 ($n = 6$)	32.06 ± 0.08 ($n = 6$)	13 ± 1.1 ($n = 5$)	8.77 ± 8.18 ($n = 6$)	1.1 ± 0.38 ($n = 6$)
2022	7.44 ± 0.61 ($n = 6$)	28.73 ± 0.70 ($n = 6$)	1.85 ± 0.34 ($n = 6$)	31.85 ± 0.13 ($n = 6$)	7.4 ± 0.20 ($n = 6$)	15.58 ± 1.01 ($n = 6$)	1.3 ± 0.15 ($n = 6$)
A1							
2018	2.16 ± 0.30 ($n = 10$)	29.58 ± 1.04 ($n = 10$)	1.27 ± 0.10 ($n = 10$)	31.87 ± 0.08 ($n = 10$)	nd	nd	nd
2019	3.20 ± 0.48 ($n = 9$)	30.76 ± 0.34 ($n = 9$)	0.79 ± 0.14 ($n = 9$)	31.88 ± 0.06 ($n = 9$)	6.1 ± 1.2 ($n = 10$)	12.94 ± 4.13 ($n = 9$)	7.5 ± 2.2 ($n = 10$)
2020	4.00 ± 0.73 ($n = 13$)	29.92 ± 0.72 ($n = 13$)	1.38 ± 0.13 ($n = 13$)	32.06 ± 0.05 ($n = 13$)	7.4 ± 0.70 ($n = 11$)	17.14 ± 3.49 ($n = 13$)	3.3 ± 0.73 ($n = 11$)
2021	3.95 ± 0.67 ($n = 12$)	26.88 ± 1.43 ($n = 12$)	1.61 ± 0.09 ($n = 12$)	31.95 ± 0.12 ($n = 12$)	6.6 ± 1.9 ($n = 12$)	9.24 ± 2.11 ($n = 12$)	5.5 ± 1.4 ($n = 12$)
2022	4.13 ± 0.75 ($n = 11$)	29.60 ± 1.04 ($n = 11$)	1.68 ± 0.10 ($n = 11$)	32.22 ± 0.04 ($n = 11$)	7.5 ± 0.78 ($n = 11$)	12.45 ± 3.22 ($n = 11$)	6.7 ± 1.9 ($n = 11$)
A5							
2018	2.28 ± 0.28 ($n = 10$)	30.20 ± 0.53 ($n = 10$)	1.25 ± 0.12 ($n = 10$)	31.88 ± 0.07 ($n = 10$)	nd	nd	nd
2019	2.86 ± 0.53 ($n = 12$)	28.39 ± 1.19 ($n = 12$)	0.67 ± 0.12 ($n = 12$)	31.83 ± 0.05 ($n = 12$)	6.8 ± 1.2 ($n = 10$)	14.94 ± 3.93 ($n = 12$)	6.5 ± 1.8 ($n = 10$)
2020	3.26 ± 0.46 ($n = 12$)	30.14 ± 0.59 ($n = 12$)	1.32 ± 0.17 ($n = 12$)	32.09 ± 0.05 ($n = 12$)	7.8 ± 0.70 ($n = 11$)	18.95 ± 4.08 ($n = 12$)	3.4 ± 0.77 ($n = 11$)
2021	3.20 ± 0.60 ($n = 11$)	28.56 ± 0.88 ($n = 11$)	1.63 ± 0.11 ($n = 11$)	32.05 ± 0.09 ($n = 11$)	7.6 ± 0.92 ($n = 12$)	10.36 ± 2.15 ($n = 11$)	4.6 ± 0.89 ($n = 12$)
2022	3.44 ± 0.48 ($n = 10$)	29.77 ± 0.67 ($n = 10$)	1.56 ± 0.08 ($n = 10$)	32.24 ± 0.02 ($n = 10$)	8.6 ± 0.93 ($n = 11$)	15.88 ± 2.84 ($n = 10$)	6.1 ± 1.8 ($n = 11$)
B4							
2018	2.29 ± 0.23 ($n = 10$)	30.70 ± 0.37 ($n = 10$)	1.47 ± 0.09 ($n = 10$)	31.76 ± 0.08 ($n = 10$)	nd	nd	nd
2019	3.33 ± 0.62 ($n = 10$)	30.42 ± 0.57 ($n = 10$)	0.98 ± 0.10 ($n = 10$)	31.76 ± 0.10 ($n = 10$)	7.2 ± 1.2 ($n = 10$)	6.75 ± 2.17 ($n = 10$)	3.8 ± 1.0 ($n = 10$)
2020	3.78 ± 0.67 ($n = 12$)	30.02 ± 0.87 ($n = 12$)	1.68 ± 0.15 ($n = 12$)	31.93 ± 0.10 ($n = 12$)	7.8 ± 0.66 ($n = 11$)	11.83 ± 2.59 ($n = 12$)	3.3 ± 0.74 ($n = 11$)
2021	3.63 ± 0.61 ($n = 12$)	29.17 ± 0.88 ($n = 12$)	1.83 ± 0.10 ($n = 12$)	31.87 ± 0.14 ($n = 12$)	7.8 ± 1.0 ($n = 12$)	7.88 ± 2.30 ($n = 12$)	5.6 ± 0.94 ($n = 12$)
2022	3.35 ± 0.45 ($n = 10$)	30.33 ± 0.67 ($n = 10$)	1.80 ± 0.13 ($n = 10$)	32.13 ± 0.06 ($n = 10$)	8.4 ± 0.84 ($n = 11$)	8.76 ± 2.70 ($n = 10$)	5.8 ± 1.8 ($n = 11$)

Note: Secchi depth and in vivo chlorophyll *a* fluorescence (Chl^{Fluo}) values represent discrete sampling. Temperature, salinity, and fluorescence values are derived from CTD casts. T_{surf} : average sea surface temperature; S_{surf} : average sea surface salinity; T_{mean} : temperature averaged throughout the water column; S_{mean} : salinity averaged throughout the water column; Z_{sd} : Secchi depth; $Z_{\text{Chl Fluor max}}$: maximum chlorophyll *a* depth; $\text{Chl}^{\text{Fluo}}_{\text{surf}}$: average sea surface (1 m) in vivo chlorophyll *a* value; variability in sample size (*n*) represents missing data; nd: no data.

Table 2. Mean abundance of dominant ice algae and phytoplankton and their frequency of occurrence by habitat type assessed between 2018 and 2022 in coastal water of Koojesse Inlet and Peterhead Inlet.

