Response to RC1

RC1: 'Comment on egusphere-2026-4192', Anonymous Referee #1, 30 Jul 2026

We thank the reviewer for the evaluation of our manuscript and for the helpful and constructive comments.

General comments:

I found the manuscript very thorough in how methods were documented and results were reported, which is evidenced in the few issues I am raising below. The figures are well designed and in particular the graphical abstract and the map in figure 1 are very illustrative. At times, following the test was complicated by the number of abbreviations and their inconsistent use. Most notably, I found that while a lot of detailed information was provided, as a reader it was difficult to connect this information logically. For me, the multiple levels of grouping of the samples (by location, by water mass, by apparent bloom state) and their interspersed use made drawing connections between data across different figures complicated. While the actual scientific questions and issues I have are few and only technical, I personally think that the overall message of the manuscript regarding 'bloom regimes' requires more context to be informative and convincing.

Response: We thank the reviewer for the positive assessment of our methods and figures and for the constructive comments on readability. In the revised manuscript, we will improve the clarity of the text by reducing the number of abbreviations and simplifying the grouping of samples. Specifically, we will:

- add a table of abbreviations to the Supplement.
- no longer use the abbreviations FS, KS and RP for the Fram Strait, the Kara Sea and the River Plume.
- remove the categorical classification into bloom and non-bloom samples (see our response to the specific comment below) and use region as the primary grouping throughout the manuscript.
- move detailed information e.g. on water mass properties, nutrient distribution (Section 3.1) and chl-*a* distribution (Section 3.2) to the Supplement.
- shorten the description of the phytoplankton community (Section 3.4) to regional differences, dominant taxa and the indicator taxa used in subsequent analyses, and move detailed cluster descriptions, diversity indices and within-phylum details to the Supplement.
- restructure the Results: (1) environmental setting, including hydrography, nutrients and chl-*a*; (2) concentration and composition of dissolved combined carbohydrates (DCCHO); (3) TEP distribution and its relation to carbohydrate concentration and composition; (4) DCCHO relation to phytoplankton biomass; (5) phytoplankton community composition; (6) the relative contributions of community composition, biomass, environmental conditions and region to carbohydrate composition; and (7) taxon-specific carbohydrate signatures..

We address the reviewer's concern regarding the bloom concept in detail in our response to the specific comments below.

Specific comments:

In particular, the classification of bloom conditions requires additional support in my opinion. I am under the impression that the observational data on chlorophyll, nutrients, carbohydrates and community composition was used to deduce bloom conditions, i.e. whether a bloom had occurred or

was occurring, but that this observational data was then also interpreted in the context of the deduced bloom status. For example, ll. 333-335: "Bloom conditions were defined as both chl-a concentrations > 1 µg 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 KS, bloom samples showed a twofold increase in DCCHO concentrations compared to non-bloom samples." This logic appears circular, because if I am not mistaken, NS and DCCHO are both based on the same carbohydrate quantification. This manuscript could be a lot stronger with an orthogonal determination of bloom conditions.

Response: We thank the reviewer for raising this point. Our intention was to combine phytoplankton biomass (chl-*a*) with an indicator of freshly produced DOM, as neutral sugar yields above 5.9 %DOC have been used to distinguish fresh from diagenetically altered DOM in the Arctic Ocean (Amon & Benner, 2003). The aim was to identify samples in which recent phytoplankton production was reflected in the DOM pool, rather than relying on chl-*a* alone. We acknowledge, however, that this classification is not fully independent of the carbohydrate data subsequently compared between bloom and non-bloom samples.

In the revised manuscript, we therefore replace the categorical bloom classification by a correlation analysis that treats phytoplankton biomass as a continuous variable that is independent of the carbohydrate data. Specifically, we examine correlations between chl-*a* and total DCCHO as well as individual monosaccharides (concentrations and mol%).

These analyses show that chl-*a* was not significantly related to total DCCHO concentrations within either region (Fram Strait r_s = 0.31, p = 0.056, n = 38; Kara Sea r_s = 0.17, p = 0.43, n = 24), but to individual monosaccharides, which differed between regions. In the Fram Strait chl-*a* correlated with arabinose, rhamnose and glucuronic acid, and in the Kara Sea with glucose (Fig. R1). These results are consistent with the decoupling of DCCHO and chl-*a* previously reported for pelagic systems (Engel et al., 2012; Sperling et al., 2017). A categorical distinction between bloom and non-bloom conditions therefore adds little beyond the correlation analysis and would unnecessarily complicate the presentation of our main message. We will present these results in a new figure replacing Fig. 4 (see also our response to Reviewer 2, comment 2).

