

The work by De Jong et al. examines core tops and box cores from SW Ross Sea to study sea ice conditions and phytoplankton communities shifts during the last 200 years through a multi-proxy analysis which is guided by biomarkers and diatoms. It focusses on how the sea ice conditions have an effect on the phytoplankton blooms through time, by considering various groups of phytoplankton. The results show an increasing sea ice trend in the last 200 years, in partial agreement with other studies from the Ross Sea region, and they offer distinctive insights into the distribution of different biomarker classes in an extremely productive area.

Although the framework is interesting and the results, especially the sea ice reconstruction, are compelling, the paper requires some adjustments and improvements to clarify certain aspects and to make it more fluid for the reader.

We thank the reviewer for the valuable feedback and have addressed the comments to strengthen the paper.

GENERAL COMMENTS

I would suggest changing the title as follows: “Biomarkers and diatoms as tracers of phytoplankton communities and past sea ice conditions in the Southwestern Ross Sea, Antarctica: drivers and variability over the last 200 years”.

Thank you, we have changed the title as suggested to highlight phytoplankton communities before the sea ice conditions.

In the abstract, few groups are cited (*Phaeocystis antarctica*, *Fragilariopsis curta*, *Chaetoceros*) but the ecological role and their implications are not clear. I suggest adding a brief specification about the diatoms and/or phytoplankton groups you are considering in this study (possibly inspired to line 88, where diatoms, dinoflagellates etc., are listed) and about what these organisms represent. The abstract seems in general too technical and the references to different diatom species and specific biomarkers without context and explanation make it challenging to follow.

We thank the reviewer for this comment and have adjusted the abstract to better reflect the findings of the study with more context, and less technical jargon. The abstract now reads as follows: “The Ross Sea, Antarctica, is among the most seasonally productive regions of the global ocean, where different classes of phytoplankton, such as diatoms, dinoflagellates, and haptophytes (*Phaeocystis antarctica*), play key roles in marine ecosystems and the carbon cycle. Sea ice dynamics strongly influence Ross Sea phytoplankton blooms, yet the effects of recent sea ice changes on bloom composition

and productivity remain poorly constrained, and longer baseline records are required to understand changes in sea ice and resulting impacts on phytoplankton and climate.

The 200-year period examined here spans the final stages of the Little Ice Age and the subsequent warming and rising atmospheric CO₂ associated with industrialisation, making it critical for contextualising recent and projected change.

We investigated phytoplankton-derived lipid biomarkers (fatty acids, highly branched isoprenoids; HBIs, sterols) and diatom assemblages in six marine sediment core tops and three short sediment cores collected along a north-south transect extending from McMurdo Sound coastal polynya to south of Terra Nova Bay, to assess how sea ice dynamics and phytoplankton communities drive biomarker signatures and diatom assemblages archived in sediments. Diatoms and biomarkers in core tops reveal increased proportions of open-ocean diatom species and bacterial fatty acids towards the southern end of the transect near McMurdo Sound driven by lower summer sea ice extent, along with a phytoplankton community dominated by diatoms and higher summer biomass. In contrast, the northern end of the transect, near Terra Nova Bay, is characterised by higher proportions of diatoms associated with sea ice, as well as increased concentrations of sea ice diatom-derived fatty acids, and HBIs, driven by greater sea ice concentrations. Similarly, *Phaeocystis antarctica*-derived fatty acid biomarkers increase towards the northern end of the transect, likely driven by differences in the phytoplankton community. A Principal Component Analysis (PCA) of the biomarker and diatom dataset confirms this spatial structure, resolving three main variance groupings: diatoms and fatty acids associated with heavier sea-ice (*Fragilariopsis curta* group, C_{24:0}), which are inversely related to open-water and fast ice diatom assemblages (*Chaetoceros* resting spores, open ocean, cold water, and sea ice diatoms), while fatty acids and HBIs form a third, independent grouping consistent with shared post-depositional degradation.