Taxon	Mean abundance (10 ³ cells L ⁻¹)	Habitat frequency of occurrence (%)
Sea ice (n = 50)		
<i>Nitzschia frigida</i>	22 000	100
<i>Navicula pelagica</i>	15 000	100
Unidentified flagellate spp. (2–5 µm)	8300	100
Unidentified flagellate spp. (5–10 µm)	7900	100
Pennate diatom sp. 6	7500	70
Under ice (n = 11)		
Unidentified flagellate spp. (2–5 µm)	11	100
Unidentified flagellate spp. (5–10 µm)	6.2	100
<i>Gymnodinium</i> / <i>Gyrodinium</i> spp. (10–20 µm)	2.9	91
<i>Chrysochromulina</i> spp. (2–5 µm)	1.7	82
Coccolithophyceae sp. (5–10 µm)	1.3	100
Ice crack (n = 2)		
<i>Thalassiosira</i> spp. (20–50 µm)	70	100
Unidentified flagellate spp. (2–5 µm)	55	100
<i>Fragilariopsis oceanica</i>	54	100
<i>Pyramimonas</i> cf. <i>nansenii</i>	30	100
Unidentified flagellate spp. (5–10 µm)	28	100
Open water (n = 164)		
<i>Chaetoceros</i> spp. (5–10 µm)	1800	100
<i>Chaetoceros</i> spp. (10–20 µm)	770	95
<i>Chrysochromulina</i> spp. (2–5 µm)	420	96
Unidentified flagellate spp. (2–5 µm)	270	100
Unidentified flagellate spp. (5–10 µm)	96	100

Note: n: number of samples.

orescence at A1, A5, and B4 was deeper on average, in 2020 (16 m) relative to other years of the study (11 m). In 2020, relative values of surface water in vivo chlorophyll *a* for A1, A5, and B4 were 30%–50% lower than other years of the study.

Dissolved inorganic nitrogen, NO₃⁻ + NO₂⁻, sampled in April or May at depths between 1 and 100 m below the sea ice ranged from 7.0 to 10.7 µmol/L, reflecting winter replenishment and pre-bloom conditions. The average coefficient of variation of the duplicate samples was 3.2%. NO₃⁻ + NO₂⁻ decreased to below detection (<0.03 µmol/L) by the end of the open-water sampling period (mid-August) indicating the transition to post-bloom conditions (Fig. S5). Silicic acid and phosphate concentrations were highest in spring, with Si(OH)₄ and PO₄ concentrations reaching as low as 0.11 and 0.15 µmol/L, respectively, during the phytoplankton bloom period (Fig. S5).

3.2. Phytoplankton dataset

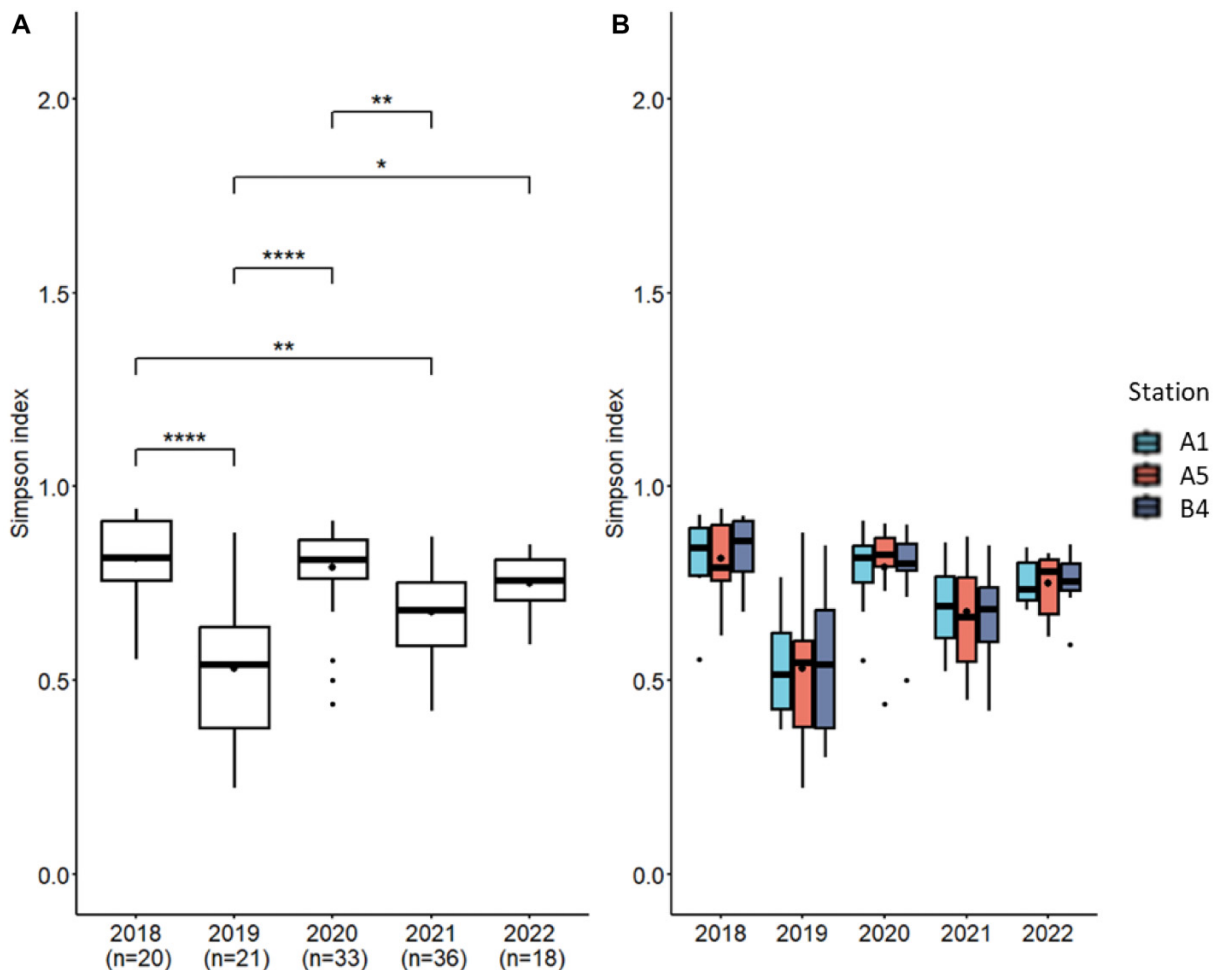
A total of 562 taxa were identified in this coastal assessment (Table S1). The frequency of occurrence indicated that the majority of taxa were rarely observed, with 129, 59, and 34 taxa occurring at one, two, or three stations, respectively (Table S1). In this study, sea ice, open-water and ice crack surface water had 140, 195, and 10 unique taxa, respectively. One hundred twenty-five taxa were common between sea ice and open-water habitats, whereas surface water samples from within the ice crack and from the open-water period

shared 132 common taxa. Species accumulation curves did not reach an asymptote for the sea-ice, open-water (bloom and post-bloom periods) or under-ice assemblages, suggesting that the total biodiversity of the study area has not yet been fully described (Fig. S2).

