



Arctic phytoplankton bloom regimes are associated with distinct dissolved carbohydrate signatures and transparent exopolymer particle (TEP) formation

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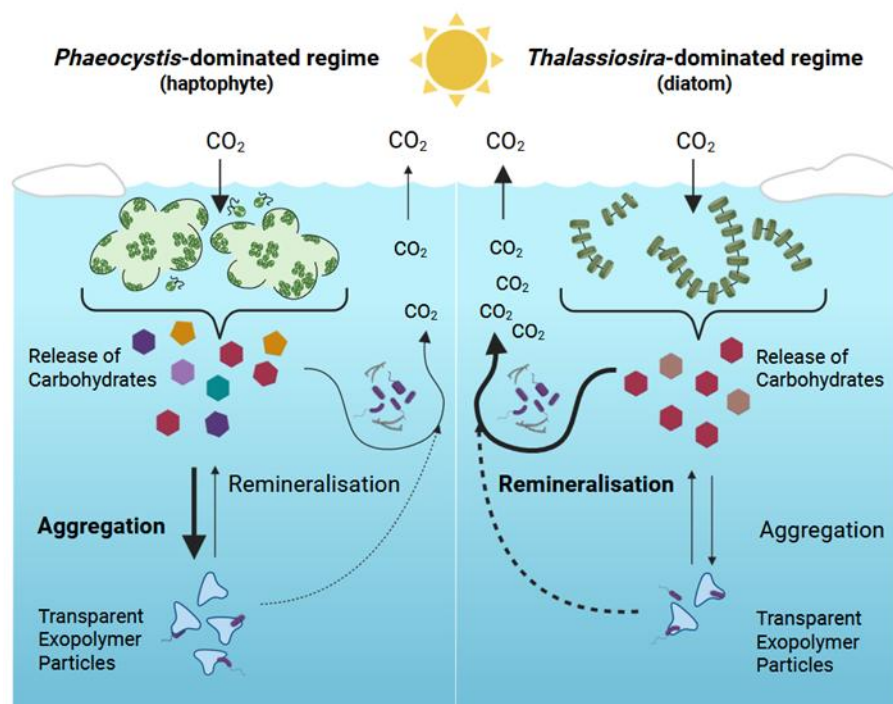
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Short summary (500 character)

Phytoplankton release dissolved organic carbon, including carbohydrates, which are either recycled by microbes or form sticky, sugar-containing gels that may contribute to carbon export via aggregation. By studying phytoplankton communities,
15 dissolved carbohydrate composition and gel formation in the Fram Strait and Kara Sea, we show that blooms dominated by different phytoplankton groups leave distinct organic signatures, suggesting that community shifts could alter carbon processing pathways.

Abstract. Phytoplankton are major producers of marine dissolved organic matter (DOM), including carbohydrates that fuel
20 microbial carbon cycling or contribute to the biological carbon pump through exopolymer particle aggregation. In the Arctic Ocean, climate-driven changes are expected to restructure phytoplankton communities, yet the consequences for the molecular composition of DOM and its fate within microbial and aggregation pathways remain unclear. Here, we examined potential linkages between phytoplankton community composition (18S-rRNA), dissolved organic carbon (DOC), dissolved combined carbohydrates (DCCHO) and transparent exopolymer particles (TEP) in the Fram Strait and the Kara Sea. An advanced spring
25 bloom dominated by the haptophyte *Phaeocystis pouchetii* coincided with a DOM pool enriched in neutral and acidic carbohydrates and elevated TEP concentrations. In contrast, ice-edge diatom blooms dominated by *Thalassiosira* spp. were characterized by glucose-enriched DOM signatures and low TEP formation. Our findings indicate an association between specific phytoplankton taxa and exopolymeric carbohydrate composition, suggesting that shifts in phytoplankton biodiversity may alter carbon processing pathways.



Contrasting phytoplankton blooms produce distinct carbohydrate signatures (hexagons: red, glucose; brown, mannose+xylose; yellow, arabinose; dark purple, rhamnose; lilac, galacturonic acid; cyan, glucuronic acid), with implications for carbon processing pathways, either promoting transparent exopolymer particle (TEP, light blue triangles) formation or coinciding with lower TEP formation and suggesting enhanced remineralization.

35 1 Introduction

Marine phytoplankton account for roughly half of global primary production and form the base of oceanic food webs by converting inorganic carbon into organic matter (Falkowski et al., 1998). A fraction of this production, typically 5-45% depending on species, growth phase, and environmental conditions, is released as dissolved organic matter (DOM) (Fogg, 1966, Prakash et al., 2024). DOM release occurs passively through leakage across cell membranes or actively via exudation associated with waste removal, substrate acquisition, communication, or defence (Sharp, 1977; Bjørrisen, 1988; Thornton, 2014). Top-down processes, including sloppy feeding by zooplankton and protists as well as viral lysis, release additional cellular material into the organic matter pool (Strom et al., 1997; Møller, 2007; Lønborg et al., 2013). DOM is a complex mixture of organic molecules that contains substantial amounts of dissolved organic carbon (DOC) and represents one of Earth's largest exchangeable carbon reservoirs, similar in scale to atmospheric CO_2 (Hansell et al., 2009; Hedges, 1992).

Carbohydrates represent a major fraction of the marine DOM pool and phytoplankton-derived organic matter (Biersmith &



Benner, 1998; Kaiser & Benner, 2009; Borchard & Engel, 2012; Sperling et al., 2017). By releasing a diverse suite of organic compounds, phytoplankton shape both the molecular composition and quantity of DOM, which in turn control its bioavailability and turnover, and consequently the fate of organic carbon in the water column (Kieft et al., 2021; Vidal-Melgosa et al., 2021).

50 Phytoplankton-derived DOC is removed from the surface ocean via two main pathways with contrasting implications for carbon cycling: it is either rapidly remineralized by heterotrophic microbes, resulting in fast recycling and CO₂ exchange with the atmosphere, or transformed into particulate organic carbon aggregation processes with implications for carbon export. Most freshly released DOC is metabolised by heterotrophic microbes (Coffin et al., 1993; Carlson et al., 1999) or transferred to higher trophic levels; however, excess DOC can accumulate in surface waters during or towards the end of a phytoplankton
55 bloom and promote the formation of gel-like particles (Azam 1998; Mari 1999; Passow 2000). Marine gel particles, such as polysaccharide-containing transparent exopolymer particles (TEP), can assemble from dissolved precursors (e.g., acidic sugars), which comprise between 5-40% of DOM (Pakulski & Benner, 1994; Engel et al., 2004a). Due to their sticky properties, TEP play an important role in the formation and sedimentation of larger aggregates, thereby linking dissolved and particulate organic matter pools and facilitating vertical carbon export (Engel, 2000; Engel et al., 2004b; Verdugo et al., 2004).

60 The influence of environmental conditions on the production and release of phytoplankton-derived DOM has been widely investigated, with experimental studies showing that factors such as nutrient and light availability, CO₂ concentration, and temperature affect both its quantity and composition (Granum et al., 2002; Borchard & Engel, 2012; Toseland 2013). In parallel, culture experiments have demonstrated that different phytoplankton taxa release distinct suites of organic compounds, suggesting a taxonomic imprint on DOM composition (Aluwihare & Repeta, 1999; Urbani et al., 2005; Eigemann et al., 2023).
65 For example, Becker et al. (2014) showed that closely related phytoplankton species produce DOM with similar molecular characteristics. Yet, it remains unclear to what extent such taxon-specific signatures are preserved in natural marine systems, and how shifts in phytoplankton community composition might affect the balance between microbial recycling and the aggregation-driven carbon export.

 The Arctic Ocean is particularly affected by ongoing environmental change (Rantanen et al., 2022). In the Eurasian
70 Arctic, the northward expansion of warmer, saltier Atlantic waters into the Arctic Basin - termed Atlantification - and increasing freshwater input from Eurasian rivers are altering stratification, heat distribution, and nutrient regimes (Peterson et al., 2002; McClelland et al., 2006; Tesi et al., 2021). In the Greenland sector, the Fram Strait (FS) serves as the only deep gateway between the Arctic and the Atlantic Ocean, where southward-flowing cold, fresh, mostly ice-covered polar waters (PW) carried by the East Greenland Current (EGC) converge with northward-flowing warm, nutrient-rich Atlantic waters
75 (AW) transported by the West Spitsbergen Current (WSC) (Rudels 2009). The resulting strong gradients between PW and AW create a highly dynamic and productive Marginal Ice Zone (MIZ) (Gradinger & Baumann, 1991; v. Appen et al., 2018) and structure phytoplankton assemblages across the strait (Nöthig et al., 2015). In contrast, the Kara Sea (KS) is a shallow Siberian shelf sea that, while also influenced by modified Atlantic waters entering from both the Fram Strait (FSAW) and the Barents Sea (BSAW) (Schauer et al., 2002; Osadchiev et al., 2022; Pérez-Tribouillier et al., 2025), is strongly shaped by riverine input.



80 The KS receives more than 40% of the total Arctic river runoff, primarily from the Ob and the Yenisei rivers. Together they deliver large amounts of terrestrial organic matter and nutrients (Ivanov, 1976; Gordeev et al., 1996;), supporting roughly one-third of total Arctic primary production (Pivovarov et al., 2003; Terhaar et al., 2021).

Shifts in phytoplankton community composition are already being reported in both the Fram Strait (Ingvaldsen et al., 2021; Ahme et al., 2023; Xi et al., 2025) and the Kara Sea (Sergeeva et al., 2025). Concurrently, annual net primary
85 production (NPP) has increased, particularly in shelf regions such as the Kara Sea, where rates rose by up to 112% due to reduced sea ice and longer growing seasons (Arrigo & van Dijken, 2015; Lewis et al., 2020). Future projections estimate pan-Arctic primary production in ice-free waters at 466-1008 Tg C yr⁻¹ (Codispoti et al., 2013; Hill et al., 2013), potentially releasing ~163-353 Tg DOC yr⁻¹ assuming an exudation rate of 35% (Amon et al., 2024). Together, these changes highlight the need to better understand the extent to which shifts in phytoplankton community composition influence DOM composition,
90 and ultimately, the balance between carbon recycling and sequestration. In this study, we investigated two hydrographically distinct regions of the Arctic Ocean – the Fram Strait and the Kara Sea – combining measurements of organic matter composition with phytoplankton community data derived from 18S rRNA gene amplicons. Specifically, we aimed to: i) assess regional differences in DOM quantity and quality across hydrographic regimes, ii) examine the potential influence of phytoplankton community structure on the composition of dissolved combined carbohydrates (DCCCHO) and TEP
95 concentration.