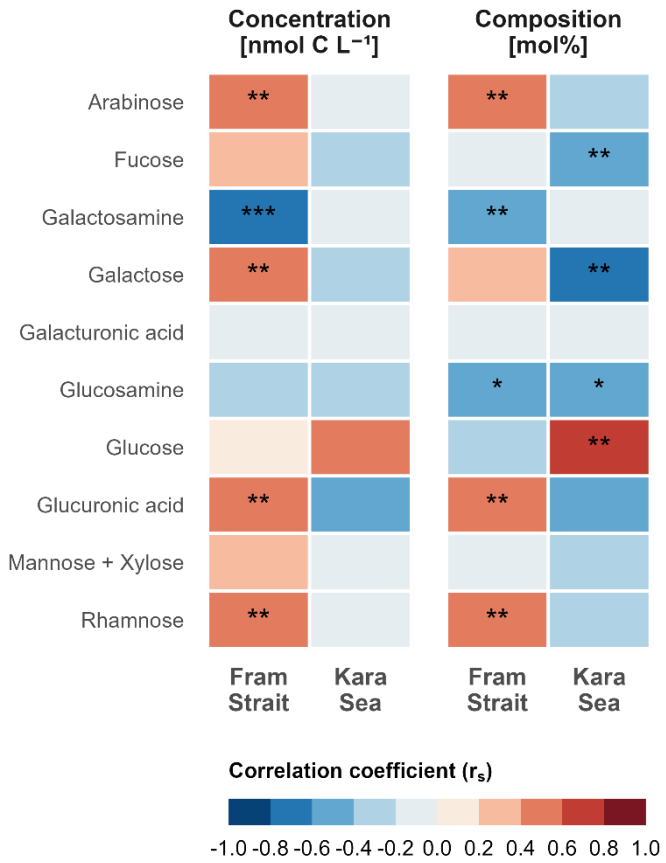


Figure R1: Spearman rank correlation coefficients (r_s) between chlorophyll-*a* (µg L^{-1}) and individual monosaccharides in the Fram Strait and Kara Sea, expressed as carbon-normalized concentration (nmol C L^{-1}) and relative composition (mol%). Significant correlations are highlighted according to significance level after Benjamini–Hochberg correction (p-values: < 0.001 ***, 0.001-0.01 **, 0.01-0.05 *, > 0.05).

Most prominently, this issue arises in section 4.1 “Regional and seasonal phytoplankton bloom dynamics”. This part of the discussion appeared to lean quite heavily on assumptions based on previous bloom dynamics, or if not then I did not understand where the information on the bloom dynamics originated from. In my opinion, interpreting the reported results in the context of bloom dynamics would highly benefit from some additional information on the time course of conditions in the sampled water masses. For example, if the authors could augment their observations with satellite or float data to interpret their observations in the context of ongoing processes, this section would stand to gain substantially in specificity. Without this context, I think it is difficult to compare the observations made on the two cruises beyond a purely descriptive standpoint.

Response: We thank the reviewer for this suggestion. In the original manuscript, our interpretation of bloom stages was based on our own observations, in particular chl-*a* concentrations, the drawdown of nitrate relative to reported winter concentrations and phytoplankton community composition and evenness, which we then compared with previously described bloom dynamics in the respective regions. Nevertheless, we agree that these observations are snapshots and do not capture the temporal development of the blooms, which limits our interpretation of bloom stages.

As the revised manuscript no longer relies on a categorical bloom classification (see our response above), we will no longer interpret our observations in terms of bloom stages. Instead, we will use the

seasonal and hydrographic context of the sampled regions to interpret differences in phytoplankton community composition and their potential influence on carbohydrate composition. We will therefore remove Section 4.1 and integrate the interpretation of seasonal differences into the Discussion where relevant, and address the snapshot nature of our observations in the new section on limitations (see also our response to Reviewer 2, comment 3).

We considered satellite-derived chl-*a* data to place our snapshot observations in a temporal context, but their use is limited in both regions by persistent cloud and sea-ice cover and, in the Kara Sea, by the frequent occurrence of subsurface chl-*a* maxima (two-thirds of the stations), which are not captured by ocean colour observations. Float data are, to our knowledge, not available for the sampled areas and periods.

Technical corrections:

For the graphical abstract, I would recommend following the Symbol Nomenclature for Glycans to depict the monosaccharides.

Response: We thank the reviewer for the helpful suggestion. The SNFG depicts glycan structures, whereas our data represent monosaccharide composition after acid hydrolysis. Therefore, depicting the monosaccharides with SNFG symbols could suggest structural information that our data do not contain. In the revised graphical abstract, we will adopt the SNFG colour scheme for the monosaccharides and depict them as linked units to indicate that they occur in oligo- or polysaccharide form, without implying specific linkages or structures.

line 191: How long did the HCl hydrolysis run, 24 hours?

Response: Hydrolysis was performed for 20 h at 100 °C, following Engel and Händel (2011). We will add this information to the methods section (Section 2.5).

line: 224: Why did you decide to compare to standardized DCCHO mol%?

Response: We thank the reviewer for pointing this out. We used molar percentages (mol%) rather than absolute concentrations because the aim of the PCA was to compare the relative composition of the carbohydrate pool independently of its total concentration, which differed considerably between regions (Fig. 3A). The mol% data were additionally standardized to give each monosaccharide equal weight in the ordination, so that differences in patterns of variation are emphasized. Without standardization, the most abundant monosaccharides, glucose and mannose + xylose, would dominate the analysis and mask compositional shifts in monosaccharides with smaller contributions. The magnitude of individual monosaccharides is addressed by other analyses in the manuscript, namely the composition of DCCHO in mol% (Fig. 3C).

e.g. l. 435: PO_4-3 should be $PO_4$3-

Response: We thank the reviewer for pointing this out; we will correct the notation to PO_4^{3-} at line 435 and check the manuscript for consistent use throughout.

lines 241ff and 453/454: Did you include any correction on the alpha-value for the many pairwise Spearman correlations?

Response: We thank the reviewer for this question. We did not apply any correction in the original submission. In the revision, we will report the corrected values using Benjamini-Hochberg false discovery rate (FDR) correction. Significance levels in the Results and in Fig. 7B–D will be updated accordingly, and the correction procedure will be described in the Methods (Section 2.7).

Figure 4a: Please specify which box depicts which water layer.

Response: We thank the reviewer for this comment. In Fig. 4, both water layers were pooled to calculate bloom-to-non-bloom ratios, which was not stated in the figure caption. As this figure will be replaced in the revised manuscript (see our response above), we will ensure that the treatment of water layers is clearly stated in the captions of all figures.

Figure 6 – legend: “relative Abundance” should not be capitalized

Response: We will correct the figure legend to “relative abundance”.

We thank the reviewer again for the constructive review of our manuscript. We expect that the proposed revisions outlined above will help to communicate the main messages of our manuscript more clearly.