Freshwater taxa were found in all years and habitats, reflecting the influence of the adjacent Sylvia Grinnell River (Table S1, Fig. 1). Associated watershed freshwater taxa, including species of diatoms, dinoflagellates, and chlorophytes had a frequency of occurrence <1%–4.4% (Table S1). All occurrences of freshwater taxa were in Koojesse Inlet except for a single occurrence at station P6 (Fig. 1). Although freshwater taxa occurred infrequently, they were present in all months of open-water sampling, and notably absent from open-water samples in 2022 (data not shown).

Marine diatoms numerically dominated sea-ice and open-water communities (Table 2), specifically *Nitzschia frigida* Grunow, 1880 and *Navicula pelagica* Cleve, 1896 in the sea ice and *Chaetoceros* spp. (Ehrenberg, 1844) (size class 5–10 µm) in the surface water. The only other taxonomic group to contribute more than 5% of ice algal/phytoplankton abundance during the sampling period were the 2–5 and 5–10 µm size classes of unidentified flagellates. Surface water in the ice crack habitat was dominated by a large centric diatom (*Thalassiosira* spp. (Cleve, 1873) 20–50 µm size class), distinct from the under-ice or open-water surface water and was the only habitat to have a notable presence of prasinophytes (*Pyrami-*

Fig. 2. Temporal variation in the Simpson diversity indices of phytoplankton (A) by year and (B) for the repeated sampling stations in Koojesse Inlet (20 July to 15 October, 1 m surface samples). In (A), significant differences are denoted by asterisks, * ($p < 0.05$), ** ($p < 0.01$), *** ($p < 0.001$), and **** ($p < 0.0001$). Error bars represent standard error ($\pm$ SE).



monas cf. *nansenii*). The under-ice surface water was the only habitat not numerically dominated by diatoms but rather a mix of potentially heterotrophic or mixotrophic taxa including flagellates, dinoflagellates, and small haptophytes (Table 2). The ice and snow cover resulted in under-ice abundances one to two orders of magnitude lower than in open-water surface water communities.

Six species known to produce toxins were identified (Table S1), including two dinoflagellates (*Protoceratium reticulatum* (Claparède & Lachmann) Bütschli, 1885 and *Prorocentrum cordatum* (Ostenfeld) J.D.Dodge, 1976). The Dictyochophyceae *Octactis speculum* (Ehrenberg) F.H.Chang, J.M.Grieve & J.E.Sutherland, 2017 and the dinoflagellate *Protoceratium reticulatum* were observed in only one surface water and one sea ice sample, respectively. *Chaetoceros convolutus* Castracane, 1886, *C. debilis* Cleve, 1894, *Leptocylindrus minimus* Gran, 1915, and the ciliate *Mesodinium rubrum* were found only in surface water with a frequency of occurrence between 5% and 24% (Table S1). *Phaeocystis pouchetii* (Hariot) Lagerheim, 1896 was identified in both sea ice and surface water samples from Koojesse and Peterhead Inlet (60% frequency of occurrence), evident in its palmelloid (i.e., colonial) stage (Table S1). This potentially harmful species did

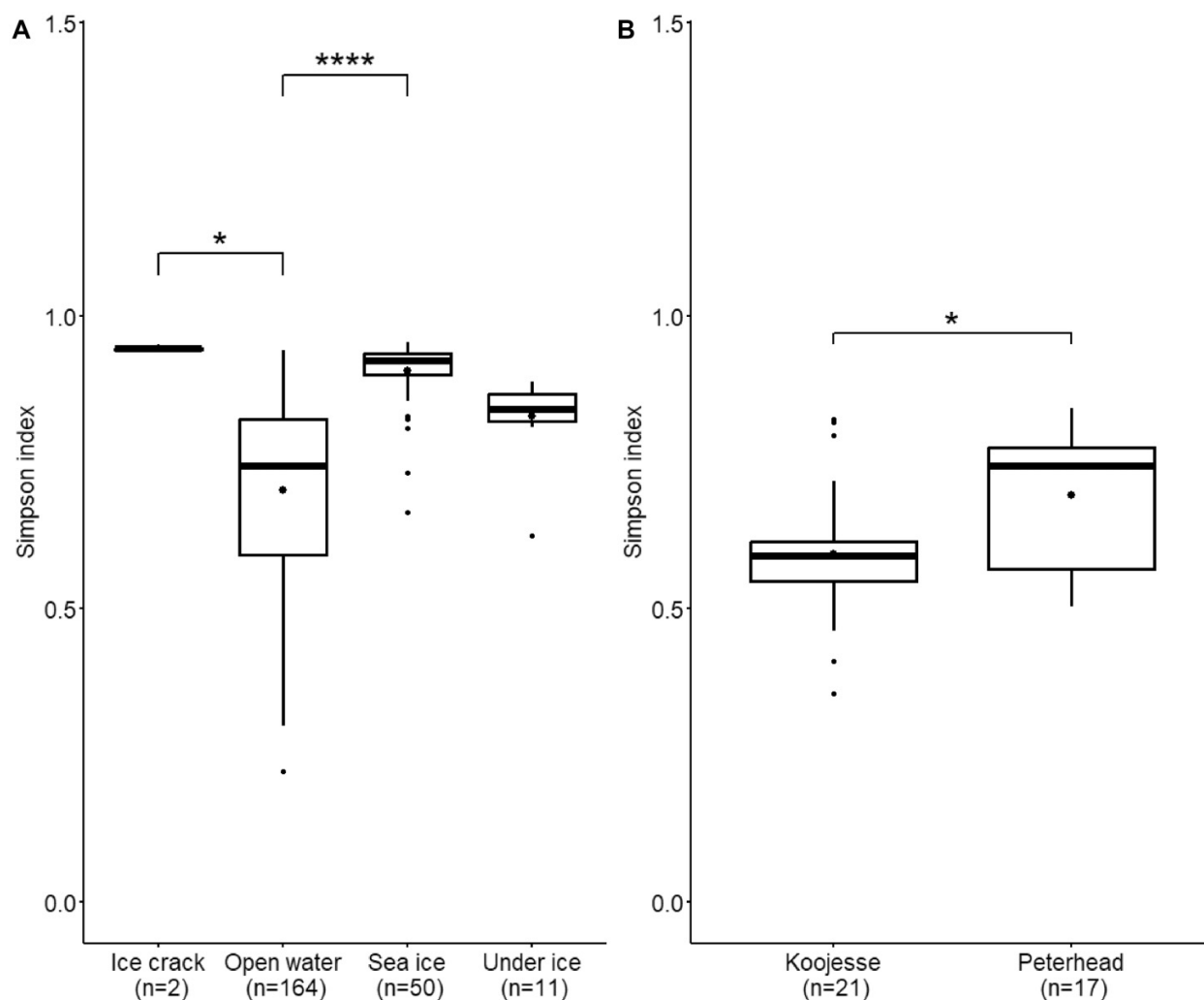
not reach bloom levels, as its mean surface water abundance was only 57×10^3 cells L^{-1} .