2. Material and Methods

2.1 Study Sites and Sampling Strategy

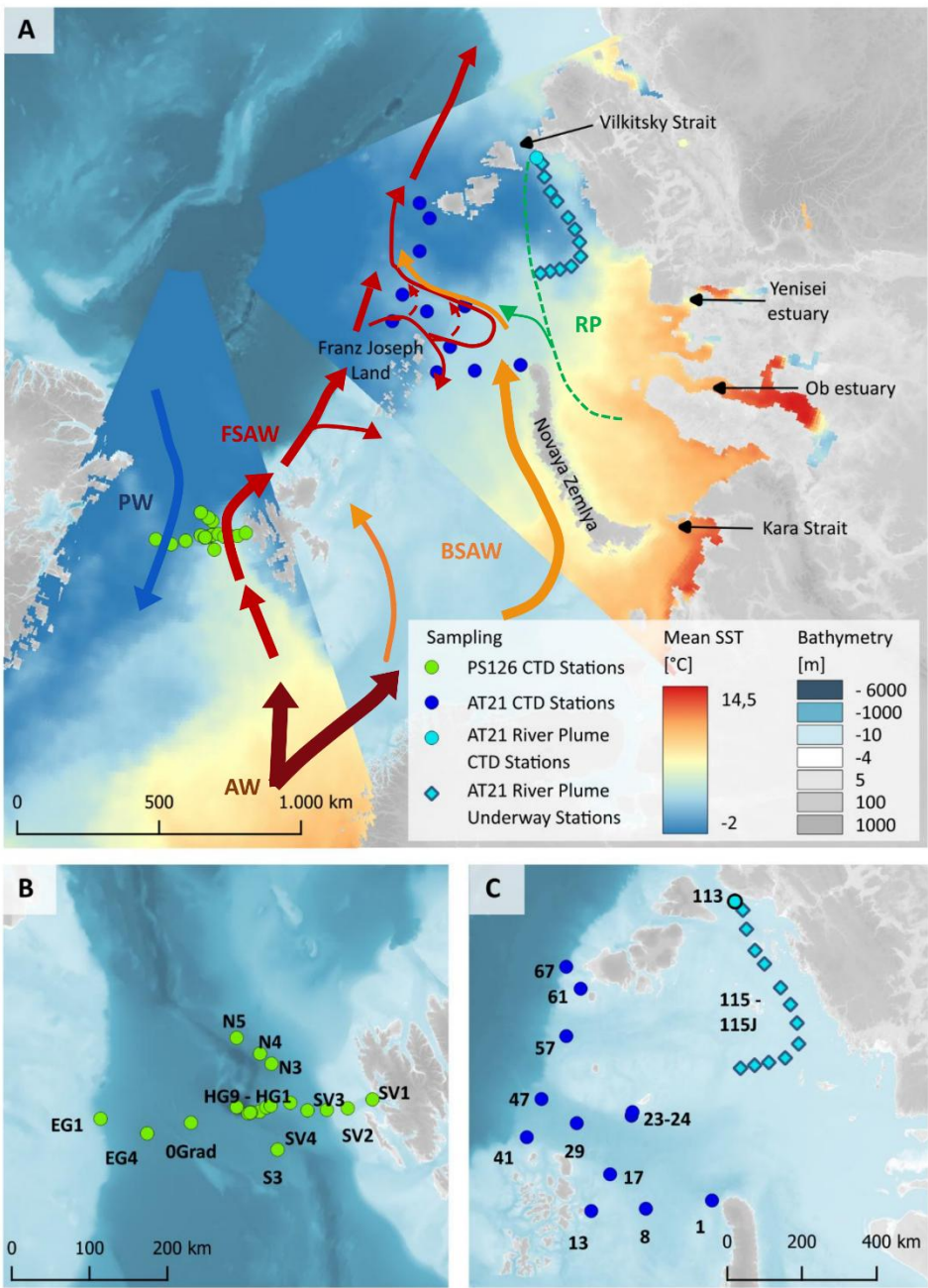
In 2021, we conducted sampling campaigns in the Fram Strait onboard the RV *Polarstern* (PS126) from 24 May to 27 June and in the Kara Sea onboard the RV *Akademik Tryoshnikov* (Arctic Century/AT21) from 5 August to 6 September (Fig. 1).
100 We collected samples from 19 CTD/Rosette stations within the Long-Term Ecological Research observatory (LTER-HAUSGARTEN) in the Fram Strait (FS), 12 CTD/Rosette stations in the Kara Sea (KS), 11 underway stations and one CTD/Rosette station in the Ob-Yenisei River Plume (RP) (Table S1). Seawater samples for biochemical and microbial analysis were collected from the surface (1.5-10m) and chlorophyll-*a* maximum (10-42m) using a CTD rosette (SBE 911plus, Sea-Bird Scientific, USA) equipped with two temperature sensors, two conductivity sensors and one chlorophyll sensor. Due to the ice
105 conditions during AT21 expedition, some samples could only be collected from the ship's underway system (~8 m depth), with temperature and salinity measurements taken in a bucket for 30 seconds using an underwater CTD system (UCTD). The full CTD data sets are publicly available on PANGAEA (Hölemann et al, 2022; Makhotin et al., 2022; Tippenhauer et al., 2023).

The data sets of both campaigns were compared by categorically assigning them into a “surface”-layer defined as 0-
110 10 m and “subsurface”-layer for samples taken in 10-42 m (Fig. S1). Based on measured chlorophyll-*a* (chl-*a*) concentrations, two-thirds of the stations displayed a chl-*a* maximum in the subsurface layer, therefore, this layer will be referred to in the



following as the subsurface chlorophyll-*a* maximum layer (SCM). Exceptions included stations without a distinct chl-*a* maximum (S3, SV1, 13, 24, 57) and stations where the maximum was located within the surface layer (EG1, 0Grad, N5, HG5, HG3, 113).

115 To illustrate the hydrographic conditions during the two expeditions, we generated overview maps of sea surface temperature (SST) for the Fram Strait and the Kara Sea using data from the Copernicus Marine Environment Monitoring Service (CMEMS). Daily data were derived from the Global Ocean OSTIA Sea Surface Temperature and Sea Ice Analysis (SST_GLO_SST_L4_NRT_OBSERVATIONS_010_001; E.U. Copernicus Marine Service Information (CMEMS), Marine Data Store (MDS), DOI: 10.48670/moi-00165, based on Good et al., 2020; Donlon et al., 2012; Stark et al., 2007) and averaged
120 over the respective sampling periods (PS126: 30 May–21 June 2021; AT21: 09 August–03 September 2021). The R packages *tidync* (v0.4.0; Sumner 2024) and *terra* (v1.8-29; Hijmans 2025) were used for processing NetCDF files and creating raster layers, respectively. Visualization and final map preparation were conducted in *QGIS* (v3.34.10; QGIS Development Team 2023). Water mass properties were calculated following the TEOS-10 framework (IOC et al., 2010) using the *gsw* package (v 1.2-0; Kelley et al. 2024) in R.



125 Figure 1: Map of sampled stations during the expeditions PS126 (light green) and AT21 (blue) in summer 2021, with a schematic
representation of the intrusion of Atlantic water masses into the Arctic (Atlantic Water (AW) in brown, Fram Strait Atlantic Water
(FSAW) in red, Barents Sea Atlantic Water (BSAW) in orange), the outflow of Arctic water through the Fram Strait (Polar Water
(PW) in blue) and the extent of the river plume (RP) in the Kara Sea (green dotted line) adapted after Pérez-Tribouillier et al., 2025.
130 Blue to white colours indicate water depth and azure to red colours indicate mean satellite-derived sea surface temperature during
the respective sampling period (A). Zoom in on Fram Strait stations and (B) Kara Sea and Ob-Yenisei River Plume stations (C).



2.2 Chlorophyll-a

Chlorophyll-*a* (chl-*a*) concentrations were determined according to Edler (1979) and Evans and O'Reilly, (1980) with modifications. In brief, up to 1 L of seawater were filtered onto 25 mm GF/F (Cytiva Whatman™, USA), which were stored at -20°C until analysis. For Fram Strait samples, pigments were extracted using acetone (90%, 2-4 hrs in the dark) and then
135 centrifuged for 10 min at 4°C at 5000 rpm before fluorometric analysis (Turner Designs, USA). For Kara Sea samples, pigments were extracted with acetone (90%) in the dark for 24 h and measured on a pre-calibrated (pure spinach Chl-A, Sigma) fluorometer (Trilogy, Turner Designs, USA) by “no acidification” protocol.

2.3 Inorganic nutrients

During PS126, 10 mL of seawater were filtered in triplicates through 0.8 µm pore-sized cellulose acetate syringe-filters
140 (Thermo Fisher Scientific, US) and stored at -20°C. At the central laboratory for chemical analysis (ZLCA) at GEOMAR, nitrate (NO₃⁻), nitrite (NO₂⁻), phosphate (PO₄³⁻) and silicic acid (Si(OH)₄) were quantified on a QuAAtro39 AutoAnalyzer (Seal Analytical Inc., USA) using salinity-adjusted (35 PSU) standards. For AT21, a detailed description of the nutrient analysis can be found in Gangnus et al. (2022).

2.4 Protist community composition analysis

145 During PS126, up to 6 L of seawater were pre-filtered (10 µm) and size fractionated using 3 µm and 0.4 µm PC filters (Millipore, USA). Filters were stored frozen (-80 °C). During AT21, up to 2 L of seawater were filtered directly onto 0.2 µm Sterivex filter units (Millipore, USA) with 1 mL of RNAlater (Thermo Fisher Scientific, USA) and then stored (-80 °C). Size fractionated samples were pooled after DNA extraction using the NucleoSpin Plant II Kit (Macherey-Nagel, Germany) for PS126 samples, and the DNeasy PowerWater Kit (Qiagen, Germany) for AT21 samples. While DNA extraction protocols can
150 introduce technical variation in microbiome studies, previous work has shown that although extraction methods may affect DNA yield and sequencing efficiency, their influence on community composition or structure is generally weaker than environmental gradients (Rubin et al., 2014). To evaluate whether observed patterns were consistent with strong ecological structuring despite methodological differences, we performed pairwise PERMANOVA analysis among regions. All three regions differed significantly in community composition (Fram Strait vs. Kara Sea: $R^2 = 0.24$, $F = 18.5$, $p = 0.001$; Fram Strait
155 vs. River Plume: $R^2 = 0.30$, $F = 19.6$, $p = 0.001$; Kara Sea vs. River Plume: $R^2 = 0.37$, $F = 19.1$, $p = 0.001$), indicating pronounced biogeographic separation between the three regions. Although sampling and extraction protocols differed between campaigns and cannot be fully disentangled from regional effects, the magnitude and consistency of community separation suggest that environmental gradients are the primary drivers. The V4 region of the 18S rRNA gene was amplified via polymerase chain reaction (PCR) using primers 528iF and 964iR (Fadeev et al., 2018). Metagenomic libraries were prepared
160 following the Illumina 16S Metagenomic Sequencing Library Preparation protocol (Part # 15044223 Rev. B). The final library pool was prepared with 20% PhiX control (Thermo Fisher Scientific, USA), adjusted to a DNA concentration of 4 nM and



paired-end sequencing was conducted on a MiSeq platform (Illumina) across five separate runs. Demultiplexing and FASTQ sequence file generation were performed using the “Generate FASTQ” workflow of the MiSeq software. 18S rRNA sequences were processed using Cudadapt (v2.8; Martin, 2011) for primer and adapter removal, and the R package *dada2* (v1.18.0; Callahan et al., 2016) for sequence trimming and filtering, denoising with the Divisive Amplicon Denoising Algorithm (DADA), and paired-end merging. Runs were processed independently and merged prior to chimera removal and taxonomic assignment against the PR2 reference dataset (v4.14.0; Guillou et al., 2012) using the *dada2* implementation of the Naïve Bayesian Classifier (Wang et al., 2007).

Following taxonomic assignment, only amplicon sequencing variants (ASVs) assigned to one of six phytoplankton phyla (Chlorophyta, Cryptophyta, Dinoflagellata, Haptophyta, Ochrophyta, Prasinodermophyta) were retained. To improve taxonomic resolution, abundant ASVs lacking species-level classification were queried against the PR2 database and annotated with the percentage identity (pid) to their closest match. To account for contamination, blanks and PCR negative controls were sequenced alongside samples. ASVs were removed if their abundance in negative controls exceeded 10% of their abundance in corresponding samples (Wangensteen and Turon, 2016). Controls with < 400 total reads were excluded. Blank correction was performed using the R package *microDecon* (v1.0.2; McKnight et al., 2019). Only ASVs representing >0.005% of total reads across the entire dataset were kept for further analysis. Further details on the data processing are provided in Supplementary Table S2. The final dataset comprised 5096621 sequences from 72 samples comprising 479 ASVs affiliated with the phyla *Chlorophyta* (48), *Cryptophyta* (17), *Dinoflagellata* (252), *Haptophyta* (41), *Ochrophyta* (119) and *Prasinodermophyta* (2). Prior to calculating diversity indices, data were rarefied to the minimum sample size of 13521 reads using the *rrarefy* function from the *vegan*-package (v2.6.4; Oksanen et al., 2024) to standardize sequencing depth across samples.

