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Spatial patterns in phytoplankton community composition and their influence on carbon export on the northwest Weddell Sea continental shelf

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Abstract. Typically, diatoms, haptophytes, and cryptophytes dominate phytoplankton biomass and abundance in the Southern Ocean, determining bloom dynamics and carbon transfer and respond to physical factors such as sea ice concentration and mixing. However, phytoplankton community composition remains understudied in many regions of the Southern Ocean. Here, we present pigment-based phytoplankton community-composition data from a summer cruise to the northwest Weddell Sea continental shelf. To our knowledge, these are the only pigment-based community composition data from this key region for deep-water formation and carbon transport. Taken together, the relative biomass of the three dominant phytoplankton groups (39.7% diatoms, 30.2% haptophytes, and 14.9% cryptophytes) explain the majority ($R^2 = 0.37 – 0.82$) of carbon export to 150 m. These findings highlight the need to consider frequently overlooked phytoplankton types, alongside diatoms, in Southern Ocean models of carbon export due to the key, but differing, roles these groups play in production-export dynamics.

1 Introduction

Phytoplankton community composition is a key driver in nutrient cycling, primary production, and carbon export across the ocean (Henson et al., 2021; Kramer et al., 2025). There is currently increased attention on the role of phytoplankton taxonomy in ocean processes with recent studies showing that climate change has already begun to shift phytoplankton abundance (Hong et al., 2025) and taxonomic patterns worldwide (Anderson et al., 2021; Cael et al., 2021). This trend is expected to continue with a restructuring of phytoplankton taxa in coming decades (Henson et al., 2021). In the Southern Ocean, some of these transitions appear to be linked to physical drivers, such as sea-ice concentration (Hayward et al., 2025), but evaluating the impacts of these shifts in ocean biogeochemistry and ecosystem functioning is complicated by regional

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differences and substantial interannual variability (Deppler and Davidson, 2017), making the need for regional measurements critical.

Despite its importance, phytoplankton community composition remains an understudied oceanographic indicator that is difficult to measure on large scales. The increase in hyperspectral capabilities on satellites (Gorman et al., 2019) and remotely-operated instruments (Suomalainen et al., 2021) has been instrumental in increasing the amount of phytoplankton community composition data collection to a level previously not possible (Cetinić et al., 2024). The launch of the NASA Plankton, Aerosol, Cloud, ocean Ecosystem (PACE) satellite was the biggest step forward to date toward achieving global, hyperspectral ocean colour data (Gorman et al., 2019). However, retrieving phytoplankton taxonomy from satellites relies on constructing relationships between remote sensing reflectance (R_{rs}) and phytoplankton community composition that must be validated by in-situ measurements (Sathyendranath et al., 2014, Bracher et al., 2017; Chase et al., 2017, Lange et al., 2020, Kramer et al., 2022). Currently, high performance liquid chromatography (HPLC) remains the standard by which phytoplankton pigments are measured and these R_{rs}-based models are validated, but the human sampling effort, cost, and analytical precision required for HPLC analysis limit the number of datasets that exist, particularly in remote regions such as the Southern Ocean.

Hayward et al. (2025) compiled HPLC datasets from the Southern Ocean (n = 14,824 samples), but their comprehensive dataset contains no HPLC samples from the Weddell Sea continental shelf. The phytoplankton community composition data that are available on high-latitude Antarctic continental shelves is highly biased towards the Western Antarctic Peninsula where repeat monitoring programs (Smith et al., 1995; Venables et al., 2023) enable data collection. Phytoplankton community composition sampling in the ice-heavy Weddell Sea is sparse, with most of our knowledge coming from several independent cruise programs occurring broadly in the Weddell Sea sector of the Southern Ocean, over varying months and years (Kang and Fryxell, 1993; Schloss and Estrada, 1994; Wright et al., 2009; Flynn et al., 2023). Here, we present results from 50 HPLC samples collected throughout the water column, and a few collected from melted sea ice, to investigate the spatial patterns of dominant phytoplankton groups and how these patterns compare with physical parameters and to POC flux across previously unsampled regions of the Weddell Sea continental shelf and slope region as part of the Processes Influencing Carbon Cycling: Observations of the Lower limb of the Antarctic Overturning (PICCOLO) program (Heywood and Bell, 2024). The patterns and relationships presented here provide novel understanding of phytoplankton community composition as it relates to carbon cycling within and out of the surface ocean in this important region for Southern Ocean deep-water formation.

2 Methods

2.1 Cruise overview

The PICCOLO cruise (SD035) occurred from 17 January (yearday (YD) 17) to 9 March (YD 69) 2024 aboard the *Royal Research Ship (RRS) Sir David Attenborough* in the northwest Weddell Sea region of the Southern Ocean (Heywood and Bell, 2024). The ship sampled across multiple, different oceanic regimes which can be classified as on the continental shelf and close to the Larsen-C Ice Shelf ("Larsen"; YD 32-33), on the continental shelf elsewhere ("shelf"; YD 47, 49, 55, 61, 129-134), from a transect sampling crossing the shelf-slope continuum ("transect"; YD 40-45), and on the continental shelf and near (approximately 0-200 m) to sea ice ("ice"; YD 48-50, 56-58; Figure 1). The Larsen samples were collected from a polynya that opened shortly before collection and proceeded to close shortly after collection. Water column samples were predominantly collected via a CTD rosette equipped with a Sea-Bird SBE 911+ CTD profiler. Sea ice samples were collected from either melted sea ice cores, in one case a particularly biomass-rich core termed "brown ice", or water pumped from the sea ice-ocean interface. The euphotic zone (measured as 1% of surface irradiance) ranged from 23 – 100 m with an average of 55 ± 21 m.