3.3. Temporal and spatial variability

Interannual variability of surface phytoplankton diversity in Koojesse Inlet (Fig. 2, Table S2) was evident with significantly lower diversity in 2019 compared to 2018, 2020, and 2022 (Dunn's test, $Z = -5.16$ to 5.22 , $p < 0.05$, Bonferroni-adjusted). Simpson diversity was highest in 2018 but was not significantly different from that in 2020 or 2022. The interannual variability in diversity was consistent among each of the three repeated sampling stations (Fig. 2B). Interannual variability in sea-ice algal diversity was only significantly different between 2019 and 2022 (Dunn's test, $Z = 2.91$, $p < 0.05$, Bonferroni-adjusted; Fig. S6), with higher diversity in 2022, when sampling effort ($n = 27$) was three-times higher than in 2019 and ice sampling extended over the longest period in the study, from February 16 to June 1 (Fig. S1).

In the different habitats assessed (Fig. 3A), Simpson diversity averaged 0.94, 0.91, 0.83, and 0.70 for ice crack, sea ice, under-ice water, and open-water, respectively. Species diversity of the ice crack (Dunn's test, $Z = -2.87$, $p < 0.05$, Bonferroni-adjusted) and sea-ice (Dunn's test, $Z = 9.50$,

Fig. 3. Simpson diversity indices for (A) sea ice algae/phytoplankton by habitat type (2018 to 2022) and (B) temporally paired open-water (8 August to 1 September) phytoplankton by Inlet in 2019, 2020, and 2022. Significant differences denoted by asterisks, * ($p < 0.05$) and **** ($p < 0.0001$).



$p < 0.0001$, Bonferroni-adjusted) habitats were significantly higher when compared to the open-water surface habitat. Simpson diversity was not significantly different between the sea-ice and under-ice habitats (Dunn's test, $Z = -2.33$, $p = 0.12$, Bonferroni-adjusted) or between the under-ice and open-water surface habitats (Dunn's test, $Z = 2.44$, $p = 0.088$, Bonferroni-adjusted). A comparison of the adjacent inlets (Fig. 3B) indicates significantly higher phytoplankton diversity in Peterhead Inlet than in Koojesse Inlet for open-water surface samples (8 August to 1 September) collected in 2019, 2020, and 2022 (Kruskal-Wallis test, $H = 2.04$, $df = 1$, $p < 0.05$).

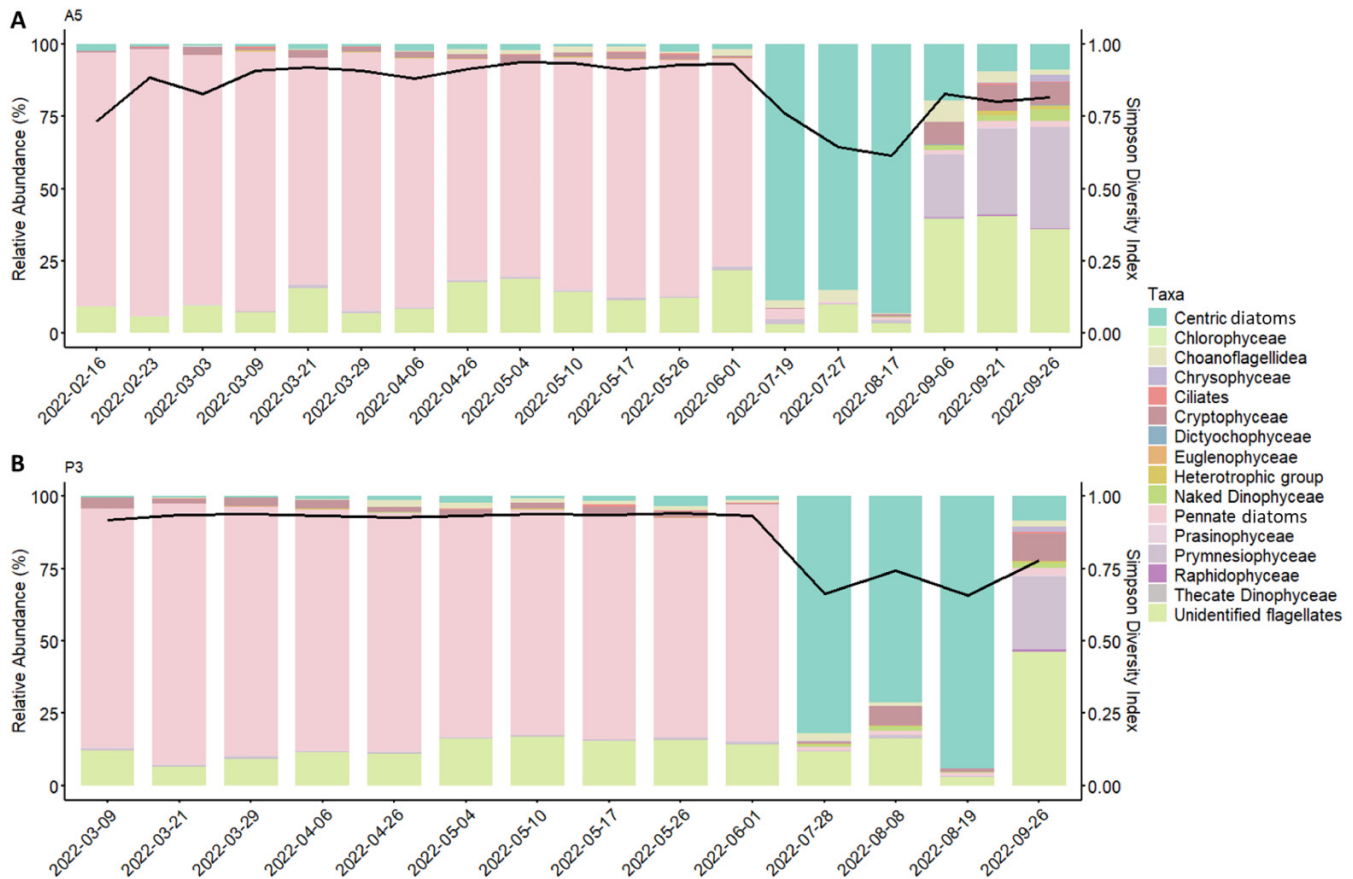
The seasonal variability of major taxonomic groups in Peterhead (station P3, Fig. 4A) and Koojesse (station A5, Fig. 4B) inlets shows a clear progression from pennate diatom to centric diatom-dominated bloom communities during the 2022 sampling period. Relative abundances are similar between inlets, with notably more Cryptophyceae in Peterhead Inlet on 8 August 2022. The relative abundance of the sea-ice community, spanning February to early June, shows small increases in heterotrophic communities including flagellates, ciliates