Within the short cores, sea ice associated diatoms such as *Fragilariopsis curta* and the sea ice proxy, PIPSO₂₅, indicate an increase in sea ice extent over the last 200 years, accompanied by declining open ocean diatom species, a trend not captured by phytoplankton-derived fatty acids alone, which show little change in community composition over the same period. Overall, our records reveal a 200-year increasing sea ice trend in the southwestern Ross Sea, consistent with existing regional sea ice extent reconstructions from ice cores. Biomarkers in the southwestern Ross Sea sediment independently distinguish between pelagic diatoms, *P. antarctica*, and sea ice-associated diatoms, offering a valuable tool for developing longer decadal resolution records of sea ice and phytoplankton community changes."

The introduction has also been adjusted to better capture which phytoplankton groups are considered in this study and more context has been added to section 2.7 where individual species are discussed.

Beware of keeping the same tense throughout the whole text, avoid shifting between past and present tense.

We thank the reviewer for this comment. The tenses were checked throughout the manuscript. The manuscript is now consistently presented in past tense, while the abstract findings are presented in present tense.

Some things are not specified enough for age models: how are the raw ^{210}Pb profiles? Is there any trace of bioturbation? Core-tops in gravity cores are preserved and you have evidence for that? The method section talking about this is extremely scarce and also the suppl. material is lacking critical information. Besides, there is no information on the sedimentological and lithological aspects of these cores (HD images, x-ray, etc).

Thank you for these comments. First, we have included more information about the sediment cores. There was bioturbation in all three box cores, and we have clarified this in text and added the following core log to the manuscript (Figure 1). We have also included more core descriptions in text, "The three box cores (BC02, BC03, BC04) are mainly composed of olive grey diatomaceous mud, with evidence of bioturbation throughout (Figure 1). Crude lamination is observed at 42-45 cm in BC03 and at 0-5 cm in BC04 (Figure 1). Only the top 0-1 cm of the gravity cores (GC72, GC78, GC80) were subsampled and are composed of olive grey diatomaceous mud and no noticeable sediment loss or disturbance was observed during coring and recovery." We have also added X-ray images to the manuscript appendix (Figure 3 below).

We have also revised the age model section to describe the raw ^{210}Pb profiles. A surface mixed layer was identified in raw ^{210}Pb profiles in BC02 and BC04, with the uppermost two samples in BC02 and one sample in BC04 excluded from the least-squares regression. No mixed layer was identified in BC03. Below the mixed layer, excess ^{210}Pb activity decreased exponentially with depth in all three cores. We acknowledge that bioturbation represents a limitation of the age model, and that the ages in the uppermost sections of BC02 and BC04 should be treated with caution. We have included this information in the text, and made an adjustment to the lead dating figure in the supplementary materials and added the raw ^{210}Pb values that were excluded from the least-squares regression onto the plot (see Figure 2 below) to be transparent about the

removed values. This figure has also been moved to an appendix to make the information more visible.

Regarding the gravity core tops, no noticeable sediment loss or disturbance was observed, however, we acknowledge that this is a possibility.