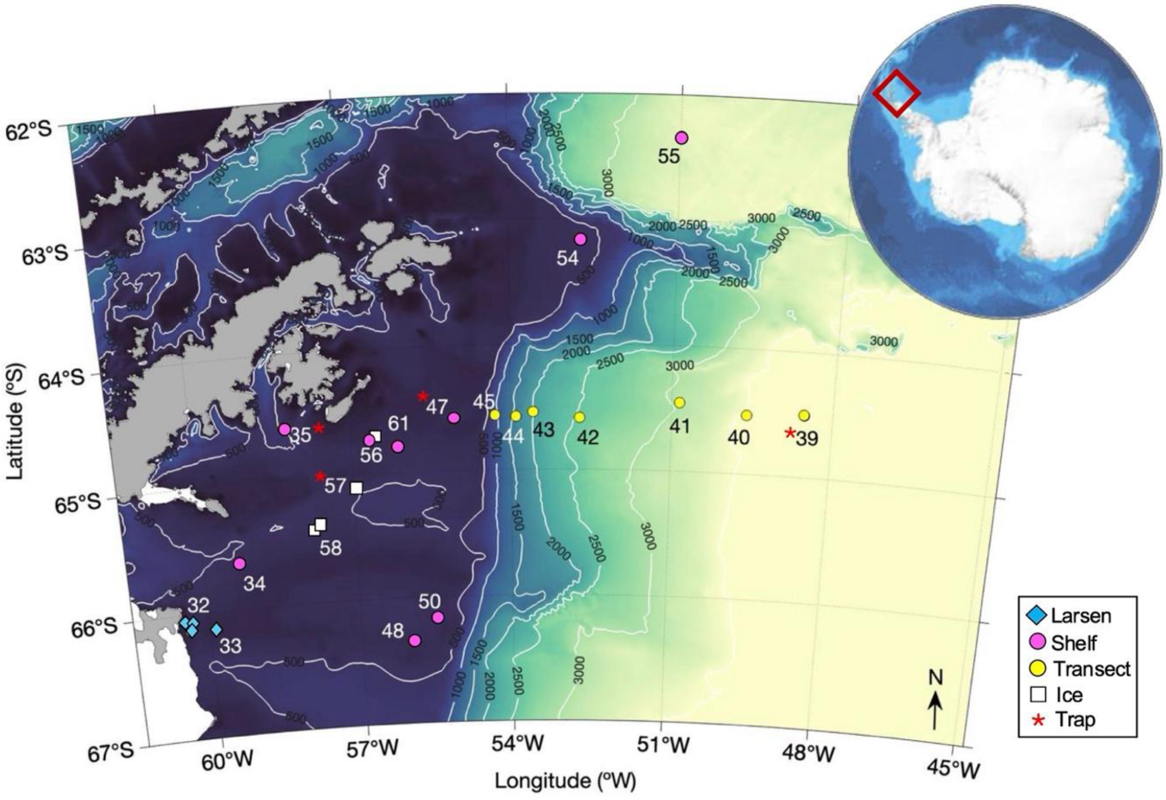

Figure 1. Map of HPLC sample locations by yearday of sampling. Global inset shows the location of sampling within the Southern Ocean generally. Isobaths are shown in white.

2.2 High Performance Liquid Chromatography Pigment Concentrations

HPLC pigment samples were collected from both discrete water column depths and the ship's underway system, which has a seawater intake at approximately 7 m depth. For the underway sampling, in addition to bulk water samples, size-fractionated HPLC pigment samples were collected by passing seawater through cartridge filters that isolate distinct size classes (here, <25 µm and <3 µm; Polygard CR cartridge filters). For all samples, 360–2000 mL of seawater was filtered through Whatman GF/F glass microfiber filters (0.7 µm nominal pore size, 25 mm diameter) under low vacuum pressure. Filters were placed in cryovials, flash-frozen in liquid nitrogen, and stored at −80 °C until onshore transport and subsequent analysis.

Filters were shipped to DHI Analytics where they were analysed according to the method of Van Heukelem and Thomas (2001). HPLC results were analysed for key accessory pigments including: alpha-beta-carotene (a-b caro), total chlorophyll b, zeaxanthin, diatoxanthin, alloxanthin, diadinoxanthin, 19'-hexanoyloxyfucoxanthin (hex-fuco), fucoxanthin, 19'-butanoyloxyfucoxanthin (but-fuco), peridinin, total chlorophyll c, and total chlorophyll a. The analytical limit of detection for this analysis ranged between 0.0003 – 0.0006 µg L^{-1} with a coefficient of variation of 0.22% for this dataset. Pigments concentrations below the detection limit were set to zero. Proportional contributions of each key accessory pigment were calculated by dividing the concentration of each key pigment by the sum of the total concentration of all accessory pigments. Accessory pigment distribution relative to dominant phytoplankton functional types, and analysis specific information are included in the Supplemental Material.