and choanoflagellidea. The extended duration of sampling captured the transition to a flagellate and Prymnesiophyceae dominated assemblage in September in the nutrient replete surface waters. In both inlets, open-water diversity (Figs. 3A and 4) was lower than the ice algal and post-bloom (September) communities given the dominance of a few taxa, with corresponding lower evenness in the July and August samples (Table S2). During the 2022 sampling, phytoplankton taxonomy was assessed at the chlorophyll maximum depth (Table 1) in addition to the surface water ($n = 28$ paired samples). Although only surface taxonomy is reported herein for consistency with other years of sampling, a comparison of the 2022 samples revealed no significant difference in phytoplankton diversity between the surface and chlorophyll maximum depths ($t = -0.587$, $df = 50.7$, $p = 0.56$, data not shown).

3.4. Community assemblages

Cluster analyses revealed three distinct assemblages reflecting the phenology of ice algae and phytoplankton (Figs.

Fig. 4. Relative abundance of taxa groups and Simpson diversity indices for stations (A) A5 and (B) P3 in 2022. Sea ice samples were collected from February to June and phytoplankton samples were collected from July to September for this time series.



5 and S7). Herein, we refer to the clusters as the open-water bloom, under ice/transitional, and sea-ice assemblages. The open-water bloom assemblage (cluster 1) includes the highest open-water abundances reaching a maximum of 3.1 , 12 , 6.4 , 20 , and 14×10^6 cells L^{-1} in 2018, 2019, 2020, 2021, and 2022, respectively. This assemblage was dominated by centric diatoms, specifically *Chaetoceros* spp. ($5\text{--}10\ \mu\text{m}$ and $10\text{--}20\ \mu\text{m}$ size classes). The under-ice/transitional assemblage (cluster 2) represents both early season under-ice taxa, and phytoplankton taxa at different stages of transition following the open-water bloom. This assemblage is dominated by Prymnesiophyceae (e.g., *Chrysochromulina* spp. (Lackey, 1939) ($2\text{--}5\ \mu\text{m}$)), with centric diatoms (e.g., *Chaetoceros* spp. ($5\text{--}10\ \mu\text{m}$)) and under-ice unidentified flagellates spp. ($2\text{--}5\ \mu\text{m}$) also characterizing this temporally diverse assemblage. The sea-ice assemblage (cluster 3, Fig. 5) is dominated by pennate diatoms (e.g., *Nitzschia frigida* and *Navicula pelagica*). SIMPER analysis revealed the highest average dissimilarity between the under-ice/transitional and sea-ice assemblages (45%) with diatoms contributing 21%–47% of the dissimilarity between assemblages (Table 3). The same five taxonomic groups (Table 3) explained over 5% of the dissimilarity between the open-water bloom and under-ice/transitional assemblages and between the under-ice/transitional and sea-ice assemblages, with the addition of naked Dinophyceae when the open-water bloom and sea-ice assemblages are compared. Groups contributing

over 5% represented 70%–77% of the total dissimilarity between assemblages.

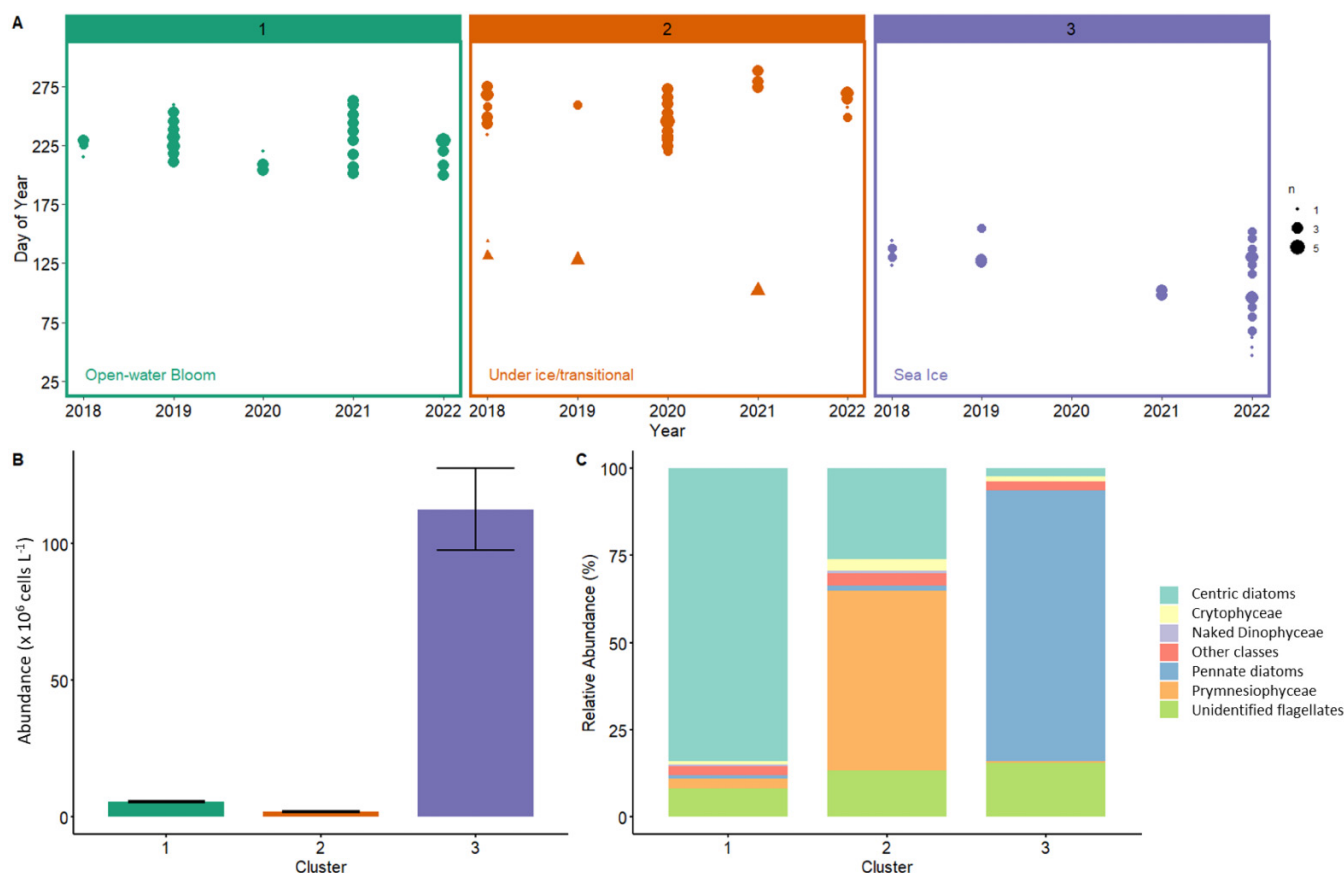
Relative abundance of the taxonomic groups in the open-water bloom and sea-ice assemblages shows greater seasonal than interannual variability (Fig. 6A, 6C). In comparison, the under-ice/transitional assemblage has notable differences between years reflecting interannual variability in bloom seasonality (Fig. 6B). In contrast to the *Chaetoceros* spp. dominated open-water bloom assemblage, post-bloom Prymnesiophyceae *Chrysochromulina* spp. ($2\text{--}5\ \mu\text{m}$ size class) and unidentified flagellates both contributed significantly to the dissimilarity between the open-water bloom and under-ice/transitional assemblage (Table 3). The two distinct sampling events in the sea ice cluster in 2019 indicate the in-situ production and/or advection of centric diatoms from the surface water of ice cracks (Fig. 6C). In contrast, pennate diatoms strongly differentiate the sea-ice assemblage with variable contributions of unidentified flagellates especially in 2018 and 2019 (Fig. 6C, Table 3).