2.5 Dissolved organic carbon, nitrogen and carbohydrates

Duplicate samples for dissolved organic carbon (DOC), total dissolved nitrogen (TDN), and high-molecular-weight (>1 kDa) dissolved combined carbohydrates (DCCHO) were collected in pre-combusted glass vials (500 °C for 8h). For DOC and TDN, 20 mL of seawater was filtered through a 0.45 µm GMF GD/X filter (Whatman, GE Healthcare Life Science, UK), acidified with 20 µL of hydrochloric acid (30% Suprapure, Sigma-Aldrich, Germany), and stored (+4°C). DOC and TDN were analysed simultaneously by applying the high-temperature catalytic oxidation method (TOC-VCSH, Shimadzu) following Engel and Galgani (2016) with a detection limit of 1 µmol L⁻¹. Seawater samples for DCCHO (20 mL) were filtered through 0.45 µm Acrodisc syringe filters (Pall Life Sciences, USA) and stored (-20 °C). After thawing, samples were desalted by membrane dialysis (1 kDa, Spectra Por) to exclude polysaccharides <1 kDa, oligosaccharides, and monosaccharides. Next, samples were hydrolysed with HCl (1 mol L⁻¹), neutralized by acid evaporation under a dinitrogen atmosphere and ultrapure water and analysed with high-performance anion exchange chromatography coupled with pulsed amperometric detection (HPAEC-PAD, DIONEX ICS3000DC) with a detection limit of 1 µg L⁻¹. A detailed description is given in Engel and Händel (2011). The analysis allows the quantification of neutral sugars (glucose, arabinose, fucose, galactose, rhamnose, mannose, and xylose),



195 amino sugars (galactosamine, glucosamine and muramic acid) and acidic sugars (galacturonic acid, glucuronic acid and gluconic acid). Mannose and xylose coeluted and were, therefore, quantified as a mixture. Muramic acid and gluconic acid were below the detection limit. Monomer concentrations and the individual numbers of carbon atoms were used to calculate the carbon concentration per litre, expressed as DCCHO-C and subsequently carbon-normalized sugar yields (%DOC) (eq. 1).
$$Yield (\% DOC) = [dCCHO - C] / DOC * 100 \quad (1)$$

200 Neutral sugar (NS) yields (%DOC; including fucose, rhamnose, arabinose, galactose, glucose, mannose and xylose) were used as an index of the relative contribution of freshly produced DOM and calculated according to equation 1.

Ratios of dissolved organic carbon (DOC) to dissolved organic nitrogen (DON) were calculated using measured DOC, total dissolved nitrogen (TDN) and inorganic nutrient (NO_3^- and NO_2^-) concentrations. DON was determined as the difference between TDN and the sum of inorganic nutrients.

205 2.6 Transparent exopolymer particles (TEP)

The gel-like particle species TEP was analysed according to Passow and Alldredge (1995) In brief, seawater samples were filtered in triplicates for spectrophotometric analysis. For each replicate 30-250 mL were filtered (<0.2 bar) onto 0.4 μ m pore size polycarbonate filters (25 mm Nucleopore, track-etched, Whatman, GE Healthcare Life Sciences, UK), stained with 1 mL Alcian Blue Working Solution (0.02% final concentration, Alcian Blue 8GX, pH 2.5, Sigma Aldrich, Germany) for 5s and
210 subsequently stored (-20°C). Prior to staining, the dye was stored at +4°C and filtered through 0.2 μ m syringe filters (Acrodisk, Sigma Aldrich) right before use. Blanks were prepared from 10 mL of distilled water and processed like the samples. In preparation for the spectrophotometric analysis, each filter was covered in 6 mL of sulfuric acid (H_2SO_4 , 80%) and incubated for 2 hours. The absorbance of Alcian Blue was measured at 787 nm in a 1 cm cuvette against distilled water. Finally, concentrations are given in micrograms of Xanthan equivalents per litre (μ g Xeq. L^{-1}) and calculated using the following
215 equation:

$$TEP (\mu g Xeq. L^{-1}) = \frac{(E_{787} - C_{787})}{V} \times F(x) \quad (2)$$

with E_{787} being the absorption of the sample, C_{787} the absorption of the blank, V the filtered volume in L and F the determined calibration factor for the standard polysaccharide Gum Xanthan.

2.7 Statistical analysis

220 All figures were generated using the ggplot2 package (v3.5.2; Wickham, 2016) and all statistical analyses and calculations were conducted using R (v4.3.3) and the R Studio interface (v2023.12.1). Differences in chl-*a* and DOM concentration among water masses and regions were assed using the *kruskal.test* function for Kruskal-Wallis rank sum tests (*stats* package) and mean chl-*a* concentrations were evaluated via Fisher-Pitman permutation test (*oneway_test*, *coin* package, v1.4.3; Hothorn et al., 2006). Principal Component Analysis (PCA) was performed on standardized DCCHO data (mol%) using the *rda*-function
225 in the *vegan* package (v2.6.4; Oksanen et al., 2024) to identify patterns in carbohydrate composition across regions.



Community analyses of the 18S amplicon data were based on Hellinger-transformed relative abundances of ASVs using Bray-Curtis dissimilarity distances and included non-metric multidimensional scaling (NMDS), permutational multivariate analysis of variance (PERMANOVA), hierarchical clustering and an indicator species analysis. NMDS and a PERMANOVA with 999 permutations were performed to test for differences in protist community composition between geographical regions and water layers, using the functions *metaMDS* and *adonis* from the *vegan* package (v2.6.4; Oksanen et al., 2024). Then, hierarchical clustering was applied to assess community patterns within regions previously identified by applying the *hclust* function set to average linkage (*stats* package). The reliability of the clusters and the optimal number of groups were evaluated with silhouette widths using *silhouette* from the *cluster* package (v2.1.6; Maechler et al., 2023). Furthermore, an indicator species analysis was performed on relative abundance data to detect ASVs significantly associated with the three identified. The analysis was conducted using the *multipatt* function of the *indicspecies* package (version 1.8.0; De Cáceres & Legendre, 2009), applying the *r.g* option (point biserial correlation coefficient) and 9999 permutations to assess statistical significance. The indicator statistic value (*stat*) represents the strength of association between ASVs and habitats, with values close to 1 indicating a perfect association. In doing so, the *stat* value accounts for both the occurrence of an ASV in a given group (presence/absence) and its relative abundance across all samples. As a result, ASVs that occur exclusively in one group, even at low abundances, as well as ASVs that are present in more than one group but are more abundant in a specific group, can yield high association values. The top 30 ASVs with the highest *stat* values and $p < 0.01$ were then selected for further analysis and correlated with DCCHO (mol%). Correlations were calculated using Spearman's rank correlation coefficient with *cor* and *cor.test* functions in *stats* package (v4.3.3). To further evaluate the relationship between protist community composition and DCCHO, a Mantel test with 999 permutations and Spearman's rank correlation was performed using the *mantel* function (*vegan* v2.6.4), comparing Bray-Curtis distances of Hellinger-transformed ASVs with Euclidean distances of standardized mol% DCCHO. The redundancy analysis (RDA) was conducted using *rda* function from the *vegan* package to assess the abiotic drivers of protist community composition. Prior a detrended correspondence analysis (*decorana*, *vegan*) was performed to confirm the use of linear methods. Collinearity was checked via variance inflation factors (>10 excluded, *vif.cca*, *vegan*) and forward selection (999 permutations, *ordiR2step*, *vegan*) identified key environmental predictors. The significance of the overall model, individual axes and each term was tested using permutation tests (999 permutations, *anova.cca*, *vegan*). Significance of environmental vectors was assessed using permutation tests of vector-ordination correlations using *envfit* function (999 permutations) in the *vegan* package.

3. Results

3.1 Hydrographic conditions and inorganic nutrients

Four different water masses were identified based on potential temperature and absolute salinity, following Rudels et al. (2000) and Meyer et al. (2017): Atlantic Water (AW), Mixed Atlantic Water (MAW), Polar Surface Water (PSW) and warm Polar Surface Water (wPSW) (Fig. S3). All four water masses occurred in the Fram Strait (FS), whereas AW was absent from both



the Kara Sea (KS) and the Ob-Yenisei River Plume (RP) (Table 1). The FS was characterized by a pronounced east-west gradient, with warm ($2.9 \pm 0.2^\circ\text{C}$), saline (34.9 ± 0.1) AW occurring in the east and colder ($-1.1 \pm 0.3^\circ\text{C}$), less saline (33.4 ± 0.7) PSW in the west, while wPSW and MAW prevailed in the transition zone. The observed spatial distribution is consistent with established EGC and WSC flow patterns. In the KS, MAW and wPSW were primarily associated with the western Kara Sea along the St. Anna Trough. The wPSW generally dominated the surface layer, while the more saline MAW (34.6 ± 0.1) was exclusively detected in the SCM layer. In contrast, colder (-1.1 ± 0.6) and fresher (33.2 ± 0.9) PSW was found along the northern shelf edge. Vertical salinity differences between the surface and the SCM were slightly more pronounced in the KS (surface 33.3 ± 0.8 ; SCM: 34.2 ± 0.4) than in the FS (surface: 33.8 ± 0.9 ; SCM: 34.2 ± 0.8). In the RP, only wPSW was observed, with a single exception. This water mass was markedly warmer (4.3 ± 1.5) and substantially less saline (15.5 ± 5.5) than wPSW in either FS or KS.

Nutrient concentrations varied by water mass and region (Table 1). In wPSW, nitrate decreased sharply from $3.4 \pm 2 \mu\text{mol L}^{-1}$ in the FS to $1.4 \pm 3 \mu\text{mol L}^{-1}$ in KS, reaching a minimum in the RP ($0.2 \pm 0.6 \mu\text{mol L}^{-1}$). Highest nitrate and phosphate concentrations were generally observed in AW and MAW, with nitrate reaching $\sim 7 \mu\text{mol L}^{-1}$ in the FS and $\sim 3 \mu\text{mol L}^{-1}$ in the KS, while phosphate ranged from 0.4 to $0.7 \mu\text{mol L}^{-1}$. Regional contrasts were pronounced, with nitrate, phosphate and silicate concentrations more than twice as high in the FS than in the KS, whereas nitrite concentrations were approx. fivefold higher in the KS. In the RP, concentrations of most nutrients were near or below the detection limit, except for silicate, which remained high, reaching $34.5 \pm 13.7 \mu\text{mol L}^{-1}$ in wPSW and $39.2 \mu\text{mol L}^{-1}$ in PSW.

Table 2: Arithmetic mean $\pm$ standard deviation of temperature, salinity and inorganic nutrient concentrations for four water masses Atlantic Water (AW), Modified Atlantic Water (MAW), warm Polar Surface Water (wPSW) and Polar Surface Water (PSW) sampled in the Fram Strait (FS; $n = 38$), Kara Sea (KS; $n = 24$) and Ob-Yenisei River Plume (RP; $n = 11$). Water masses were defined following Rudels et al. (2000) and Meyer et al. (2017).