2.3 *Phytoclass* Analysis

To estimate phytoplankton community composition, HPLC data were analysed via the R program *phytoclass* (phytoclass.github.io/phytoclass/; Hayward et al., 2023). This Southern Ocean-trained model assesses the distribution of diatoms, dinoflagellates, haptophytes, cryptophytes, and *Synechococcus* from simulated annealing of accessory pigment concentrations (Hayward et al., 2023). *phytoclass* is based on a similar approach to the CHEMTAX method (Mackey et al., 1996). While both of these methods make assumptions about the relationships between and among phytoplankton pigments that are not upheld in statistical analyses of pigment-based datasets (Kramer and Siegel, 2019), CHEMTAX has historically shown good agreement with microscopy and 18S rRNA gene sequencing data from the Western Antarctic Peninsula (e.g., Lin et al., 2019; Brown et al., 2019; Lin et al., 2021). Emerging studies have also shown general agreement between *phytoclass* outputs with microscopy and Flowcam data in open-ocean regions of the Southern Ocean, providing enhanced confidence in applying the method in this ecosystem.

2.4 Particulate Organic Carbon Flux

Particulate organic carbon (POC) was collected from a drifting sediment trap with three collection carousels at 50, 100, and 150 m. This design enables one trap containing three separate carousels with collection canisters (for seawater) at each depth. The trap was deployed for 11-22 hours. Upon drifting sediment trap recovery, a messenger was released, triggering a custom closing mechanism and preventing contamination and potential overestimation of the flux as the trap was hauled onboard. Once onboard, the trap material was processed immediately.

For processing, the collection cannisters were descended into carboys, thoroughly mixed, and 600 ml of collected water was filtered onto pre-combusted (450°C, 16 hrs), pre-weighed 25 mm Whatman glass fibre filters (0.45 µm pore size, air dried for 24 hours) and frozen at -20ºC until onshore analysis at the British Antarctic Survey. POC samples were fumed for 24 hours with 37% HCl in a desiccator and placed in sterile nickel capsules. POC samples were then analysed and blank corrected using a CE Instruments NA2500 elemental analyser which was calibrated using an acetanilide calibration standard with a known % C and % N (71.09 % and 10.36 % respectively). For full details, see Atherden et al. (2026).

2.5 Phytoplankton Community Composition vs. POC Flux Analysis

HPLC results were compared with rates of particulate organic carbon (POC) flux measured via sediment traps, following a similar analysis to that of Kramer et al. (2025). In their analysis, the authors compared the summed relative sequence abundance of diatoms + photosynthetic hacrobia (haptophytes and cryptophytes) / all other phytoplankton groups (in that study, chlorophytes and dinoflagellates) using metabarcoding data (18S rRNA gene V4 region) to POC flux. Here, we combine the diatom, haptophyte, and cryptophyte percent contribution relative to dinoflagellate and *Synechococcus* percent contributions from pigments in surface samples (≤10 m) using the *phytoclass* output according to the following equation (1):

$$\mathrm{PCC_{ratio}} = (\mathrm{Diatoms} + \mathrm{Haptophytes} + \mathrm{Cryptophytes}) / (\mathrm{Dinoflagellates} + \mathit{Synechococcus}) \qquad (1)$$

where $\mathrm{PCC_{ratio}}$ stands for diagnostic phytoplankton community composition. POC export fluxes from four drifting sediment traps were compared with co-located HPLC samples from the YD 47 (shelf), YD 35 (shelf), YD 39 (transect), and YD 57 (ice) locations. See supplemental material for a full discussion on the considerations and uncertainty associated with pigment-based community composition.

2.6 Method Uncertainties

Phytoplankton accessory pigment analysis has inherent uncertainty for interpreting taxonomy due to (1) the large fraction of accessory pigments shared between broad phytoplankton groups, (2) the relatively plastic nature of phytoplankton pigments in response to changes in nutrient and light regimes, and (3) the high degree of co-linearity between all phytoplankton pigments, which is a violated assumption of many popular pigment-based algorithms such as CHEMTAX and *phytoclass* (Kramer and Siegel, 2019). However, HPLC pigments remain the gold standard for developing and validating ocean colour algorithms, so examining relationships between POC flux and pigment-based phytoplankton groups enhances potential for improving remotely-sensed export models. Further, HPLC pigment-based phytoplankton groups broadly compare well with other metrics for determining phytoplankton community composition across numerous coastal and open ocean ecosystems (e.g., Garibotti et al., 2003; Lin et al., 2019; Kramer et al., 2024). Additionally, certain methodological caveats may be introduced by the differences in methods between this study and Kramer et al. (2025), namely the use of HPLC pigments instead of gene-based community composition, and the difference (~40-45 m) in depth and collection time between our surface seawater HPLC samples and our sediment trap POC flux samples. In the work by Kramer et al. (2025), the rRNA gene samples were collected directly from the sediment trap, which was deployed for an average of 2-4 days, alongside the POC flux samples. Despite these broad differences, the methods used here still allow for the relative contribution of pigment-based $\mathrm{PCC_{ratio}}$ to be assessed as a potential indicator of carbon export flux magnitude across sampling depths.