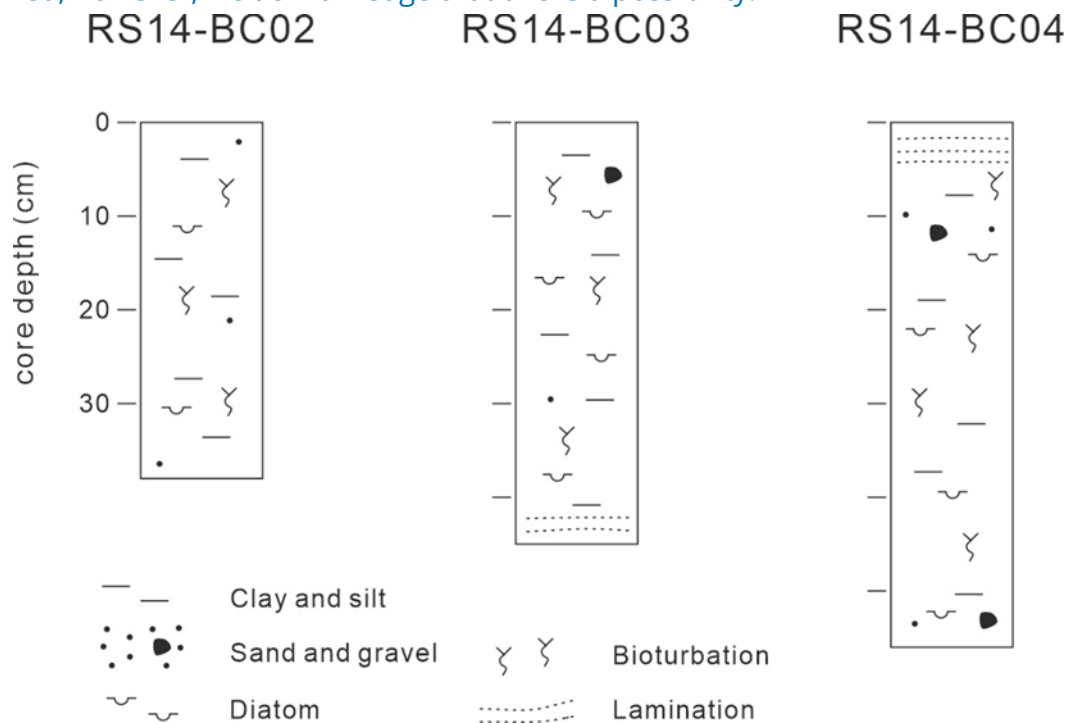


Figure 1: Core logs for RS14-BC02, RS14-BC03, and RS14-BC04 from the southwestern Ross Sea, Antarctica. Lithology and sedimentary structures shown against depth (cm).