Region	Water mass	Temperature [$^\circ\text{C}$]	Salinity	NO_3^- [$\mu\text{mol L}^{-1}$]	NO_2^- [$\mu\text{mol L}^{-1}$]	PO_4^{3-} [$\mu\text{mol L}^{-1}$]	$\text{Si}(\text{OH})_4$ [$\mu\text{mol L}^{-1}$]
Fram Strait	AW (n=7)	2.93 ± 0.2	34.9 ± 0.1	7.11 ± 1.1	0.1 ± 0.01	0.5 ± 0.1	1.8 ± 0.6
	MAW (n=1)	0.7	34.6	7.8	0.02	0.7	3.1
	wPSW (n=11)	2.5 ± 1.4	34.5 ± 0.5	3.4 ± 2	0.1 ± 0.03	0.3 ± 0.1	1.4 ± 0.5
	PSW (n=19)	-1.1 ± 0.3	33.4 ± 0.7	1.6 ± 1.6	0 ± 0.01	0.3 ± 0.1	1.5 ± 1.3
Kara Sea	MAW (n=4)	-0.1 ± 0.7	34.6 ± 0.1	3.1 ± 2.2	0.3 ± 0.2	0.4 ± 0.3	1.1 ± 0.8
	wPSW (n=11)	1.6 ± 1	33.9 ± 0.4	1.4 ± 3	0.1 ± 0.1	0.2 ± 0.2	0.8 ± 1.5



River Plume (OY)	PSW (n=9)	-1.1 ± 0.6	33.2 ± 0.9	1.6 ± 1.9	0.09 ± 0.09	0.1 ± 0.08	0.4 ± 0.5
	wPSW (n=10)	4.3 ± 1.5	15.5 ± 5.5	0.2 ± 0.6	0.07 ± 0.03	0.14 ± 0.07	34.5 ± 13.7
	PSW (n=1)	-0.55	23	0.1	0.1	0.1	39.2

280 **3.2 Chlorophyll-a distribution**

While the depth of the SCM layer was on average 18 m in the FS and 31 m in the KS (Fig. S1), chl-*a* concentration did not differ significantly between regions (Fisher-Pitman, $p = 0.85$) or among water masses (Kruskal-Wallis, $p = 0.08$). Generally, chl-*a* appeared to be highly patchy across the sectors with less pronounced vertical differences in the FS (surface: $2.1 \pm 1.1 \mu\text{g L}^{-1}$; SCM: $2.2 \pm 1.1 \mu\text{g L}^{-1}$), yet the highest (SCM: $3.3 \pm 2.9 \mu\text{g L}^{-1}$) and lowest concentrations (surface: $1.1 \pm 2.2 \mu\text{g L}^{-1}$) across water layers in the KS (Fig. 2). Although no underway measurements were available, data from CTD station 113 in the RP showed values comparable to the KS surface layer ($1.1 \mu\text{g L}^{-1}$). At the regional scale, differences between selected water masses emerged. In the KS, chl-*a* was fourfold lower in the wPSW ($0.8 \pm 1.2 \mu\text{g L}^{-1}$) than in the PSW ($4.1 \pm 3.4 \mu\text{g L}^{-1}$; Table S3). In the FS, differences were less pronounced, ranging from $1.2 \mu\text{g L}^{-1}$ in AW to $2.6 \mu\text{g L}^{-1}$ in wPSW. Notably, exceptionally high concentrations were measured at the SCM of stations 41 and 47 and at both the surface and SCM of station 61 ($7\text{--}8 \mu\text{g L}^{-1}$; $n = 4$).

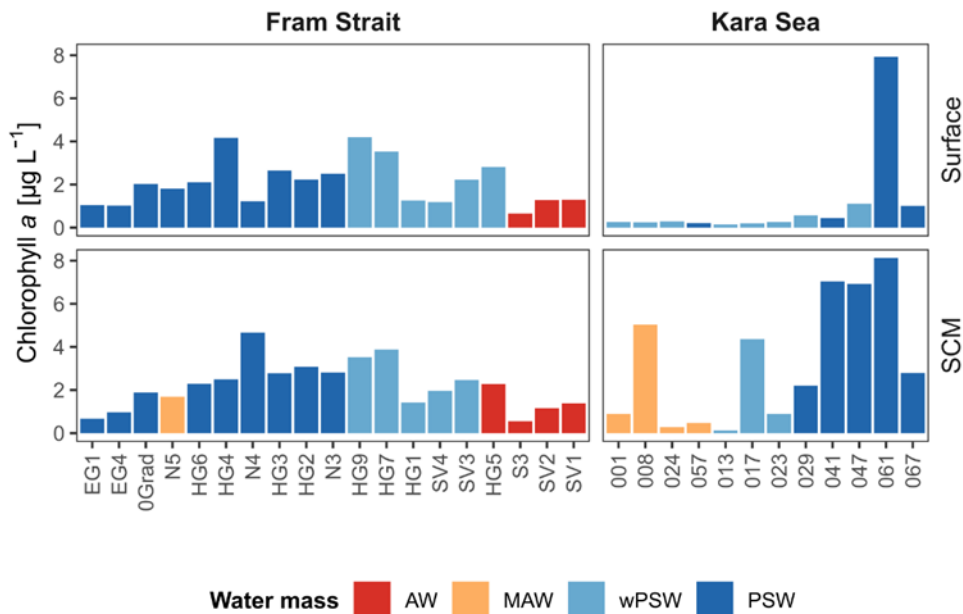




Figure 2: Chlorophyll *a* concentration ($\mu\text{g L}^{-1}$) at the surface and subsurface chlorophyll *a* maximum (SCM) layer at each station. Colours indicate water mass: AW (Atlantic Water), MAW (Modified Atlantic Water), PSW (Polar Surface Water), wPSW (warm Polar Surface Water).

3.3 Spatial distribution of dissolved biopolymers and transparent exopolymer particles (TEP)

295 Clear regional patterns emerged with the highest DOC and DCCHO concentrations in the RP, whereas TEP concentrations peaked in the FS (Fig. 3A). DOC varied significantly among regions (Kruskal–Wallis: $\chi^2 = 32.17$, $df = 2$, $p < 0.001$), peaking in the RP ($335 \pm 94 \mu\text{mol L}^{-1}$) and being consistently higher in the FS (surface: 81 ± 13 ; SCM: $79 \pm 16 \mu\text{mol L}^{-1}$) than in the KS (surface: 75 ± 11 ; SCM: $69 \pm 9 \mu\text{mol L}^{-1}$). DCCHO showed a similar regional trend (Kruskal–Wallis: $\chi^2 = 30.03$, $df = 2$, $p < 0.001$), with the highest values in the RP ($2609 \pm 862 \text{ nmol L}^{-1}$), roughly twofold higher than in the FS (surface: $1250 \pm$
300 576 nmol L^{-1} ; SCM: $990 \pm 376 \text{ nmol L}^{-1}$) and about fourfold higher in the KS (surface: 735 ± 154 ; SCM: $786 \pm 426 \text{ nmol L}^{-1}$). In contrast, TEP concentrations were highest in the FS (surface: 226 ± 115 ; SCM: $219 \pm 210 \mu\text{g Xeq L}^{-1}$, $n=19$), approximately fourfold greater than in the KS (surface: 41 ± 22 ; SCM: $47 \pm 32 \mu\text{g Xeq L}^{-1}$, $n=12$) or the RP ($59 \mu\text{g Xeq L}^{-1}$, $n=1$), with significant differences among regions (Kruskal–Wallis, $\chi^2 = 24.80$, $df = 2$, $p < 0.001$). Differences among water masses were generally less pronounced, but DOC, DCCHO and TEP concentrations were highest in PSW compared with AW and MAW
305 (Table S3), with TEP reaching maxima at the northern stations (surface: $472 \pm 31 \mu\text{g Xeq L}^{-1}$ at N3; SCM: $949 \pm 143 \mu\text{g Xeq L}^{-1}$ at N4; Fig. S4). Although DCCHO concentrations in the FS were less than twofold higher than in the KS, TEP concentrations were more than fourfold higher, leading to markedly higher TEP:DCCHO ratios in the FS, particularly in the PSW and wPSW in the SCM (FS: ~ 0.7 ; KS: ~ 0.2 ; Fig. S5).

Furthermore, we observed regional differences in DOM quality and origin (Fig. 3A). Neutral sugar yields (NS %DOC)
310 were highest in the FS (surface: $9 \pm 5\%$; SCM: $7 \pm 3\%$), followed by the KS (surface: $5 \pm 1\%$; SCM: $6 \pm 3\%$) and RP ($4 \pm 1\%$). In contrast, DOC:DON ratios peaked in the RP (29 ± 4), while FS (surface: 11 ± 3 ; SCM: 9 ± 5) and the KS (surface: 12 ± 3 ; SCM: 8 ± 3) ratios were similar, with greater vertical variability in the KS. Together, these proxies indicate terrestrial influence in the RP and surface KS layers and fresher material in the FS.

Compositional analysis of DCCHO (mol%) using principal component analysis (PCA) revealed that PC1 (33.4%
315 variance explained) separated RP and FS, whereas PC2 (29.2%) distinguished RP and KS samples (Fig. 3B). Glucose and mannose + xylose dominated across all regions (FS: 34–42 and 29–35 mol%; KS: 34–36 and 33–42 mol%; RP 24 and 29 mol%, respectively) (Fig. 3C). Rhamnose and arabinose were enriched in FS (surface: 4.8 mol% and 8.7 mol%; SCM: 5.3 mol% and 8.1 mol%, respectively), while galactose and fucose were highest in RP (14.2 mol% and 9.6 mol% respectively). KS samples contained on average a higher proportion of amino sugars (galactosamine: 0.8–0.9 mol%; glucosamine: 5–6.4 mol%).

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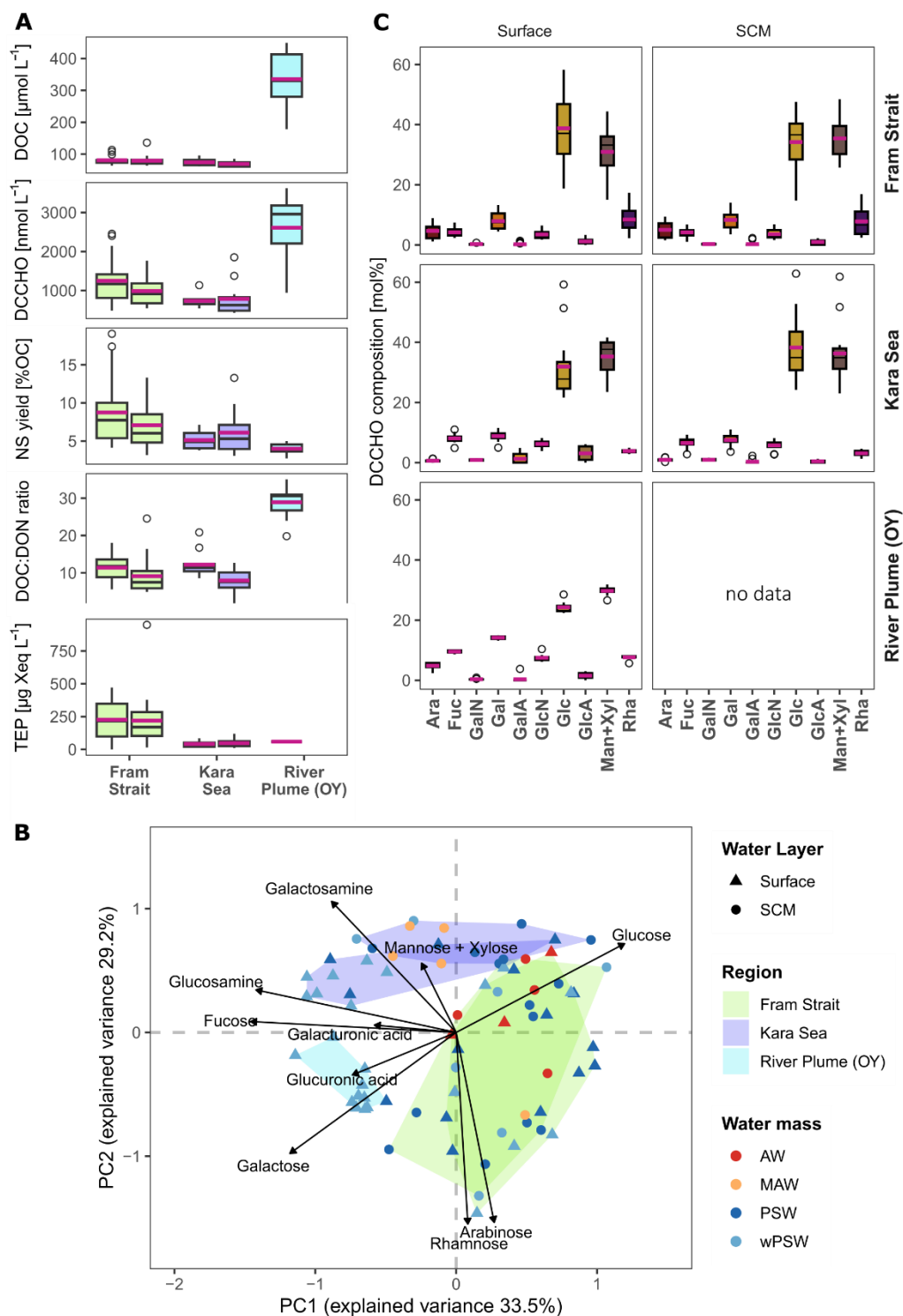


Figure 3: Characteristics of dissolved organic matter (DOM) properties across three Arctic regions at the surface and in the subsurface chlorophyll *a* maximum (SCM) layer. (A) Boxplots of DOM characteristic top to bottom: dissolved organic carbon (DOC)



325 in $\mu\text{mol L}^{-1}$, dissolved combined carbohydrates (DCCHO) in nmol L^{-1} , neutral sugar yields (NS yields %DOC) of DOC, DOC:DON
ratios and transparent exopolymer particles (TEP) expressed in $\mu\text{g Gum Xanthan L}^{-1}$ equivalents for each water layer. The
horizontal black line indicates the median, the magenta line the mean, the box shows the interquartile range, and whiskers extend
to $1.5\times$ the interquartile range. Colours represent geographical regions. (B) Principal component analysis (PCA) based on DCCHO
composition (mol%). Colours indicate geographical region, and shape indicates water layer, and point colour denotes water mass:
AW (Atlantic Water), MAW (Modified Atlantic Water), PSW (Polar Surface Water), wPSW (warm Polar Surface Water). Arrow
length illustrates the strength of the contribution of individual sugars in driving sample distribution. (C) Composition of DCCHO
330 (mol%) grouped by water layer and region. Abbreviations: Ara, arabinose; Fuc, fucose; GalN, galactosamine; Gal, galactose; GalA,
galacturonic acid; GlcN, glucosamine; Glc, glucose; GlcA, glucuronic acid; Man+ Xyl, mannose + xylose; Rha, rhamnose.