3 Results and Discussion

3.1 Overarching Phytoplankton Community Distribution

Across all samples, the proportionally dominant pigments were fucoxanthin, hex-fuco, and chlorophyll c with variable, but sometimes high, percent contributions of alloxanthin and chlorophyll b (Figure 2). Broadly, this finding is consistent with previous HPLC studies which found the community in the Weddell Sea open-ocean region to be dominated by diatoms (fucoxanthin and chlorophyll c), haptophytes (hex-fuco, but-fuco, fucoxanthin, and chlorophyll c), and cryptophytes (alloxanthin; Wright et al., 2010; Hayward et al., 2025). Accordingly, the *phytoclass* output found a predominance of diatoms (mean = 40 ± 26%) followed closely by haptophytes (30 ± 22%) and cryptophytes (15 ± 24%) across the dataset (Figure 2). *Synechococcus* made up a non-negligible fraction with a mean percent contribution of 13 ± 10%, although caution should be taken with this finding because, while *Synechococcus* can be found in the Southern Ocean, they are more commonly associated with lower latitudes and the results may be skewed due to the sharing of zeaxanthin between *Synechococcus* and haptophytes (Hayward et al., 2023; Hayward et al., 2024). The pigments exhibited strong spatial variability, with haptophytes dominating at the Larsen-C Ice Shelf locations while diatoms dominated in the ice core and interface samples and at most non-Larsen water column locations (Figure 2G-J). Cryptophytes exhibited temporal variability, increasing in contribution on YD 58 and 61 (Figure 2).

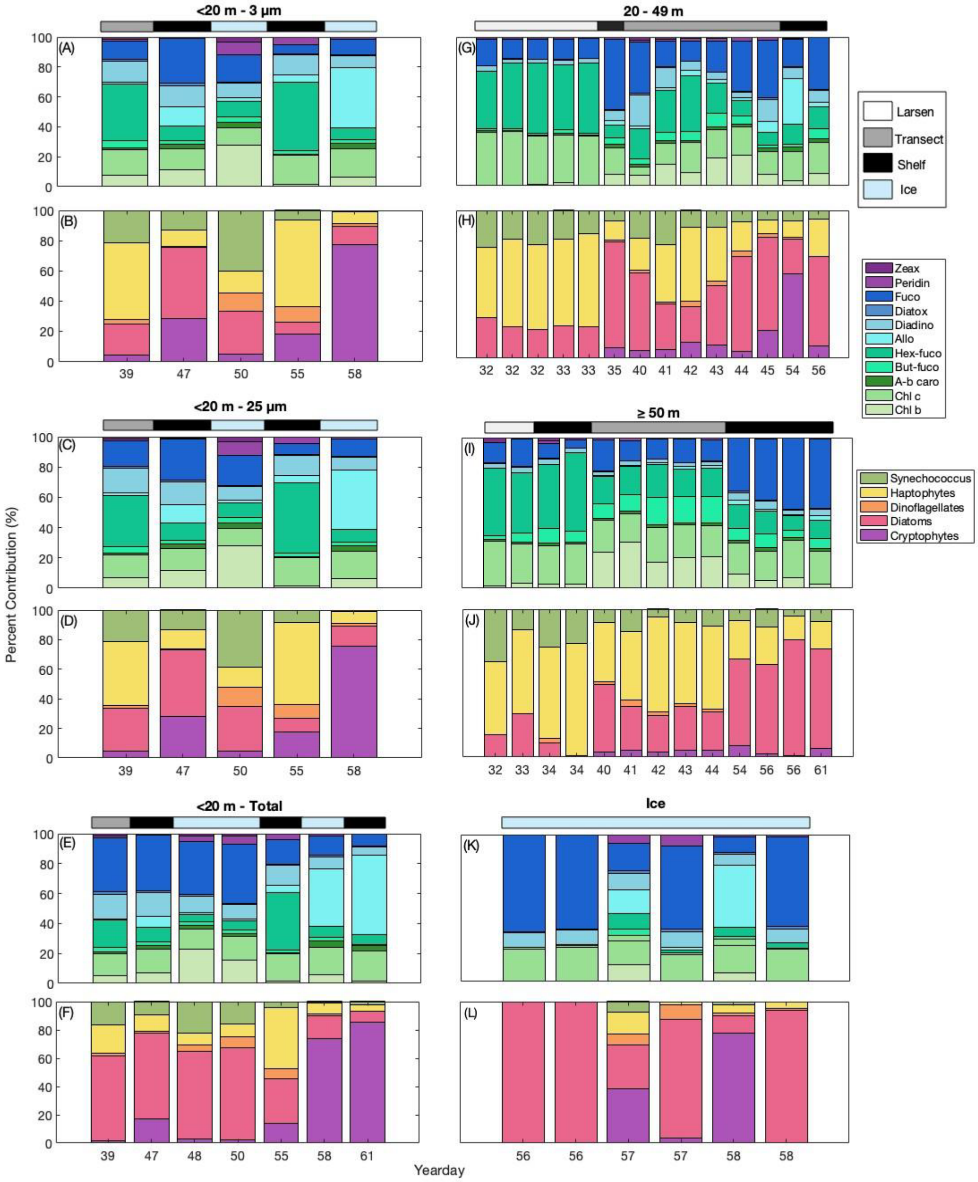

Figure 2. Percent contribution (%) of HPLC-derived accessory pigments by depth of sampling and yearday. Samples collected from <20 m were size fractionated, producing 3 (A-B), 25 (C-D), and total (E-F) concentrations. All other samples (-) were whole seawater (total) samples. Accessory pigment abbreviations stand for alpha-beta-carotene (a-b caro), chlorophyll b (chl b), zeaxanthin (zeax), diatoxanthin (diatox), alloxanthin (allo), diadinoxanthin (diadino), 19’-hexanolyoxyfucoxanthin (hex-fuco), fucoxanthin (fuco), 19’-butanolyoxyfucoxanthin (but-fuco), peridinin (peridin), and chlorophyll c (chl c).