4. Discussion

4.1. Diversity

Koojesse Inlet, home to the only deep-water port in the eastern Canadian Arctic, is at high risk for the

Fig. 5. (A) Temporal distribution of assemblages, and (B) mean abundance and (C) relative abundance of taxa groups contributing up to 75% dissimilarity based on SIMPER analysis in the open-water bloom (cluster 1-green), under ice (Δ)/transitional (cluster 2-orange), and sea ice (cluster 3-purple) assemblages. n = number of stations, error bars represent standard error ($\pm$ SE).



introduction of non-indigenous species (Chan et al. 2012, 2013). Some of these species have the potential to be harmful due to their production of toxins or blooms, which can disrupt the flow of energy to consumers (Sampei et al. 2021). The Iqaluit deep-water port construction, increased vessel activity (Dawson et al. 2018), and population growth associated with ongoing coastal development highlighted the need for improved ecosystem knowledge, including the assessment of current diversity baselines (Fisheries and Oceans Canada 2024) against which changes and potential stressors could be measured in this Arctic coastal ecosystem. Sampling across multiple temporal scales documented interannual variability in diversity (Fig. 2) without a clear trend between 2018 and 2022. Unexpectedly, open-water surface diversity was significantly higher in Peterhead Inlet (Fig. 3B), despite greater river and anthropogenic influences in Koojesse Inlet. Improved understanding of coastal circulation within inner Frobisher Bay may help explain the distribution of diversity in the adjacent inlets.

This study revealed that ice-associated and surface water diversity were dominated by rare taxa that occur infrequently and contribute little to the total community abundance. This finding is consistent with global patterns of marine phytoplankton biodiversity (Ignatiades and Skretas 2014; Laraib et al. 2024). Abundant taxa influenced spatial, seasonal, and in-

terannual variability in community composition (Figs. 4 and 6) although trends in relative abundance are not greatly affected by rare occurrences. In this study, taxa observed from three sampling events or fewer, comprise 40% of the total taxa. These species may influence the size-abundance relationship of the community, contributing to morphologically related functional diversity of the coastal system (Laraib et al. 2024). Advection and mixing related to the high tidal cycle of inner Frobisher Bay (Hsiao 1992a) could potentially increase the diversity of rare species (Villa Martín et al. 2020) and influence their detection and impact at this port location compared to other Arctic coastal zones.

The current study adds approximately 130 species-level identifications (Table S1) relative to earlier (1970–1980s, 2015, 2019) known taxonomic assessments in inner Frobisher Bay that included ice algae (Hsiao 1979; Grainger and Hsiao 1982; Hsiao 1992a) and phytoplankton (Hsiao 1979; Grainger and Hsiao 1982; Hsiao and Pinkewycz 1983, 1984, 1985; Hsiao 1992a, 1992b; Dhifallah et al. 2022) taxonomy. With the expanded knowledge of taxa present, the asymptote of accumulation curves was still not reached (Fig. S2). Similar to other taxonomic assessments, multiple identifications could only be resolved to class (Table S1), such that additional species could be identified with the use of other taxonomic tools, including sequence-based approaches (Ribeiro et al. 2024).

Table 3. Ranked taxa contributing more than 5% dissimilarity (SIMPER analysis) between the open-water bloom (cluster 1), under-ice/transitional (cluster 2), and sea-ice (cluster 3) assemblages.

Cluster 1 versus Cluster 2				
Average dissimilarity: 37.18%				
Taxa	Average abundance (Cluster 1)	Average abundance (Cluster 2)	Diss./SD	Contribution %
Centric diatoms	0.58	0.61	1.29	21.39
Prymnesiophyceae	0.27	0.43	1.32	18.69
Pennate diatoms	0.28	0.17	0.79	15.12
Unidentified flagellates	0.39	0.37	1.17	8.93
Cryptophyceae	0.14	0.15	1.22	6.04
Naked dinophyceae	0.11	0.09	1.06	5.24
			Cumulative %	75.41
Cluster 1 versus Cluster 3				
Average dissimilarity: 43.64%				
Taxa	Average abundance (Cluster 1)	Average abundance (Cluster 3)	Diss./SD	Contribution %
Pennate diatoms	0.28	0.52	1.15	23.73
Centric diatoms	0.58	0.40	1.24	23.21
Prymnesiophyceae	0.27	0.16	1.10	12.06
Unidentified flagellates	0.39	0.39	1.25	8.76
Naked Dinophyceae	0.11	0.05	1.16	5.16
Cryptophyceae	0.14	0.16	1.31	5.05
			Cumulative %	77.97
Cluster 2 versus Cluster 3				
Average dissimilarity: 45.02%				
Taxa	Average abundance (Cluster 2)	Average abundance (Cluster 3)	Diss./SD	Contribution %
Pennate diatoms	0.17	0.52	1.13	23.61
Centric diatoms	0.61	0.40	1.41	22.46
Prymnesiophyceae	0.43	0.16	1.34	17.97
Unidentified flagellates	0.37	0.39	1.34	7.65
Cryptophyceae	0.15	0.16	1.31	5.24
			Cumulative %	76.92

Note: Average abundances (based on Hellinger transformed data), ratio (dissimilarity/standard deviation–Diss./SD), and percentage contribution to dissimilarity are included.