The composition of DCCHO also varied within regions and across bloom conditions (Fig. 4, Table S4). Bloom conditions
were defined as both chl-*a* concentrations $> 1 \mu\text{g L}^{-1}$ and NS yields $> 5.9 \%$ DOC, with the latter threshold indicating fresh
DOM (Amon & Benner, 2003). Samples not meeting the criteria were classified as non-bloom samples. In both the FS and
335 KS, bloom samples showed a twofold increase in DCCHO concentrations compared to non-bloom samples. However, this
increase was accompanied by region-specific changes in the relative contributions of individual carbohydrates (Table S4).

In the FS, several carbohydrates contributed more strongly under bloom conditions, including arabinose, which
increased from 4% to 5.5%, rhamnose from 7% to 9%, and glucose from 34.3% to 38.3%, alongside a twofold increase in
acidic sugars. To assess whether these shifts represented enrichment trends, bloom-to-non-bloom molar ratios were calculated
340 and tested against 1 using Wald tests on log-transformed ratios, with standard errors estimated by Gaussian error propagation.
Ratios exceeded 1 for rhamnose, arabinose, glucose, galacturonic acid, and glucuronic acid, indicating a broader enrichment
trend across neutral and acidic sugars (Fig. 4). Although most enrichments were not statistically significant across the full FS
bloom dataset, restricting the analysis to samples with particularly high NS yields ($>10 \%$ DOC, above the upper limit of 9.6
reported by Amon and Benner (2003)) revealed significant enrichments in arabinose, glucose, and glucuronic acid, together
345 with significant decreases in fucose and amino sugars (Table S4). In contrast, the compositional shift in the KS was mainly
limited to glucose, which increased from 32.3% to 49.3%, while the relative contributions of most other carbohydrates
decreased under bloom conditions. Accordingly, glucose was the only carbohydrate with a significant bloom-to-non-bloom
molar ratio above 1 (1.5), whereas most other compounds showed ratios below 1. Significant declines occurred in fucose,
rhamnose, arabinose, galactose, glucuronic acid, and the amino sugars, while mannose + xylose showed no significant change.

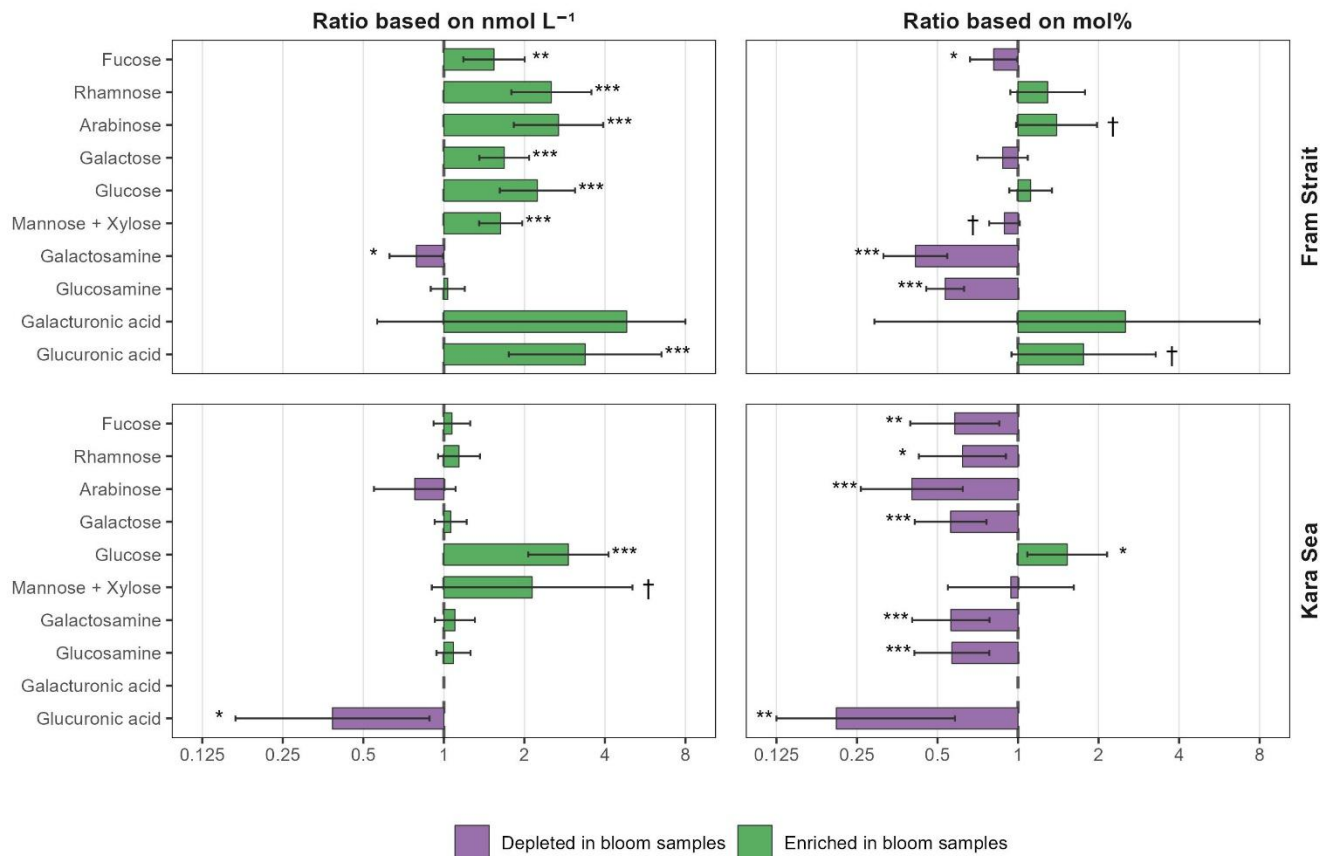


Figure 4: Bloom vs. no-bloom ratios of dissolved combined carbohydrate concentrations and molar percentages in Kara Sea and Fram Strait. Ratios are plotted on a log₂-transformed axis for symmetry, while x-axis labels show the corresponding untransformed ratio values. Green bars indicate enrichment in bloom samples and purple bars indicate depletion. Error bars show 95% confidence intervals and symbols denote p-value thresholds: † p < 0.10, * p < 0.05, ** p < 0.01, and * p < 0.001.**

3.4 Protist community composition

3.4.1 Differences among geographical regions

Protist communities grouped into three significantly distinct clusters corresponding to the FS, KS and RP (PERMANOVA, R² = 0.33, F = 16.79, p = 0.001; Fig. 5A). The FS represented the largest cluster (38 samples, 390 ASVs), followed by the KS (23 samples, 375 ASVs) and RP (11 samples, 315 ASVs; Fig. S2). The FS assemblage showed the highest ASV richness, particularly within the SCM (200), yet low evenness resulted in a low overall Shannon diversity (surface: 2.8; SCM: 2.7) (Fig. S6). Conversely, the RP and the KS surface layer exhibited the highest Shannon diversity (3.2 and 3.3, respectively) driven by high evenness (0.66 and 0.62) but low richness (158 and 169), whereas the SCM in the KS was characterised by low richness (142) but highly variable evenness and diversity.



Community composition differed among regions, even at the phylum level (Fig. 5B, Table S5). In the FS, dinoflagellates (43% in the surface) and haptophytes (39% in the SCM) dominated the community, with *Phaeocystis pouchetii* (~89%) as the most prevalent haptophyte ASV (Table S6). Ochrophytes 18% surface and 20% SCM), the third largest group, were dominated by the diatom *Chaetoceros gelidus* (48% and 71%). Across depth layers, no significant differences in community composition were observed (PERMANOVA, $R^2 = 0.028$, $F = 1.02$, $p = 0.41$).

In the KS, haptophytes accounted for only a small proportion of the community (4% surface and 2% SCM), and overall community composition differed significantly with depth (PERMANOVA, $R^2 = 0.107$, $F = 2.51$, $p = 0.007$). Dinoflagellates prevailed at the surface (56%), while Ochrophyta dominated the SCM (52%). Among Ochrophyta, the diatom *Thalassiosira rotula* dominated the surface (19%), while an ASV matching *Eucampia groenlandica* (100% pid) prevailed in the SCM (46%), followed by *T. rotula* (11%). Among dinoflagellates *Gyrodinium helveticum* (20%) and *Karlodinium veneficum* (14%) were most abundant.

As in the KS, dinoflagellates strongly dominated the RP cluster (57%), followed by ochrophytes (25%), while cryptophytes reached up to fivefold higher abundances (8%) than in the other regions. The most abundant ASVs were an unknown dinophyte (35%; highest similarity to *Karenia papilionacea* (pid 99.7) and *Prorocentrum* sp. (pid 99.7), the diatom *Chaetoceros neogracilis* (32%), and the cryptophyte *Teleaulax gracilis* (64%). Interestingly, chlorophytes varied only slightly among regions (4–8%), but were dominated by *Micromonas polaris*, whose relative abundance within Chlorophyta ranged from 29% in the RP to 94% in the KS surface. Within the Ochrophyta, diatoms (*Bacillariophyceae*) were most abundant in all clusters (77–94%), yet slightly declined as golden algae (*Chrysophyceae*) increased to 15% in the RP and 13% in the surface KS, with ASVs belonging to the genus *Dinobryon* being the most abundant (38–94%; Table S7).