These data show multiple phytoplankton groups coexisting in a mixed assemblage with the absence of a substantive phytoplankton bloom during most of the expedition (HPLC chlorophyll *a* concentrations, without Larsen-C samples, ranged from 0.06 - 2.0 µg L^{-1}). While the phytoplankton bloom succession in this region is poorly documented, studies from the marginal ice zone of the Weddell Sea suggest phytoplankton bloom peaks prior to mid-January, suggesting our samples represent bloom decline conditions (von Berg et al., 2020). The exceptions to this finding were the samples collected at the Larsen-C Ice Shelf, discussed below.

These pigment concentration patterns and *phytoclass* output provide important advances for both our understanding of the region's ecosystem structure and biogeochemical processes as well as motivation for future investigations of the region using advanced technology, including hyperspectral satellites. Our results provide quantifiable relationships between key phytoplankton groups and indicate co-location of diatoms, haptophytes, and cryptophytes in nearly all samples, at all depths. However, size fraction and depth patterns exist with haptophytes accounting for a larger proportion of pigments in the smaller size fractions and higher proportions of haptophytes and cryptophytes at the surface to mid-water column (Figure 2A-F; discussed further below). Additionally, the current impact of the PACE satellite is limited by validation data, namely HPLC samples, in remote regions, particularly at high latitudes (Cetinic et al., 2024). These data represent one of the only, if not the only, HPLC dataset and one of the only phytoplankton community composition datasets, generally, from the Weddell Sea continental shelf. Without this type of data, satellite algorithms will continue to be biased towards the North Atlantic and mid-latitude regions (Chen et al., 2021) which, combined with the limited in-situ data, limits our understanding of the ecological and biogeochemical characteristics of the region.

3.2 The Larsen-C Ice Shelf Bloom

The Larsen-C Ice Shelf samples (n = 7) were notably different from the rest of the samples. Both mid-water and deep samples were dominated by hex-fuco, which comprised on average 44 ± 3% of total accessory pigments. Contrastingly, in this region, fucoxanthin displayed its lowest percent concentration (average = 15 ± 2%) to total accessory pigments of the entire dataset. The proportional increase of hex-fuco and decrease of fucoxanthin concentrations were both significant (*P*-value < 0.05) and corresponded to a substantial increase in hex-fuco with average Larsen-C concentrations of 0.64 ± 0.64 µg L^{-1} (relative to the total sample average of 0.13 ± 0.31 µg L^{-1}) as well as a substantial decrease in fucoxanthin with average Larsen-C concentrations of 0.19 ± 0.17 µg L^{-1} (relative to the total sample average of 1.1 ± 4.6 µg L^{-1}). These changes in pigment concentration and fucoxanthin and hex-fuco pigment proportions, combined with peak Chl *a* concentrations, reinforce the presence of a haptophyte bloom in this region. This represents a noteworthy deviation from community composition observations from the Western side of the Antarctic Peninsula where blooms are typically diatom or cryptophyte, not haptophyte dominated (Brown et al., 2021).

Because the dominant haptophyte throughout the Southern Ocean is known to be *Phaeocystis antarctica* (*P. antarctica*; Smith and Trimborn, 2024), we presume that the enhanced proportional and discrete concentration of hex-fuco in this region corresponds to a high concentration of *P. antarctica*. This assessment is supported by Flowcam data collected during the PICCOLO cruise sampling, which showed the presence of *Phaeocystis* colonies (Fileman et al., 2026). Additionally, *P. antarctica* has been known to generate large blooms (both in spatial extent and biomass concentrations), leading to very high chlorophyll-*a* concentrations and rates of primary production (Smith et al., 2014; Meyer et al., 2025). The HPLC-derived concentrations of total chlorophyll *a* at Larsen C were the highest of any water column sample in this study, with a maximum concentration of 3.4 µg L^{-1} (Fig. 2A), representative of bloom concentrations. Total accessory pigment concentrations were similarly high (Figure S3). The Larsen C region also had the shallowest Secchi depth (6 m) and greenest water (Forel Ule colour of approximately 7) of any location, consistent with a large *Phaeocystis* bloom.

The consistency in relative hex-fuco concentrations between samples that were collected at varying depths from 20-70 m is noteworthy. This result suggests that *P. antarctica* dominated the community throughout the euphotic zone and supports previous findings, which describe *Phaeocystis* clades in general as cosmopolitan phytoplankton with a remarkable capacity to capitalize upon alleviation of resource limitation (Fussy et al., 2025). In the case of Larsen-C, alleviation of resource limitation likely corresponds to light and potential iron stress, as satellite imagery shows that the region had been sea-ice covered until a few days prior to sampling (Figure S1). Additionally, δ18O samples suggest enhanced ice shelf meltwater and dissolved iron concentrations in the region (Heywood and Bell, 2025). The magnitude of the bloom (total chlorophyll-*a* concentrations > 3 µg L^{-1}) supports the conclusion of Oliver et al. (2025) that the Larsen-C Ice Shelf hosts one of the top 15 most productive polynyas in the Antarctic. This region had previously been somewhat overlooked in importance due to a combination of lacking in situ data and ice-adjacency effects, which bias satellite-derived chlorophyll estimates (Oliver et al., 2025).