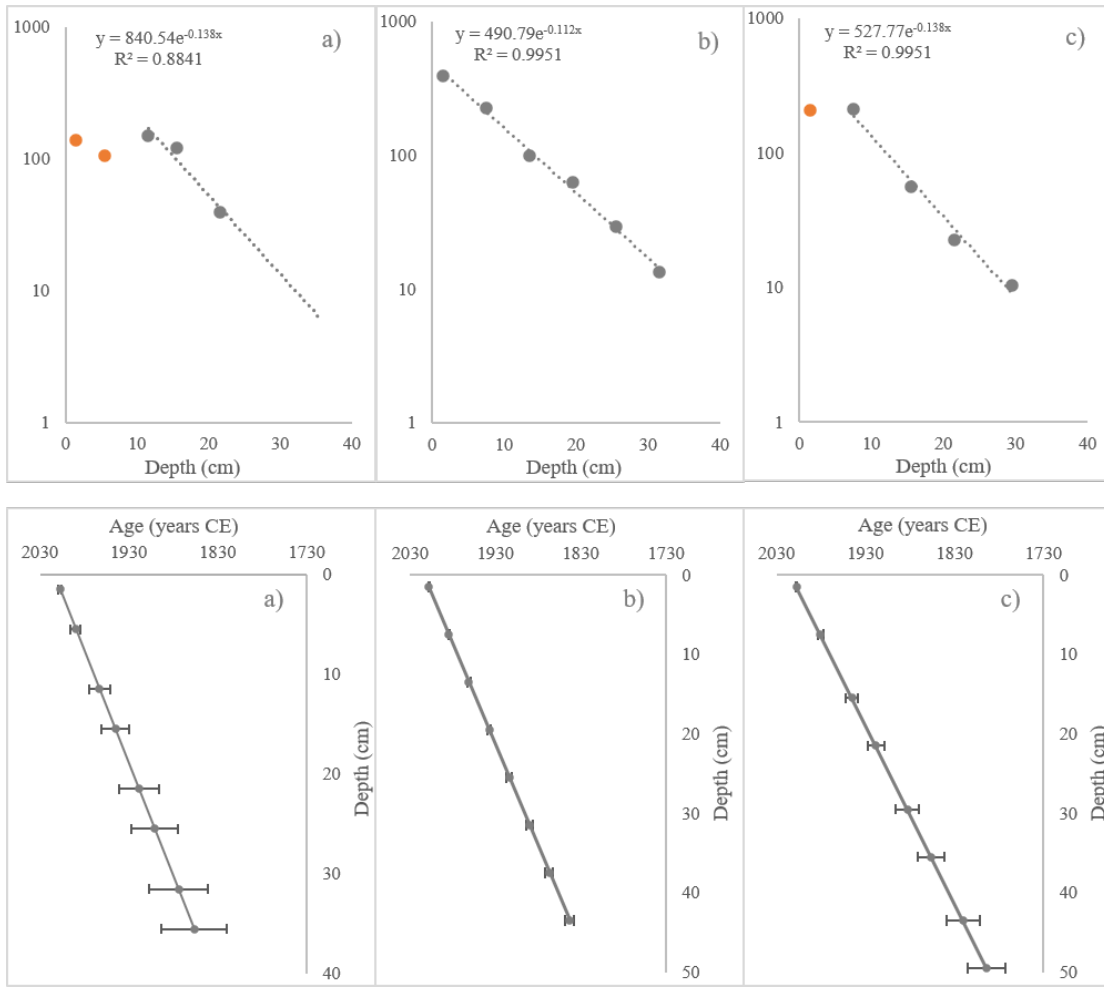


Figure 2: Lead dating age-depth models for a) BC02, b) BC03, c) BC04, and d) BC04. Top: Sedimentation rates were calculated from the least-squares fit slope of $^{210}\text{Po}_{\text{supported}}$ on a logarithmic scale against depth (Appleby, 2001). The orange dots show evidence of a mixed layer in the ^{210}Po and were not included in the least-squares fit slope. Bottom: The constant flux and constant sedimentation rate (CFCS) model was applied to determine sediment ages (Bruehl et al., 2020). Errors were estimated using R package 'serac' (Bruehl et al., 2020).

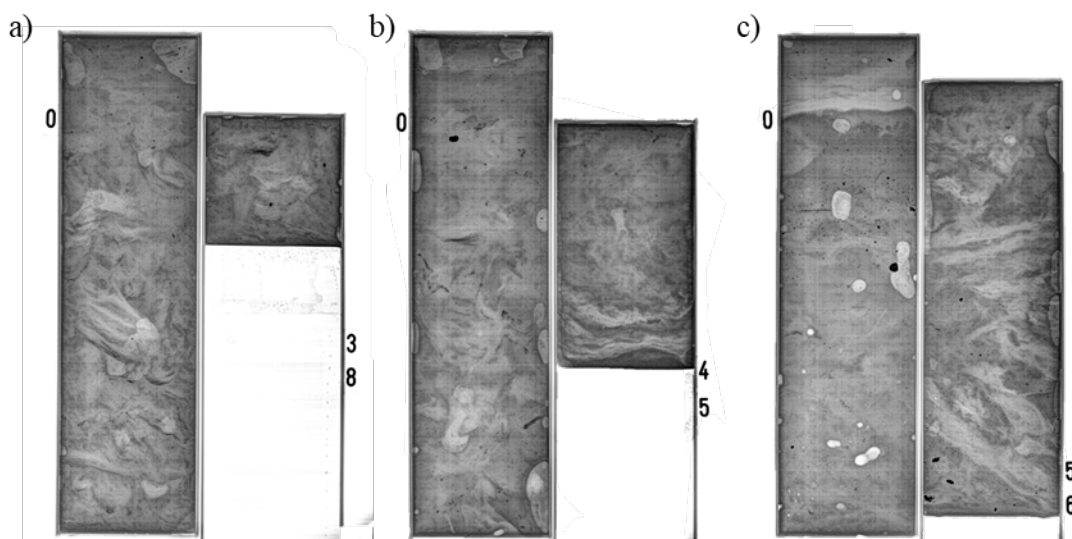


Figure 3: X-radiographic images of RS14-BC02 (a), RS14-BC03 (b), and RS14-BC04 (c). Depth (cm) is noted beside each X-ray. Images were taken on 1 cm thick sediment slabs with Softex M-100W X-ray source and NTB EZ-320 digital X-ray scanner, and were processed with iX-Pect EZ imaging software.

Why HBI III and IV were not used? Are they absent? Since you separated a ketone fraction, did you have the chance to look for alkenones from haptophytes blooms? From what I know they are not present, or at least not detected, in Antarctic species but it would be interesting if they were indeed present.