We found no difference in phytoplankton diversity between the surface and chlorophyll *a* maximum depth in 2022. However, Hsiao (1992b) found that phytoplankton diversity exhibited vertical variation when assessed at a single station near Iqaluit. Nevertheless, the evenness of the species was uniform throughout the water column. In addition, community composition may vary over a tidal cycle (Hsiao 1992a). Consequently, in the strong tidally influenced coastal waters of inner Frobisher Bay, using a single monitoring depth to assess phytoplankton diversity may be limiting, even though it could reasonably represent the most abundant species and the phenology of key food web contributors.

Hsiao (1992a) found that 16 taxa from ice and water samples were consistent contributors to more than 5% of the community in inner Frobisher Bay. From the sea-ice community of this study, only pennate diatoms including *Nitzschia frigida* and *Navicula pelagica* and unidentified flagellates contributed to more than 5% of the community in each year. Whereas

only *Chaetoceros* spp., *Chrysochromulina* spp. and unidentified flagellates spp. contributed more than 5% of the surface water community. Such dominance by a small number of taxonomic groups was reflected in decreased diversity during the bloom period relative to under-ice and post-bloom communities (Figs. 3A and 4). These dominant taxa represent a potential focal monitoring group to assess shifts in phenology as well as key prey for herbivorous copepods and amphipods (e.g., *Themisto libellula* Lichtenstein, 1822) that are dominant contributors to the diets of Arctic Char and other coastal fish in inner Frobisher Bay (Rauf et al. 2025).

From a monitoring perspective, the presence of harmful phytoplankton is also of interest given potential impacts on food web function and species health (Amiriaux et al. 2021; Schiffrine et al. 2024). This study identified the prevalence of *Phaeocystis pouchetii*, a species that can form harmful algal blooms causing hypoxic benthic waters (Smith and Trimbom 2024), and is already known to be increasingly dominant in

Fig. 6. Interannual and seasonal variation in the relative abundance of phytoplankton in the (A) open-water bloom period (cluster 1), (B) under-ice/transitional (cluster 2), and (C) sea-ice (cluster 3) assemblages. Each bar represents a sampling event in the years indicated. Sampling events span from July–September, April–May/August–October, and February–June for the bloom, under ice/transitional, and ice assemblages, respectively.



Arctic waters (Orkney et al. 2020). However, there was no evidence of *P. pouchetii* bloom formation in this study. Species capable of producing toxins occurred infrequently (Table S1) such that documenting their seasonal progression or potential impact is challenging. Dhifallah et al. (2022) detected two potential toxin producing dinoflagellates in Koojesse Inlet: *Protoceratium reticulatum* in 2015 and *Dinophysis acuminata* (Claparède and Lachmann, 1859) in 2019. *Protoceratium reticulatum* was observed in a single sea ice sample in the current study but not *D. acuminata*. However, *Prorocentrum cordatum* was observed in four surface water samples, a species not recorded in the study of Dhifallah et al. (2022). Given the infrequent occurrence of potentially harmful or toxic species, detailed taxonomic studies are needed to document new or repeated occurrences, as well as the production of harmful species at meaningful spatial and temporal scales.

4.2. Seasonality

In Koojesse and Peterhead Inlet, seasonal variability and community assemblages reflect the transitions from ice algal to phytoplankton blooms (Table 2, Fig. 6), rather than coastal-station or inlet-scale variability (Figs. 3 and 4). Seasonal vari-

ability in community composition (Fig. 4) follows the phenology of Arctic primary producers transitioning from an ice-covered habitat to an open-water habitat (Croteau et al. 2022; Benoit-Gagné et al. 2024), and from nutrient-repleted to nutrient-depleted conditions in surface waters (Fig. S5, Ardyna and Arrigo 2020). Diatom-dominated communities were evident through taxonomy and the drawdown of silicic acid in surface waters, a macronutrient essential for diatom growth.

Sampling events included in the open-water bloom assemblage were few in 2018 and 2020, with most open-water events corresponding to the post-bloom transitional assemblage (Fig. 5A), suggesting an earlier start of the phytoplankton bloom in those years. An earlier bloom is supported by the deeper chlorophyll *a* maximum and Secchi depths, along with lower in vivo chlorophyll *a* measurements during the open-water period in 2020 (Table 1). The apparent shift in bloom seasonality resulted in a higher presence of flagellates in July 2020 (Fig. 6A) and a higher presence of Prymnesiophyceae in August 2018 and 2020 (Fig. 6B), relative to other years of this study, contributing to observed variability in the open-water bloom and under ice/transitional assem-

blages. Additional years of sampling would better constrain the identification of early versus expected timing of the open-water phytoplankton bloom in inner Frobisher Bay, in order for bloom timing to act as an indicator of potential disruptions in ecosystem energy flow (Renaud et al. 2024).

The peak of the ice algal and phytoplankton bloom is a transient condition common to the extreme seasonality experienced by Arctic ecosystems. In this coastal study, the presence of freshened surface water (Figs. S3 and S4) from ice melt, river output, and coastal runoff provides seasonal or event-based habitat for freshwater and brackish taxa. Freshwater taxa were infrequently observed in all open-water months of this study (Table S1) and were not specifically associated with the freshet of the Sylvia Grinnell River. Their presence constitutes a transient allochthonous contribution to coastal diversity within Koojesse but not Peterhead Inlet, reflecting the inflow and local dispersion of the Sylvia Grinnell River.