3.3 The Continental Shelf Community

Samples collected from the continental shelf (YD 34, 45, 47, 54-56, 61) had on average lower (0.41 µg L^{-1}) accessory pigment concentrations than those at Larsen-C but higher accessory pigment concentrations than the more offshore samples along the shelf-slope transect. Shelf samples had some of the highest percent contribution of fucoxanthin, particularly at 20 m and below where fucoxanthin dominated (32%), followed by chlorophyll c (22%; Figure 2G; 2I). This pigment composition resulted in diatom dominance in the *phytoclass* analysis from the deeper shelf samples (Figure 2I-J). However, cryptophytes dominated (57%) at 20-49 m at one of the most Northern sampling locations (63.15 ºS, 52.74 ºW) on YD 54 and in the total size fraction surface sample on YD 61. Interestingly, haptophytes dominated on YD 55 in both the 3 and 25 µm size fractions, but diatoms played a disproportionally larger role in the total sample (31% in the total vs. 8.1 and 9.4% in the 3 and 25 µm, respectively), suggesting that this station has a substantial population of large (>25 µm) diatoms (Figure 2C-D). The contrast between continental shelf and Larsen-C samples is noteworthy, with the shelf samples likely reflecting continental shelf community composition outside of bloom conditions. These “standard” conditions are more similar to that of the Ross Sea, another cold continental shelf sector, than to the West Antarctic Peninsula, a warm continental shelf sector (Thompson et al., 2018), which may suggest hydrography plays an important role in determining which species are most acclimated to dominate in the region. The rapid warming of the West Antarctic Peninsula is thought to contribute substantially to community composition changes (namely a shift from diatoms toward flagellates; Nardelli et al., 2023) in recent years whereas the colder temperatures and heavier ice concentrations common to the Weddell Sea likely enable the high concentrations of diatoms and haptophytes in the region.

3.4 The Shelf-Slope Transect Community

The zonal transect spanned approximately 225 km. Despite this large longitudinal gradient, the pigment composition from both the surface (<50 m; n = 6) and depth (>50 m; n = 5) was remarkably similar across the transect. Both depths were dominated by fucoxanthin, hex-fuco, and chlorophyll c with percent concentrations ranging from 13-39%, 8-37%, and 5-23%, respectively (Figure 2). The homogeneity across samples suggests a consistent community composition in the shelf-slope region. This finding was further supported by *phytoclass* results, which showed the highest concentrations of diatoms (41%), followed by haptophytes (38%) and substantially smaller contributions from cryptophytes and *Synechococcus* (Figure 2). The consistency of the phytoplankton community is somewhat surprising given the changes in hydrography across the shelf-slope region, suggesting these hydrographic changes are not substantial controls on community composition in the region. The relative homogeneity across the shelf to shelf-slope is consistent with homogeneity of the phytoplankton community across the continental shelf, as has been hypothesized for the Ross Sea (Smith and Kaufman, 2018) but contrasts with what has been found along the West Antarctic Peninsula where the influence of spatial gradients for differing community composition appear large (Moreno et al., 2024).

The contrast between community composition at Larsen-C and the shelf-slope transect is noteworthy when considering the foodweb dynamics of the region. Typically, diatoms are thought to support shorter, more efficient foodwebs (Michaels and Silver, 1988) while smaller cells such as cryptophytes and *Synechococcus* are thought to contribute to longer foodwebs with higher rates of recycling and more energy loss (Schmidt et al., 2020). Additionally, *P. antarctica* colonies are thought to be unpalatable for many krill and zooplankton species (Caron et al., 2000; Smith et al., 2014), leading to disruptions in the Antarctic food chain. The relative dominance of *P. antarctica* in our Larsen-C samples suggests that there are likely substantial, spatiotemporal differences between the Larsen-C region and the rest of the Weddell Sea in terms of zooplankton grazing, nutrient cycling, and carbon export. Further research should investigate whether *P. antarctica* blooms commonly occur across the Weddell Sea as sea ice retreats and polynyas form. Understanding how frequently these blooms occur and quantifying the associated increases in *P. antarctica*, particularly relative to diatom concentrations, would help better quantify regional primary production and carbon export rates.

3.5 The Sea Ice Community

The six samples collected from sea-ice cores, the ice-ocean interface, and brown ice had extremely high concentrations of total accessory pigments (Figure S3), which was predominant predominately fucoxanthin (ranging from 11 - 66%), particularly in the brown ice samples (Figure 2K). Alloxanthin and chlorophyll c also contributed substantially, ranging from 0 - 42% and 16 – 23%, respectively. This pigment composition led to a clear prevalence of diatoms in the *phytoclass* results (Figure 2L). Cryptophytes were also an important proportion of the community, particularly in the ice-ocean interface samples. These findings show a noteworthy difference in community composition between sample types despite the fact that the two communities live in the same geographic space, i.e., near complete dominance of diatoms in core samples whereas ice-ocean samples have a more mixed composition (Figure 2K-L). As has been previously shown, sea-ice dwelling diatoms, and to some degree cryptophytes, must have unique physiological or adaptive traits to enable them to survive in colder, less saline, and less viscous environments (Ligowski et al., 2012). Furthermore, the difference in community composition between the sea-ice community and all other samples (Figure 2) suggests ice or ice-adjacent communities should be considered independently in models and climatologies.