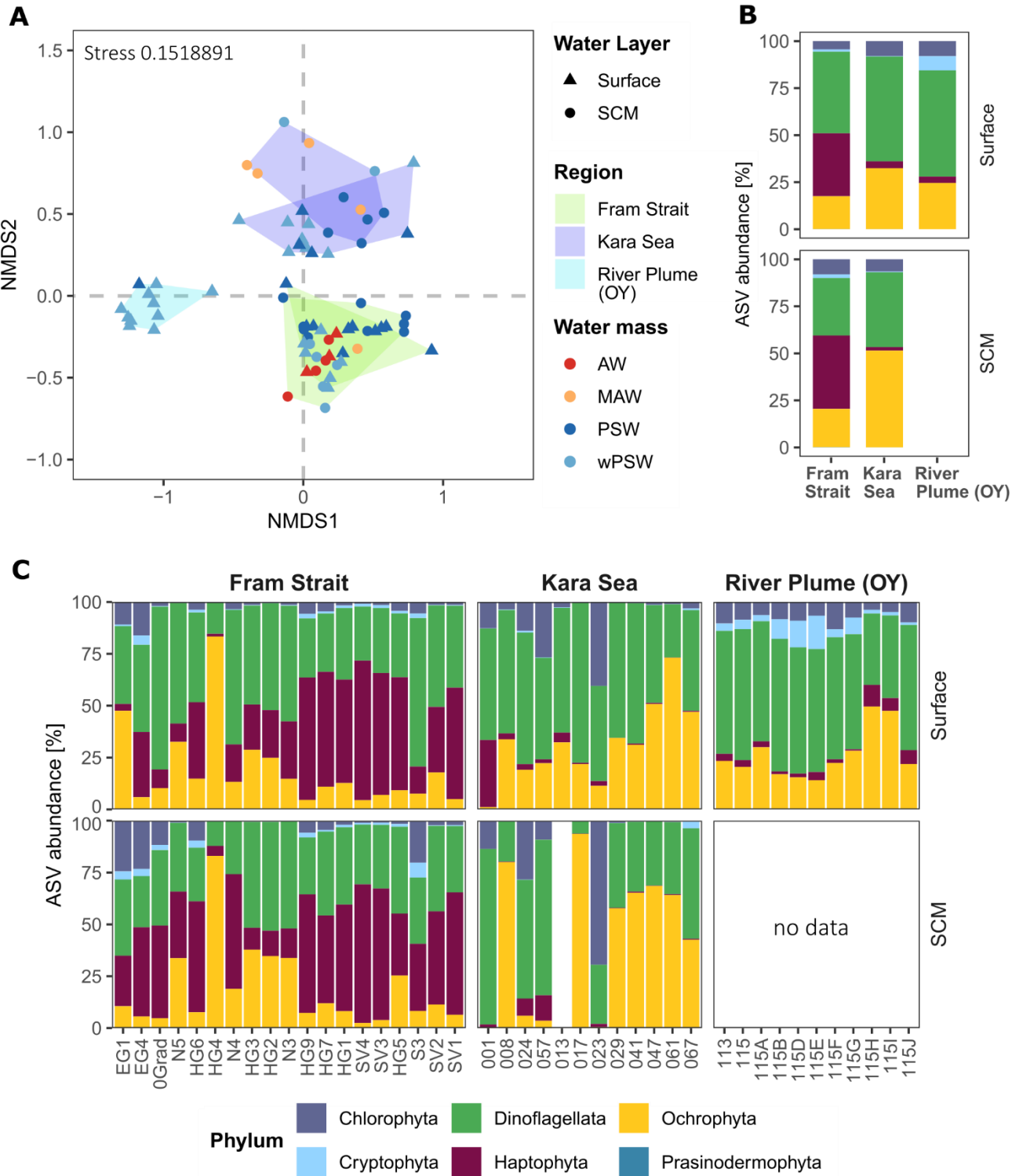


Figure 5: Spatial distribution patterns of phytoplankton community composition at the surface and in the subsurface chlorophyll *a*



385 **maximum layer (SCM): (A) Non-metric multidimensional scaling (NMDS) plot illustrating differences in protist community composition between regions. The ordination is based on Bray-Curtis dissimilarity distances of Hellinger-transformed amplicon sequence variants (ASVs). Colours indicate geographical region, shape indicates water layer, and point colour denotes water mass: AW (Atlantic Water), MAW (Modified Atlantic Water), PSW (Polar Surface Water), wPSW (warm Polar Surface Water). The 2D stress value is displayed in the plot. (B) Mean relative abundance of ASVs grouped by phytoplankton phylum level for each region. (C) Relative abundance of phytoplankton ASVs grouped at the phylum level across individual samples. Colours represent phytoplankton phyla.**

3.4.2 Variability within geographical regions

While protist community composition differed strongly among regions, notable within-region variability was also observed (Fig. 5C). Hierarchical clustering identified two to four robust clusters per region (Fig. S7). Although cluster numbers were similar between depth, station assignment differed, particularly in the KS.

395 In the FS, two clusters were observed across depth. One cluster was dominated almost entirely by a single ASV assigned to *Chaetoceros gelidus*, accounting for 72% at the surface and 79% at SCM of HG4, with lower contributions at nearby stations (25% SCM HG3 and 21% SCM HG2). The second cluster was characterized by low ochrophyte contributions and instead a dominance of *Phaeocystis pouchetii*, (~32% surface; ~40% SCM).

In the KS, clustering differed strongly between surface and SCM samples. In surface waters, two of the three clusters
400 corresponded to station 61, dominated by ochrophytes (73%), with the two most abundant ASVs assigned to the genus *Thalassiosira* (38%), and station 29, dominated by the dinoflagellate *Gyrodinium helveticum* (44%). The remaining stations formed the third cluster defined by *Gyrodinium* spp. and the chlorophyte *Micromonas* sp. In the SCM, the largest cluster (stations: 8, 17, 41, 29, 47, 61, 67) was characterised by diatoms, primarily *Thalassiosira* spp. and *Eucampia* spp. Stations 8 and 17 were dominated by *Eucampia* sp. (77–88%), stations 29, 41 and 47 exhibited mixed assemblages, while stations 61 and
405 67 had higher *Thalassiosira* spp. contributions (45% and 16%). The second SCM cluster (stations: 24, 57) was characterised by *Micromonas polaris* (~19%), followed by *Karlodinium* sp. (~9%), while in the third cluster (stations: 1, 23) an unknown Dinophyceae lineage (~39%) and *M. polaris* (~34%) prevailed.

Four subclusters were identified in the RP. The first (stations: 113, 115, 115A) and second (stations: 115B-G) cluster were dominated by *Gymnodinium* sp. (16% and 11%) and unidentified dinoflagellates (single ASVs between 16 and 26%),
410 with Cluster 2 showing higher cryptophyte contributions, particularly *Teleaulax gracilis* (7%). A third cluster (stations: 115H, 115I) was defined by the diatom *Chaetoceros neogracilis* (22%), whereas a fourth cluster (115J) was characterised by a *Gymnodinium* sp. ASV (15%) distinct from those in the other clusters, and notable contributions of dinoflagellates *Biecheleria* sp. (10%) and *Gyrodinium spirale* (9%).

3.4.3 Region-specific protist indicator species

415 To identify individual taxa with a high prevalence for a specific geographical region, we conducted an indicator species analysis. In total, 236 ASVs were identified as significant indicators ($p \leq 0.01$ & $\text{stat} \geq 0.3$) for FS (68), KS (52), and the RP (116). Identified indicator taxa were distinct among regions, but not restricted to them (Fig. 6 and Table S8). We focused on



abundant indicator taxa, as we expect them to exert a stronger influence on biogeochemical processes. For the FS, *Phaeocystis*
pouchetii ($p=0.0001$, $\text{stat}=0.8$) was most abundant $\sim 32.4\%$, even reaching $\geq 50\%$ (stations: SV1, SV3, SV4, HG9), followed
420 by *Heterocapsa* sp. with $\sim 1.7\%$ and up to 11% at station N3. In the KS, the most abundant ASV was assigned to the diatom
genus *Eucampia* ($p=0.0006$, $\text{stat}=0.43$), with an average of 15.4% and a wide range from less than 1% to 63% across stations,
along with the dinoflagellate *Karlodinium* sp. ($\sim 3.4\%$). The RP was characterised by dinoflagellate indicator species, the most
abundant ASV ($p=0.0001$, $\text{stat}=0.82$, averaging 19.1%) being an unidentifiable dinoflagellate showing 99.7% similarity the
genera *Gyrodinium* and *Prorocentrum*.

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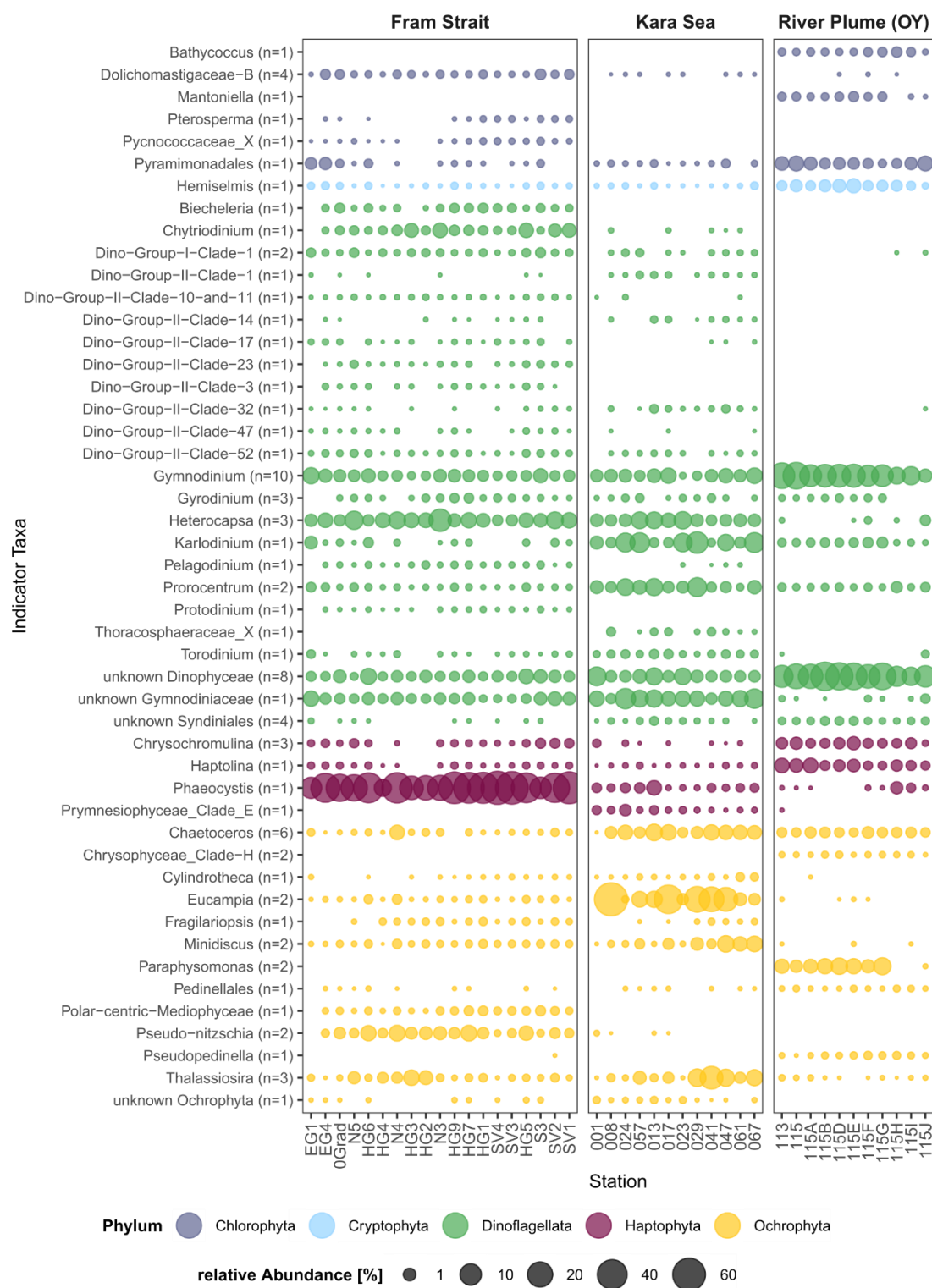


Figure 6: Bubble chart of protist indicator taxa abundance across stations, grouped by region. The 30 ASVs with the highest stat



values per region were grouped at the genus level whenever possible, with n denoting the number of ASVs contributing to a given taxon. Where genus-level assignment was not feasible, higher taxonomic groups were used. Bubble sizes are proportional to the square root of relative abundance (%) and coloured by phylum. Note that indicator taxa identified for a particular region are not restricted to that region and are also present in other regions (Table. S7).

3.5 Environmental drivers of community composition

The RDA model explained approximately 23% of protist community variation (Fig. 7A). Forward selection identified salinity, nitrite (NO_2^-) and phosphate (PO_4^{3-}) as significant predictors, whereas temperature showed only a weak effect and silicate (SiO_2) as well as nitrate (NO_3^-) were excluded due to multicollinearity. Permutation tests confirmed that the overall model was significant ($F = 5.04$, $p = 0.001$) and that salinity ($F = 10.57$, $p = 0.001$), NO_2^- ($F = 4.09$, $p = 0.001$) and PO_4^{3-} ($F = 3.66$, $p = 0.001$) contributed significantly, whereas temperature was not significant at $\alpha = 0.05$ ($F = 1.82$, $p = 0.068$). Only the first two canonical axes were significant (RDA1: $F = 11.85$, $p = 0.001$; RDA2: $F = 5.89$, $p = 0.001$) and retained for interpretation. Assemblages from the KS were primarily associated with elevated NO_2^- , whereas FS communities were more strongly related to PO_4^{3-} . RP assemblages aligned with lower salinity, higher temperatures, and higher Si(OH)_4 concentrations.