We thank the reviewer for these suggestions. Regarding HBI III and IV, these compounds were not detected in our samples. A sentence has been added to the results to clarify this: "Other HBIs, such as the commonly found triene (Belt, 2018), were not detected." Regarding alkenones, we ran the ketone fraction for a small selection of samples and did not detect any alkenones. This is expected, as the source organisms (i.e. coccolithophore *Emiliania huxleyi*) are not typically present in the Ross Sea (Chen et al., 2021; Sikes et al., 1997).

Talking about decay rate to describe the vertical decrease of a certain biomarker seems odd. A downcore decrease of concentration could be of course due to decay/degradation, but at the same time concentrations can change during time, and thus at different depths, due to environmental conditions (less productivity, advection, etc). This also raise another problem, that is, it is really challenging to discriminate between different biological sources using almost only absolute concentrations, which are extremely dependent on several uncontrolled variables (same as before, productivity, advection, etc). Both these issues are not clearly mentioned and discussed in the text.

We thank the reviewer for this important comment. We use the term 'decay rate' to describe the downcore decrease in concentration because post-depositional degradation of organic matter is a well-documented process in marine sediments, and the marked decrease we observe within the upper ~20 cm is consistent with this process. However, we agree that there are two processes influencing the fatty acid concentrations in the upper section of the sediment. Changes in environmental factors such as primary production changes and phytoplankton species can influence the absolute concentrations of fatty acids, as well as the profiles of fatty acids. Degradation can also impact the absolute concentration of fatty acids. We note that all biomarker concentrations are normalised to total organic carbon (TOC), which partially accounts for fluctuations in bulk organic input to the sediment, though it does not fully resolve variability arising from changes in productivity or advection. A Principal Components Analysis was conducted on the diatom groupings and biomarker results to better highlight the main sources of variance and the relationship between key variables. The PCA analysis (Figure 4) groups the fatty acids and HBIs together suggesting shared post-depositional processes such as degradation. In contrast, the sterols, which do not show the same marked decrease as the fatty acids and HBIs consistent with their low reactivity (Vorrath et al., 2019; Rontani et al., 2019; Rontani et al., 2012), do not follow the same grouping as the fatty acids. However, the profiles provide evidence of different sources such as diatoms and *Phaeocystis antarctica*, alongside independent evidence from diatom analysis.

We have revised the manuscript to highlight this point. In particular, in section 4.2 we have adjusted the section: "Fatty acids in the surface sediments reflect inputs from a mixture of phytoplankton sources, including diatoms and *P. antarctica*. The PCA analysis (Figure 4) groups the fatty acids and HBIs together, suggesting shared post-depositional processes such as degradation. In contrast, the sterols do not follow the same grouping as the fatty acids and HBIs, consistent with their comparatively low reactivity and limited downcore decrease (Vorrath et al., 2019; Rontani et al., 2019; Rontani et al., 2012). Downcore profiles of fatty acids show a marked decrease in concentrations within the upper ~20 cm (corresponding to ~76-95 years), consistent with early post depositional degradation. Below this interval, fatty acid concentrations remained relatively stable. This pattern suggests that post-depositional alteration is an important driver of fatty acid concentrations; however, it is unlikely to be the sole factor influencing downcore variability. Changes in primary production, organic matter flux, and sedimentation processes also contribute to the observed trends. Beyond the ~20 cm fatty acid decrease, no consistent downcore trends were observed, which may suggest relatively little change in phytoplankton community

composition over the past ~200 years, despite increasing sea-ice influence (Yuan et al., 2017; Dalaiden et al., 2021)."