3.6 POC Flux vs. Community Composition

The POC flux vs. PCC_{ratio} shows positive but non-significant relationships between surface community composition and carbon export at 50, 100, and 150 m (Figure 3). Interestingly, the relationship was weakest ($R^2 = 0.37$) at 50 m, the shallowest depth, but strongest (even stronger than the relationship observed by Kramer et al. (2025)), at 100 m ($R^2 = 0.83$; Figure 3C) which is a depth of enhanced krill grazing and faecal pellet production (Atherden et al., 2026). No matter the depth of POC export evaluated in this study, the observed relationship is substantially different from that reported by Kramer et al. (2025), where PCC_{ratio} values were much lower but rates of POC flux were much higher. This deviation is likely due to substantial ecological and biogeochemical differences between the Southern Ocean relative to the North Pacific and the North Atlantic. Specifically, the Southern Ocean continental shelf is known to be dominated by a mixed assemblage of diatoms, *P. antarctica*, and cryptophytes (Wright et al., 2010; Hayward et al., 2025) while the North Pacific and the North Atlantic are dominated by much more mixed assemblages of dinoflagellates, diatoms, haptophytes, chlorophytes, and *Synechococcus* (Sharpe et al., 2023; Meyer et al., 2024; Kramer et al., 2025). Therefore, it is unsurprising that our PCC_{ratio} values were all >1 and much larger (4.6 – 11). Contrastingly, rates of carbon export were lower than those found by Kramer et al. (2025). The dominance of diatoms, haptophytes, and cryptophytes lead to high PCC_{ratio}, but some studies suggest a substantial proportion of *Phaeocystis* is remineralized in the surface, reducing the rates of POC flux to depth (Meyer et al., 2022). These differences in ecosystem characteristics between Kramer et al. (2025) and this study, along with the limited number of northwest Weddell Sea samples, necessitate different linear equations to describe the relationship between community composition and carbon export. This result may suggest a strong relationship exists, but unique linear regression coefficients should be derived to calculate export in highly different ecological regions, or at least polar versus non-polar regions.

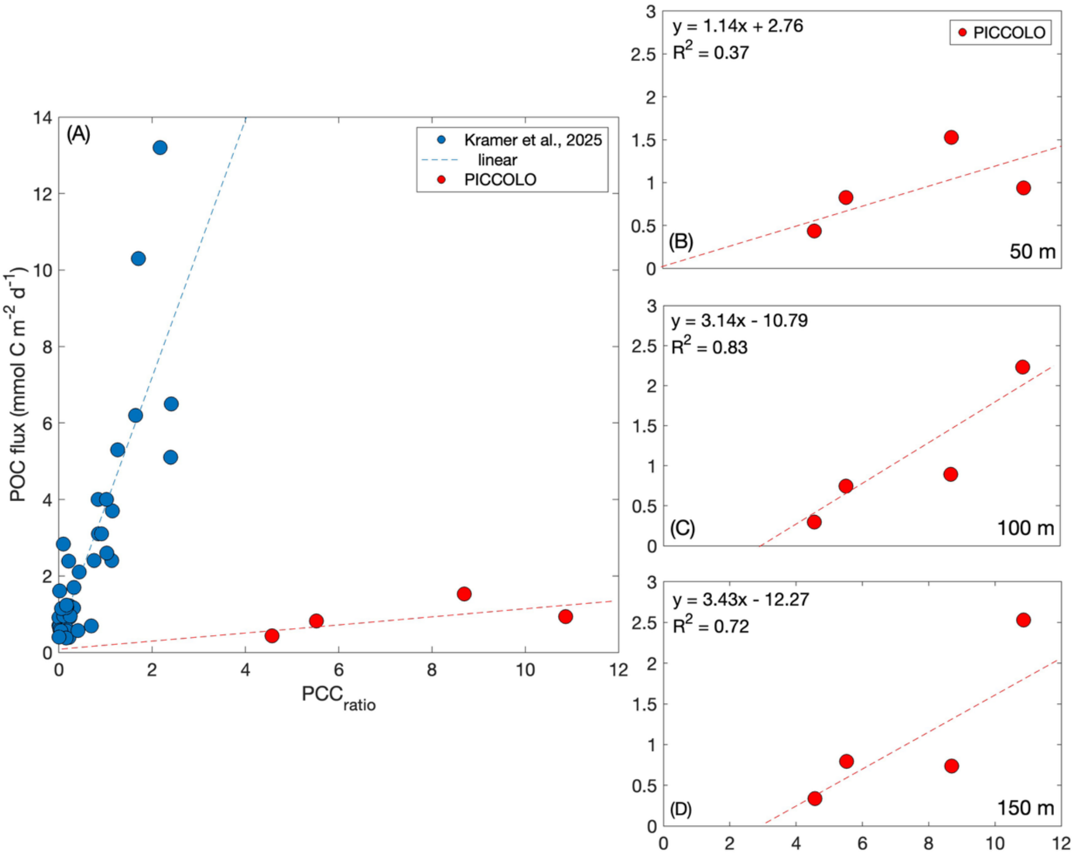

Figure 3. POC flux (mmol C m^{-2} d^{-1}) versus the contribution of diatoms and hacrobia to phytoplankton community composition (PCC$_{ratio}$). (A) includes HPLC and 50 m sediment trap data from the PICCOLO campaign compared to data from Kramer et al. (2025). (B-D) presents PICCOLO HPLC and sediment trap data from 50, 100, and 150 m, respectively. The R^2 values for (B-D) are 0.37, 0.83, and 0.72, respectively, and p-values were > 0.05 for all plots.