Ice cracks also represent a seasonally transient, primarily autochthonous, contribution to diversity. The surface water of the ice cracks hosted the highest level of diversity (149 taxa in the two samples, Fig. 3A) with a distinct community within the sea-ice assemblage (Fig. 6C). The 10 ice crack taxa that were not identified in any other ice or water sample from this study included *Pyramimonas* spp., cells similar to *Dinobryon sertularia* (Ehrenberg, 1834), and *Euglena* spp. (Ehrenberg, 1830) (size class 10–20 µm) that may inhabit fresh or brackish environments. Diversity within the ice crack also included the coastal presence of taxa previously recorded in offshore studies of the western Canadian Arctic, e.g., *Laboea strobila* (Lohmann, 1908) (Jiang et al. 2013) and unidentified species of the genera *Diploneis* Ehrenberg ex Cleve, 1894, *Coscinodiscus* Ehrenberg, 1839, *Navicula* Bory, 1822, and *Tetraselmis* F. Stein, 1878. Distinct communities are known to develop during ice melt in surface melt ponds and melt layers directly below the sea ice (Mundy et al. 2011), as well as through the physical concentration of cells around sea ice structures (Fernández-Méndez et al. 2018). This sampling took place when the snow was melting, and river water was slowly flowing beneath the sea ice. The freshwater trapped under the sea ice may have flowed and pooled within the cracks, as evidenced by a water surface salinity near 15 psu (data not shown), concentrating cells from the surrounding area.

4.3. Community assemblages

In the current study, the sea-ice algal and open-water blooms were numerically dominated by *Nitzschia frigida* and *Chaetoceros* spp., respectively (Table 2), representing the expected community structure for coastal and offshore Arctic ecosystems (Leu et al. 2015; Mundy and Meiners 2021). This suggests that significant community restructuring in response to sea-ice change or potential port-related species introductions has not occurred in recent years. Ice algae and phytoplankton assemblages exhibited spatial homogeneity (Fig. 6), integrating known small-scale variability in ice communities under differing snow cover (Róžańska et al. 2009; Duncan et al. 2024) and potential coastal patchiness of Arctic phytoplankton (Trudnowska et al. 2022). This heterogeneity

suggests that the repeated sampling at stations A1, A5, and B4 in Koojesse Inlet (Fig. 1) is sufficient to monitor community assemblages in the vicinity of the deep-water port.

Although the study area is a diatom dominated ecosystem it is interesting to note that only unidentified flagellates had 100% frequency of occurrence in all habitats (Table 2) suggesting that the ecosystem role of this functionally diverse group should not be overlooked. Diatoms, more so than the unidentified flagellates, differentiated the observed assemblages (Table 3, Fig. 6) and would be expected to facultatively support the diet of zooplankton in ice-covered and open-water conditions (Kohlbach et al. 2022; Kaiser et al. 2025). The high diatom-driven abundance of the sea-ice assemblage (Fig. 5B) was likely supported by strong tidal forcing, which sustains photosynthesis by resupplying nutrients to the brine channel and interstitial assemblages (Gosselin et al. 1985; Mundy et al. 2025). In contrast the under-ice/transitional assemblage included potential mixotrophic taxa (e.g., *Chrysochromulina* spp.), which may increase heterotrophic feeding in low light conditions under the sea ice (Stoecker and Lavrenko 2018), as well as phytoplankton adapted to post-bloom nutrient levels. Taxa such as *Dinobryon* spp. Ehrenberg, 1834, *Monosiga* spp. Kent, 1878, and Cyanophyceae, were absent or only present at low abundances during the open-water bloom but were notable during the post-bloom period. The detection of these groups in open waters (Fig. 6B) may be due to their ability to thrive in waters with low concentrations of nitrate (flagellates) or dissolved silicon (prymnesiophytes) (Ardyna and Arrigo 2020), which facilitates their production and detection compared to the prevalent diatoms, which require higher nutrient availability.

The dominant taxa in this coastal study differed from those in recent sequence-based assessments of microalgae in offshore Baffin Bay (Ribeiro et al. 2024). For example, Ribeiro et al. (2024) identified the centric diatom *Melosira arctica* Dickie, 1852 and the pennate diatom *Pseudo-nitzschia seriata* (Cleve) H. Peragallo, 1899 as indicators of offshore marginal ice zone taxa. However, these taxa were not dominant, nor a differentiated assemblage in the current coastal study (Tables 2 and 3). Furthermore, the picoeukaryote *Micromonas* Manton and Parke, 1960, an early bloomer observed in the offshore study (Ribeiro et al. 2024), was not detected by the light microscopy method employed in the current study. These results underscore the importance of coastal-focused studies in identifying regional indicator species and the necessity of employing multiple methods to comprehensively monitor diversity.

5. Conclusion

Changes in the Arctic affect the foundation of the marine ecosystem, including the phenology, community composition, and diversity of ice algae and phytoplankton. Because they respond rapidly to environmental variability (Ardyna et al. 2020; Forgereau et al. 2023; Duncan et al. 2024), ice algae and phytoplankton can serve as early indicators of anthropogenic impacts in developing coastal ecosystems, when monitored appropriately. This work provides a current benchmark of sea-ice algae and phytoplankton diversity, including species of potential concern, in a developing Arc-

tic coastal community. The prevalence of rare taxa indicates that monitoring for new introductions or potentially harmful taxa continues to require detailed taxonomic studies over extended spatial scales. However, monitoring to inform diversity related to food web function can be focused on scale, given the numerical dominance of a few taxa that differentiate assemblages, and the homogeneity of community composition observed between stations and inlets. In the vicinity of the Iqaluit port, seasonal observations are needed to ensure that phenological variation is not incorrectly attributed to port-related impacts, as phytoplankton bloom seasonality is evident.

A comprehensive description of surface-associated communities during both the ice-covered and open-water periods highlights the need for further assessment of the environmental drivers of diversity and community composition. This assessment should consider the significant tidal influence of inner Frobisher Bay, as tides may affect the diversity of ice algae and phytoplankton relative to other Canadian Arctic coastal locations, including ports. This multi-year and seasonal description of surface-associated communities provides critical knowledge for developing integrated, ecosystem-based responses to potential events (e.g., oil or fuel spills) associated with the only deep-water port in the eastern Canadian Arctic.

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Community involvement

Data collection priorities for the larger Coastal Environmental Baseline Program near Iqaluit were identified through close engagement with co-management partners, namely the Amaruq Hunters and Trappers Association (HTA). The Amaruq HTA is responsible for the management of harvesting among its membership. Specifically, this project provided a current baseline of sea-ice algae and phytoplankton biodiversity for a key coastal port in the Canadian Arctic. Community members from Iqaluit played an integral role in the collection of data for this project. Engagement meetings between the corresponding author and HTA took place before, during, and after research on an annual basis for the duration of this study. The HTA also provided annual letters of support for this research.

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Data availability

Data available upon request.

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Supplementary material

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