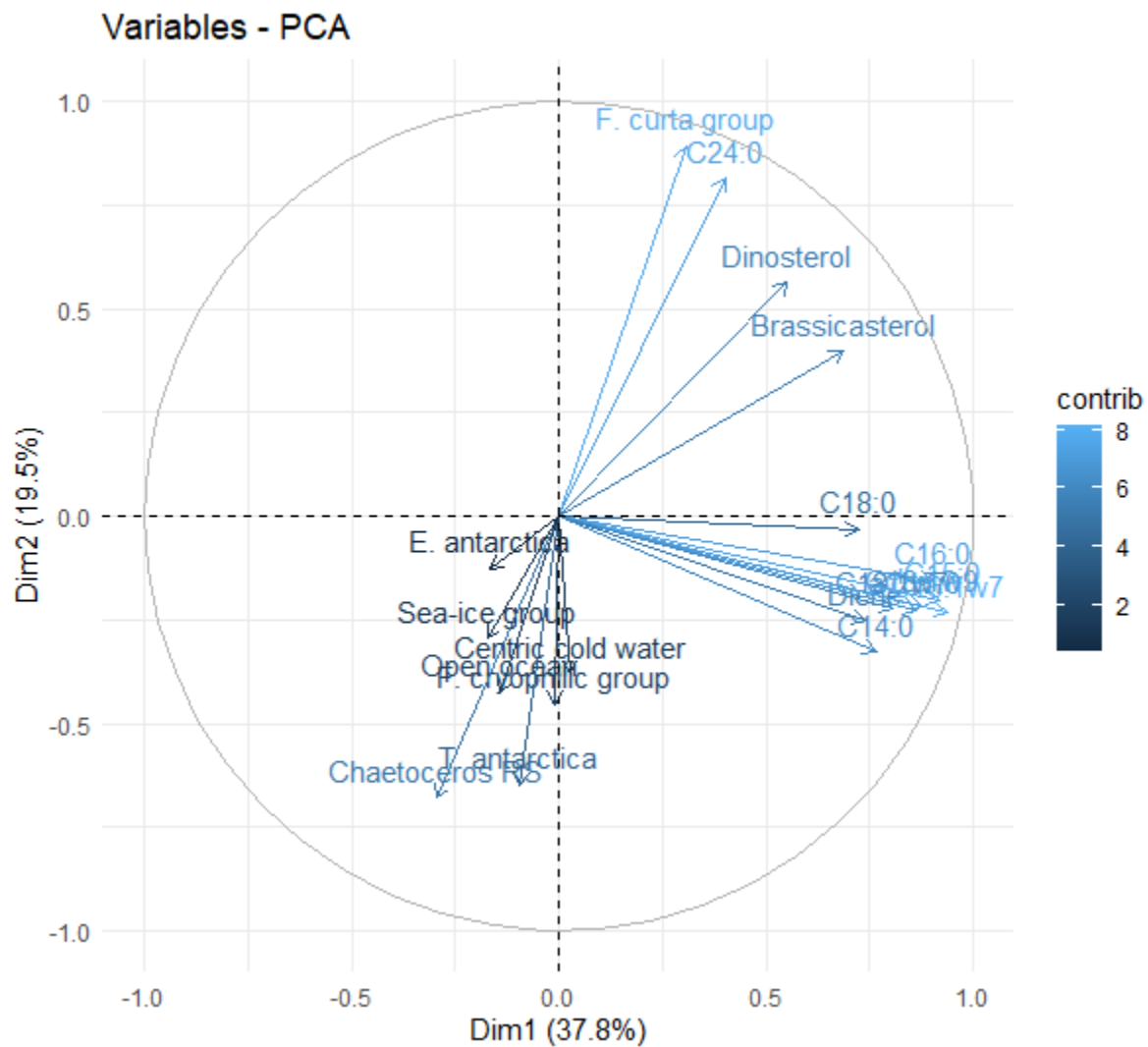


Figure 4: Principal Component Analysis (PCA) of biomarker and diatom variables ($n = 27$), showing the correlation circle for the first two principal components (Dim1 = 37.8 %, Dim2 = 19.5 % of total variance). Arrow color indicates the contribution of each variable to the plotted dimensions.

The results section is not adequately presented. The description need to be homogenized and uniformed, otherwise it could also be a possibility to unite results and discussion sections if the editor agrees.

We thank the reviewer for this comment. We agree that the results were not presented in a uniform way. The results have been modified to follow a clearer structure. First, the biomarker section has been split into three subheadings (Fatty Acids, Sterols, and Highly

Branched Isoprenoids), and second, each section follows the same structure where general results are presented first, followed by spatial differences, and then downcore trends. We have also checked for inconsistent language such as 'core tops' and 'surface sediments', and used core top consistently throughout.