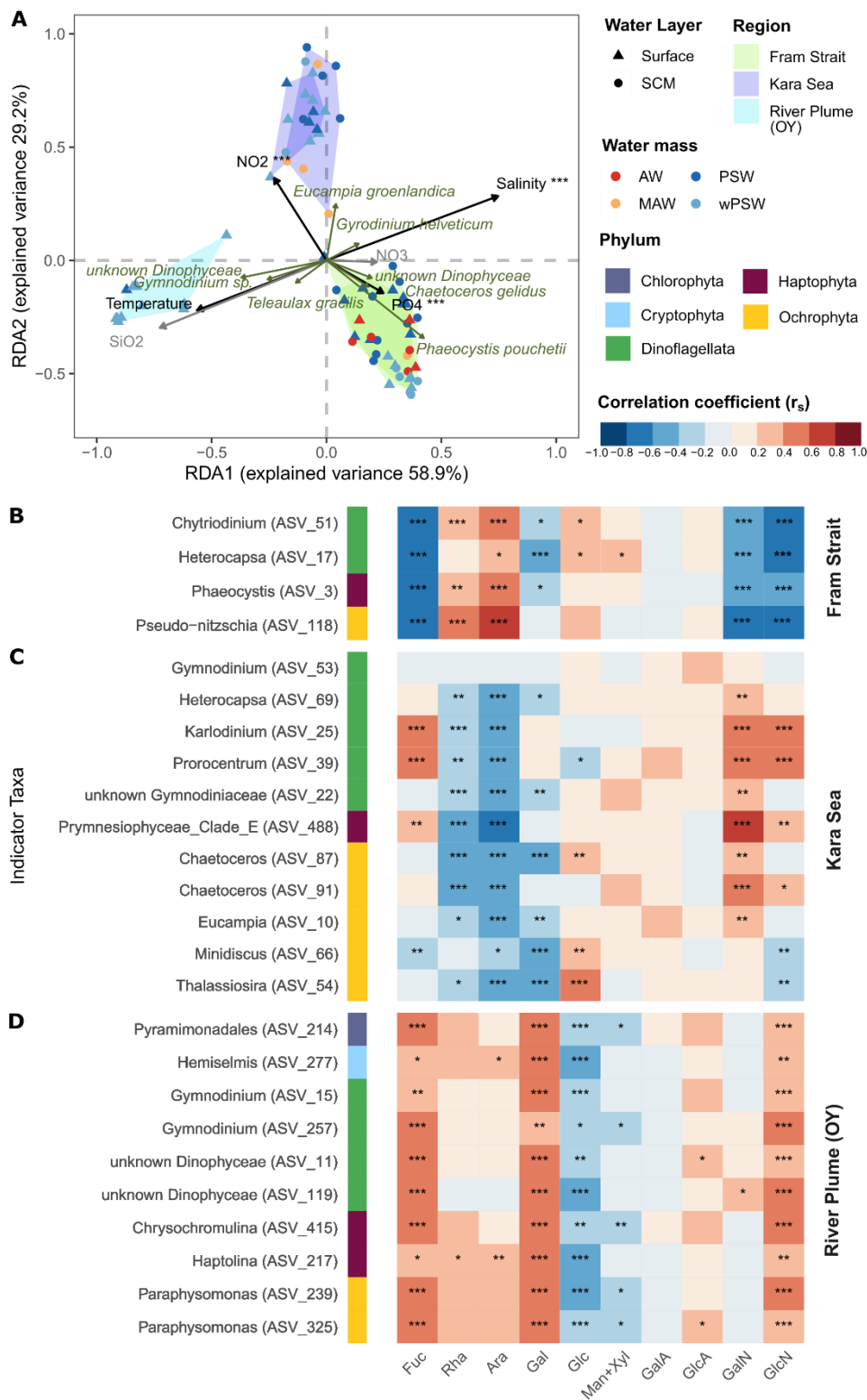


Figure 7: Redundancy Analysis (RDA) of phytoplankton community composition and environmental drivers (A). Convex hulls show



geographical regions, point colours indicate water masses and shapes denote water layers. Arrows represent environmental variables identified via forward selection (black = selected, gray = excluded), with significance assessed by permutation tests of RDA model terms (999 permutations). Green arrows indicate the 8 most abundant ASVs across all samples, highlighting taxa contributing most strongly to community variation. Panels B - D illustrate pairwise Spearman correlations of relative abundances of phytoplankton indicator ASVs (relative abundances >1%) with dissolved carbohydrates (DCCHO, mol%) for Fram Strait (B), Kara Sea (C) and the Ob-Yenisei River Plume (D). DCCHO abbreviations are: Ara, arabinose; Fuc, fucose; GalN, galactosamine; Gal, galactose; GalA, galacturonic acid; GlcN, glucosamine; Glc, glucose; GlcA, glucuronic acid; Man+ Xyl, mannose + xylose; Rha, rhamnose. Colour-coded bar indicates phylum affiliation, while the blue-to-red scale reflects correlation strength. Significant correlations are highlighted according to significance levels (p-values: < 0.001 ***, 0.001-0.01 **, 0.01-0.05 *, > 0.05).

3.6 Linking protist community to carbohydrate composition

A Mantel test analysis revealed a significant correlation between phytoplankton community structure and DCCHO composition (Spearman's $r = 0.31$, $p < 0.001$). To further examine the relationship between individual indicator taxa of each region and specific monomeric sugars, we applied pairwise Spearman correlations. In the FS, the haptophyte *Phaeocystis* sp. and the diatom *Pseudo-nitzschia* sp. were strongly positively correlated with rhamnose and particularly arabinose, whereas the dinoflagellate *Heterocapsa* sp. showed weaker positive correlations with arabinose, galactose and glucose (Fig. 7B). Across all taxa, significant negative associations were observed with fucose and amino sugars. In contrast, indicator taxa in the KS were positively associated with fucose and amino sugars, including dinoflagellates of the genera *Karlodinium* and *Prorocentrum* as well as an unidentified prymnesiophyte (Fig. 7C). Only diatoms showed significant positive correlations with glucose, with *Thalassiosira* sp. exhibiting the strongest relationship, followed by *Minidiscus* sp. and *Chaetoceros* sp. *Eucampia* was the only diatom lacking a significant association with glucose but instead showed a positive correlation with galactosamine. In the RP, all indicator taxa, regardless of phylogenetic affiliation, were negatively correlated with glucose and mannose+xylose but positively associated with galactose, fucose and glucosamine and to a lesser extent with glucuronic acid (Fig. 7D). Notably, galactosamine showed no significant correlations with any taxa except for a single unidentified dinoflagellate.

4. Discussion

Our study examined how regional and seasonal differences in phytoplankton community composition are associated with the quantity and quality of DOM and the formation of TEP across contrasting Arctic sectors. Disentangling these relationships is critical to understanding how shifts in phytoplankton communities influence the balance between carbon recycling in the microbial loop and carbon export. To address this, we assessed DOM origin and diagenetic state using established biogeochemical proxies, including DOC concentrations, DCCHO composition and DOC:DON ratios (Repeta, 2015), allowing us to interpret regional patterns in organic matter sources and microbial processing within the context of bloom dynamics and hydrography.



4.1 Regional and seasonal phytoplankton bloom dynamics

475 The primary spring bloom in the FS is initiated by sea-ice retreat and increasing light availability (Cherkasheva et al., 2014). In late May to late June, we observed main bloom events in the transition zone between the WSC and the EGC, particularly at wPSW- and PSW-dominated HAUSGARTEN (HG) and northern stations (N), confirming earlier observations that spring blooms tend to develop first in polar waters before spreading into Atlantic waters (Lampe et al., 2021; 2026). Elevated chl-*a* concentrations ($\sim 2\text{--}4\ \mu\text{g L}^{-1}$) exceeded the majority of previously reported values for June to October ($\sim 1.5\ \mu\text{g L}^{-1}$; Piontek et al., 2014; Nöthig et al., 2020; von Jackowski et al., 2020). Concurrently, nitrate concentrations were substantially reduced (~ 3.4 and $\sim 1.6\ \mu\text{mol L}^{-1}$) relative to winter-replenished levels ($\sim 11\ \mu\text{mol L}^{-1}$; von Appen et al., 2021). Together, the elevated chl-*a* concentrations and substantial nitrate drawdown indicate that the spring bloom already reached an advanced stage, further supported by low phytoplankton evenness and the dominance of single phytoplankton taxa (ASVs), consistent with reduced community complexity during late bloom stages.

485 The spring bloom community was dominated by either diatoms or haptophytes. One bloom event, confined to HG4, was strongly dominated the diatom *Chaetoceros gelidus* and occurred under partial ice coverage ($\sim 80\%$), which is consistent with a typical ice-edge diatom bloom (Rat'kova & Wassmann, 2002; Weiß et al., 2024). Another bloom event was characterised by high proportions of *Phaeocystis pouchetii* and frequent occurrences of the dinoflagellate genus *Gyrodinium* and the order Syndiniales. The co-occurrence of *Gyrodinium* spp., a reported grazer of *Phaeocystis* (Grattepanche et al., 2011) and Syndiniales, an order that includes many parasitic lineages known to recycle phytoplankton biomass (Clarke et al., 2019), suggests that multi-trophic interactions may have contributed to bloom dynamics and biomass turnover.

In contrast to the FS, depleted nitrate, phosphate, and silicate concentrations, alongside slightly elevated nitrite levels indicative of active microbial remineralization and nitrification (Tuerena et al., 2021), point to nutrient-limited post-bloom regime in the KS and RP. Such conditions favoured a mixotrophic, phagotrophic and bacterivorous community dominated by 495 dinoflagellates (*Karlodinium* spp., *Gymnodinium* spp., *Gyrodinium* spp.), as well as taxa from Cryptophyceae (*Teleaulax* sp., *Hemiselmis* sp.), Chrysophyceae (*Dinobryon* spp.), and Chlorophyta (*Micromonas* spp.), characteristic of resource limitation and enhanced recycling within the microbial loop (Stoecker & Lavrentyev, 2018; Li et al., 2022). Consistently low surface chl-*a* concentrations and frequent subsurface chlorophyll *a* maxima are in accordance with previous late-summer observations for this region (Demidov et al., 2021; Bukatov et al., 2025).

500 The weak correspondence between chl-*a* distribution and distinct water mass boundaries suggests that bloom development was primarily governed by local-scale processes such as nutrient regeneration, and ice-edge dynamics. Exceptionally high chl-*a* concentrations (~ 6.5 to $8\ \mu\text{g L}^{-1}$) along the shelf break of the KS, likely related to the sea-ice edge (Fig. S8), were dominated by *Thalassiosira* spp., large cold-water diatoms commonly associated with first-year ice (Makarevich et al., 2015; Pautova et al., 2024). *Thalassiosira* spp. are typically observed during the second stage of ice-edge-bloom succession, following an initial phase dominated by small diatoms such as *Chaetoceros socialis* (Rat'kova & Wassmann, 2002). The advanced stage of this bloom is further supported by pronounced subsurface chl-*a* maxima (e.g.,



stations 41, 47, 67), consistent with the under-ice to ice-edge to deep open-water progression described by Mayot et al. (2018). Only station 61 showed elevated surface and subsurface chl-*a* concentrations under ~40% sea-ice cover, indicative of an ongoing ice-edge bloom.