The water overlying the four floating trap stations presented here was dominated by diatoms with percent contributions of 84, 61, 72, and 60% compared to the haptophyte percent contributions of 13, 20, 12, and 2% for YD 35 (shelf sample), YD 39 (transect), YD 47 (shelf sample), and YD 57 (ice sample), respectively. To test whether diatom abundance alone could be used as a predictor of carbon export in the euphotic zone, the percent contribution of just diatoms was regressed against carbon export (Figure S4). At 50, 100, and 150 m, the R^2 values decreased substantially from those of PCC$_{ratio}$ to 0.01, 0.06, and 0.08, respectively. R^2 values were similarly weak if just haptophytes or just cryptophytes were regressed versus carbon export (0.10, 0.01, and 0.01 for haptophytes at 50, 100, and 150 m and 0.03 and 0 for cryptophytes at 100 and 150 m;

Figure S4). The one exception to this finding was the relationship between percent contribution of cryptophytes to carbon export at 50 m, which had an exceptionally high R^2 value of 0.93 (*P*-value < 0.05; Figure S4). With this relationship, and all the presented relationships, caution should be taken given the small sample size (n = 4). However, this result suggests that overall it is not solely the relative diatom, haptophyte, or cryptophyte abundances that are a good predictor of carbon export, but diatoms + hacrobia together are the most robust metric at multiple depths and should be evaluated together against POC flux in remote sensing products and global models.

While some previous studies have shown that diatoms are highly correlated with carbon export due to their fast sinking rates and potential to be readily grazed (Michaels and Silver 1988; Zuniga et al., 2021; Siegel et al., 2025), other studies (Cassar et al., 2015; Williams et al., 2024) have found that diatoms are not always a good indicator of export efficiency in the Southern Ocean. Our results support a growing body of evidence which suggests that the balance between diatoms and *Phaeocystis* is critical for determining the magnitude of both primary production and carbon export rates globally. Numerous studies (Smith et al., 1991; Meyer et al., 2022; Smith and Trimborn, 2024; Meyer et al., 2025; Roca-Marti et al., 2025) have found that *Phaeocystis sp.* contributes to high rates of primary production, but the high remineralization rate of *Phaeocystis* in the surface ocean means that rates of production become uncoupled from export rates, keeping export rates low or consistent with non-bloom conditions. Unfortunately, we could not directly assess the relationship between phytoplankton community composition to POC flux during the *Phaeocystis* bloom but suggest this should be investigated in future studies. Furthermore, cryptophytes have not been as large a focus in Southern Ocean carbon export analyses, but our results suggest that they too play a large, perhaps overlooked, role in carbon flux. Typically, cryptophytes have been believed to shorten food webs and decrease carbon flux and are frequently mixotrophic (Brown et al., 2021), so overlooking these organisms in models could potentially lead to overestimates of flux.

More sampling of concurrent community composition and carbon export data is needed to better test the relationships found here within the Weddell Sea and the whole Southern Ocean, generally. The robustness of the relationships shown here and by Kramer et al. (2025) should be further tested in space and time in order to evaluate this predictive relationship between PCC_{ratio} measured from next generation ocean colour satellite products and POC flux (Kramer et al., 2022).

4 Conclusions

This study presents the only HPLC dataset (to our knowledge) from the Weddell Sea continental shelf region. Here, we confirmed an expected dominance of diatoms and haptophytes throughout the region. We presented new geographic and depth patterns that highlight understudied phytoplankton community dynamics such as the stable contribution of haptophytes (presumably *P. antarctica*) in the surface and at depth during a bloom, the higher contribution of cryptophytes in surface waters, the decrease of cryptophyte abundance in haptophyte dominated waters, and the overwhelming dominance of diatoms in sea-ice samples. The results presented here showcase the importance of understanding variable phytoplankton community composition, and show a strong predictive relationship between POC flux and diatoms, typically thought to enhance flux, and hacrobia, typically thought to reduce flux.

While more research is needed, the predictive capacity of diatom + photosynthetic hacrobia community composition to estimate the magnitude of POC flux appears strong and holds across oceanic systems. Currently, some Earth Systems models have begun to differentiate between key phytoplankton groups like diatoms and *Phaeocystis* (Enright et al., 2009), but not all. Our findings suggest that including key hacrobia, such as *Phaeocystis* and cryptophytes, as independent groups in earth system models is a key step in developing a more comprehensive, mechanistic understanding of the relationship between changing phytoplankton community composition and key ecosystem and biogeochemical processes, particularly in critical areas such as the Weddell Sea and Southern Ocean.

Code and data availability

All data are available at the British Oceanographic Data Centre (https://doi.org/10.5285/4D5D158B-3CF9-AD21-E063-7086ABC01540).

Author contributions

MGM is responsible for conceptualisation, data curation, formal analysis, investigation, validation, visualisation, writing (original draft preparation), and writing (review and editing). RJWB, XS, CM, FA, and GD are responsible for data curation, methodology, validation, visualisation, writing (original draft preparation), and writing (review and editing). SJK is responsible for conceptualisation, methodology, validation, writing (original draft preparation), and writing (review and editing). KJH is responsible for validation, visualisation, resources, project administration, writing (original draft preparation), and writing (review and editing).

Competing interests

K. Heywood is an editor of Ocean Science.

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