510 Mesoscale hydrographic processes, including riverine inputs and Atlantic inflow, further influence phytoplankton community structure and bloom development in the KS. At shelf-edge station 57, a pronounced riverine signal from the Ob and Yenisei rivers detected in the Voronin Trough during the Arctic Century expedition (Pérez-Tribouillier et al., 2025) likely modified nutrient availability, thereby influencing phytoplankton growth conditions and subsequent DOM production and transformation. In addition, the strong influence of Barents Sea-derived Atlantic waters in the St. Anna Trough (Pérez-
515 Tribouillier et al., 2025) coincided with an increasing contribution of *Eucampia groenlandica* at western stations. The pronounced occurrence of *E. groenlandica*, similar to recent observations linked to intensified Atlantic inflow in the Franz Victoria Trough (Pautova et al., 2024), together with the first reported appearance of *Phaeocystis* colonies in June 2021 (Sergeeva et al., 2025) and their confinement to stations along the Atlantic inflow pathway (stations 8, 13, 17, 29, 41, 47), suggests a hydrographically mediated community shift with potential implications for future DOM dynamics. Our observations
520 highlight pronounced regional and seasonal contrasts in bloom dynamics from an advanced spring bloom in the FS, dominated by *Phaeocystis pouchetii* and *Chaetoceros gelidus*, to predominantly post-summer bloom with nutrient-recycling regimes, and punctuated by localized ice-edge and shelf-margin *Thalassiosira* spp. blooms in the KS and RP.

4.2 Contrasting DOM sources

To interpret regional differences in DOM composition, we distinguished between autochthonous DOM produced by
525 phytoplankton and allochthonous DOM originating from terrestrial sources, as they differ markedly in composition and reactivity. Across the FS, DOM quantity and composition reflected the combined influence of hydrography and bloom dynamics. Waters influenced by the WSC exhibited lower DOC concentrations and DOC:DON ratios than PSW transported by the EGC, which carries terrigenous DOM originating from Eurasian rivers (Amon & Budéus, 2003; Engel et al., 2026). DOC concentrations were consistent with previously reported values for Atlantic (~60 $\mu\text{mol L}^{-1}$) and polar waters
530 ($79 \pm 19 \mu\text{mol L}^{-1}$) in the region (Amon et al., 2024; Engel et al., 2026), while DOC:DON ratios remained at the lower end of the regional range (10-25; Lara et al., 1998), pointing towards a substantial contribution of phytoplankton-derived DOM. Moreover, NS yields in PSW and wPSW exceeded those observed in the KS, reaching up to 19 %DOC and falling within the upper range reported for other polar marine environments (Kirchman et al., 2001; Amon & Benner, 2003; Panagiotopoulos et al., 2014). Elevated NS yields likely reflect enhanced carbohydrate exudation during active or late-stage phytoplankton
535 blooms, when neutral sugar concentrations can increase several-fold (Obernosterer & Herndl, 1995; Kirchman et al., 2001; von Jackowski et al., 2022). Taken together, DOM composition in the FS reflects a mixed signal shaped by the interplay between advected terrestrial inputs via the EGC and spring bloom-derived marine DOM.

In the KS, comparatively low DOC concentrations and DOC:DON ratios (~10) suggest a predominantly marine DOM signal with little discernible riverine influence. This is consistent with the eastward extension of the Ob-Yenisei plume toward



540 the Vilkitsky Strait rather than into the central KS, and with Barents Sea-derived Atlantic waters influencing the St. Anna
Trough surface waters (Pérez-Tribouillier et al., 2025). Low chl-*a* concentrations and amino sugar signatures, which are
indicative of microbial reworking as they accumulate due to their low decay rates (Benner & Kaiser, 2003; Kawasaki & Benner,
2006), suggest that the DOM pool was already partially degraded, reaffirming post-bloom conditions (von Jackowski et al.,
2022). However, elevated chl-*a* concentrations at selected stations influenced by PSW and ice showed increased NS yields (~7
545 %DOC), within the range reported for freshly produced phytoplankton-derived DOM (4.1-9.6 %DOC, Amon & Benner, 2003),
which indicates localized inputs of labile organic matter.

In the RP, high DOC concentrations and elevated DOC:DON ratios are consistent with a strong terrestrial influence
on the DOM pool, as previously observed from the Ob and Yenisei estuaries (Amon & Benner, 2003). Average DOC
concentrations (~340 $\mu\text{mol L}^{-1}$) were lower than previously reported values from the river mouths (423-537 $\mu\text{mol L}^{-1}$), likely
550 reflecting sampling near the plume margin. DOC:DON ratios of ~29 fall at the lower end of the range reported for these
estuaries (29-51; Köhler et al., 2003), further suggesting partial mixing with shelf waters. Despite the predominantly
terrigenous signal, NS yields were higher than typically expected for refractory terrestrial DOM (1.7–3.5 %DOC; Amon &
Benner, 2003), reaching ~3.9 %DOC and up to ~5 %DOC at the easternmost stations (113, 115). These elevated yields may
partly reflect the relatively high DCCHO content previously reported for the Ob and Yenisei compared with other Arctic river
555 systems such as the Lena and Mackenzie (Kaiser et al., 2017), while the highest values at the easternmost stations may suggest
additional “fresh” inputs from algal release under partial sea-ice cover.

Disentangling terrestrial and phytoplankton-derived signals in the river plume region is challenging, as both sources
can contribute overlapping carbohydrate signatures. Galactose, for example, accounted for a higher proportion of
carbohydrates in the RP than in the other regions, but may originate from multiple sources, including non-woody plant tissue,
560 soil bacteria, and phytoplankton-derived organic matter (Cowie & Hedges, 1984; Biersmith & Benner, 1998; da Cuhna et al.,
2002). Previously discussed DOC:DON ratios, together with very low nutrient concentrations and a predominantly
mixotrophic phytoplankton community, suggest that terrestrial inputs and subsequent microbial processing exerted a stronger
influence on the DOM pool than recent phytoplankton production. This is in line with Kaiser et al. (2017), who reported a
comparable neutral sugar composition for the Ob and Yenisei, with galactose contributions of up to 15%, and linked the
565 relatively uniform neutral sugar patterns across Siberian rivers to early degradation stages of plant-, soil-, and bacterially
derived organic matter. A notable difference from the pattern reported by Kaiser et al. (2017) is the higher contribution of
fucose relative to rhamnose in our samples, which may reflect flow-regime-related variability; however, as both sugars have
been linked to bacterial reworking in river plumes, this shift may still be consistent with a microbially influenced DOM signal
(Guggenberger et al., 1994; Panagiotopoulos et al., 2012). Thus, the carbohydrate signature in the RP likely reflects a mixture
570 of terrestrial plant- and soil-derived as well as bacterially processed DOM, rather than a predominantly phytoplankton-derived
source.



4.3 Taxonomic controls on DOM composition and implications for TEP formation

Distinct DCCHO molecular signatures across bloom types indicate taxon-associated differences in DOM quality. In the FS, *Phaeocystis*-dominated blooms were characterised by an enrichment of neutral (arabinose, rhamnose, and glucose) and acidic sugars, likely reflecting a complex heteropolysaccharide-rich DOM pool and coinciding with high TEP concentrations. These observations align with previous studies indicating that rhamnose and arabinose are major components of *Phaeocystis*-derived DOM and occur in higher relative proportions than in DOM produced by phytoplankton species from other genera (Biersmith & Benner, 1998; Aluwihare & Repeta, 1999; Alderkamp et al., 2007). Rhamnose- and arabinose-containing compounds are often associated with the production of polysaccharide-rich colonial mucus containing gel-forming acidic components. Both neutral deoxy-sugars (e.g., rhamnose and fucose) and uronic acids (e.g., glucuronic acid and galacturonic acid) have been linked to TEP formation (Alldredge et al., 1993; Skoog et al., 2008; Engel et al., 2012), with the latter playing a key role in aggregation via cation bridging (Passow, 2002; Engel et al., 2004a; Mari et al., 2005). In the present study, however, acidic sugars contributed only a minor fraction of the bloom-associated DCCHO pool (< 2 mol%), whereas previous high-TEP bloom studies reported uronic acid contributions of ~26 mol% of DCCHO in a coccolithophorid-dominated (Engel et al., 2012) and ~16 mol% of total CCHO in a diatom-dominated bloom (Sperling et al., 2017). The low abundance of acidic sugars may either reflect their rapid incorporation into TEP or indicate that acidic sugars are less dominant components of TEP produced in *Phaeocystis*-dominated systems, leaving potential taxon-specific differences in TEP composition unresolved.

In the KS, diatom-dominated blooms were characterized by a strong glucose signal alongside reduced contributions from most other sugars, indicating a simpler exopolysaccharide composition and coinciding with surprisingly low TEP concentrations. This was unexpected given the abundance of *Thalassiosira* spp., as several species within this genus are known to produce TEP precursors, although the amount released can vary among species (Burns et al. 2019). Low TEP concentrations may therefore reflect interspecies variability or additional mechanisms influencing exudation. A potential mechanism may relate to the overflow hypothesis, whereby excess fixed carbon is released when photosynthetic carbon fixation exceeds the capacity for growth under nutrient limitation (Fogg, 1966, 1983; Williams, 1990). Low nutrient conditions towards the end of the diatom bloom may therefore have favoured overflow-related glucose release, consistent with laboratory observations of nutrient-limited *Thalassiosira pseudonana* releasing carbohydrates composed almost exclusively of glucose (Urbani et al., 2005). In natural phytoplankton communities, glucose was also the dominant sugar accumulating in the DCCHO pool triggered by photosynthetic overflow (Barthelmeß et al., 2025), pointing to the importance of glucose and its role as a component of storage polysaccharides such as β -1,3-glucans in diatoms (Becker et al., 2020). Degradation of less complex polysaccharides or homopolysaccharides, composed primarily of one monomer species, requires fewer enzymatic steps and thus lower energetic investment compared to structurally complex heteropolysaccharides (Unfried et al., 2018; Sichert et al., 2020; Vidal-Melgosa et al., 2021). Thus, the pronounced enrichment of glucose could indicate a less structurally complex polysaccharide pool, which may have favoured microbial recycling over TEP formation, despite substantial carbon release.



5. Conclusion

605 In the Arctic Ocean, dissolved carbohydrate signatures and TEP dynamics varied in relation to regional hydrography, seasonal succession, and bloom identity. Distinct bloom regimes (i.e., haptophyte versus diatom dominance) were associated with contrasting DOM signatures and aggregation potential: an advanced spring bloom dominated by *Phaeocystis pouchetii* was associated with a DOM pool particularly enriched in arabinose, rhamnose, glucose and acidic sugars as well as elevated TEP concentrations, whereas localized ice-edge diatom blooms dominated by *Thalassiosira* spp. showed glucose-enriched DOM signatures indicative of simpler polysaccharides, and coinciding with comparatively low TEP formation. Under post-bloom conditions communities were characterized by mixotrophic, phagotrophic, and bacterivorous taxa, low TEP concentrations, elevated amino sugar contributions and nitrite levels, consistent with advanced DOM reworking. These observations provide direct field-based evidence that differences in phytoplankton bloom composition and stage are reflected in the molecular signature of dissolved carbohydrates and may translate into contrasting aggregation potential. The occurrence of *Eucampia* 615 *groenlandica* along Atlantic inflow pathways provides further evidence for climate-induced changes such as Atlantification and their role in restructuring planktonic communities. Changes in phytoplankton community composition may alter DOM quality by favouring either structurally complex, aggregation-prone polysaccharides or less complex, more labile biopolymers, thereby influencing whether organic carbon is primarily retained in the surface waters within the microbial loop or exported to the deep ocean via TEP-mediated aggregation. To understand the potential consequences of future community shifts, further 620 studies are needed to characterize taxon-specific polysaccharides and resolve their functional roles in TEP formation and microbial utilization.

Data availability

Environmental data will be archived in the PANGAEA World Data Centre and amplicon data will be deposited in the European Nucleotide Archive (ENA) at EMBL-EBI and is for PS126 already accessible under PRJEB108237.

625 Author contributions

Sophia Hirschmann: data curation, formal analysis, validation, visualization, writing - original draft, writing - review & editing. **Anabel von Jackowski:** investigation, funding acquisition, supervision, writing - review & editing. **Benjamin Pontiller:** supervision, writing - review & editing. **Katja Metfies:** investigation, resources, writing - review & editing. **Vasily Povazhnyi:** investigation. **Stefan Neuhaus:** data curation, writing - review & editing. **Eva-Maria Nöthig:** investigation, 630 writing - review & editing. **Anja Engel:** conceptualization, funding acquisition, resources, supervision, project administration, writing - review & editing.



Competing interests

The authors declare no conflicts of interest.

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