In the Results data from core-tops are presented, but they are not discussed later. We thank the reviewer for this comment. The core tops have been added throughout the discussion section to strengthen the evidence of spatial variability and biomarker sources. For example section 4.1.2 has been updated to read: "The study sites investigated in this study are located along a north-south transect from south of the Drygalski Ice Tongue, an area covered in sea ice for ~80 % of the year, to McMurdo Sound in the south, which is covered in sea ice for around 20-40 % of the year (Figure 1, Spreen et al. (2008). Sea ice in the southwestern Ross Sea undergoes a dramatic change every year when the warm season sea ice breakup forms ice-free biological hotspots in McMurdo and Terra Nova Bay (Brett et al., 2020). Sites BC02, GC72, and GC78 at the southern end of the transect are closest to the McMurdo polynya, where the proportion of ice-free days is the highest. The lower sea ice concentration at these sites is reflected by the lowest relative abundances of the *F. curta* group, increased proportions of open ocean diatoms, decreased C_{24:0} fatty acids sourced from sea ice diatoms (Nichols et al., 1986), and the absence of sea ice diatom-sourced C_{20:1} compounds (Fahl and Kattner, 1993). Biomarker and diatom distributions in the southern sites also reflect enhanced phytoplankton productivity, as fatty acid ACL is lower, the CRS concentration is increased, and the diatom absolute abundance in BC02 is more than 15.8 % higher relative to BC03 and BC04. The northern end of the transect (GC80, BC03, and BC04) has higher sea ice concentration with a break-up later in the summer than at McMurdo Sound (Spreen et al., 2008). Increased sea ice concentration is seen in our core sediments, with *F. curta* abundances being 7 % and 30 % higher in BC03 and BC04, respectively, than in the three southern core tops. The same trend is observable in fatty acid concentrations of C_{24:0}, which is likely a reflection of degraded sea ice diatom-produced C_{24:1ω11} and C_{24:1ω9} (Nichols et al., 1986; Nichols et al., 1993). GC80, BC03, and BC04 also have higher ACL, lower proportions of CRS, and lower diatom abundances, which all reflect the lower productivity in this region. Centric cold water diatoms also decrease on a south to north gradient, away from the polynya, likely reflecting the decreased productivity as a result of delayed sea ice opening above the northern core locations, which influences the release of nutrients and the stratification of the water column (Deppeler and Davidson, 2017)."

The conclusion chapter is messy and difficult to follow, without any structure nor organization. I suggest rephrasing the main conclusions in order to clarify the take home messages of this study.

Thank you for this comment. We have reordered and revised the conclusion chapter and it now reads as follows:

“In this study, lipid biomarkers (fatty acids, sterols, and HBIs) from surface and short sediment cores were combined with diatom assemblage data to assess their drivers and help interpret past sea ice dynamics and phytoplankton community changes in a 200-year record in the southwestern Ross Sea, an area characterised by the variable presence of coastal polynyas. Three sediment cores along a north-south transect were sampled at decadal resolution and dated using ^{210}Pb dating, with the longest core representing years 1794-2007 (± 20 years at its base). This time interval encompasses the final stages of cooling in Antarctica, during which atmospheric and oceanic dynamics influenced polynya evolution in the Ross Sea, as well as increasing atmospheric CO_2 since the Industrial Revolution (Rhodes et al., 2012). The three cores offer an opportunity to examine biosiliceous and organic records during this period and to assess the long-term behaviour of biomarkers, bacterial activity, and preservation processes.

Trends in sea ice diatoms such as *Fragilariopsis curta*, alongside HBIs and PIPSO₂₅, reveal an increase in sea ice extent in the southwestern Ross Sea over the last 200 years. This finding contributes to a growing picture of regional sea ice variability, with trends differing by proxy and location, emphasizing the importance of high-resolution records for capturing local and broader scale sea ice change.

Spatial variations in biomarker composition were primarily driven by sea ice conditions and associated phytoplankton habitats, while pelagic diatoms, haptophytes (e.g. *Phaeocystis antarctica*), and sea ice diatoms exhibit distinctive biomarker signatures. While pelagic diatom derived fatty acids ($\text{C}_{14:0}$, $\text{C}_{16:0}$, $\text{C}_{16:1\omega 8}$, $\text{C}_{16:1\omega 7}$, $\text{C}_{16:1\omega 6}$, $\text{C}_{16:1\omega 5}$) were identified in this study, polyunsaturated fatty acids (specifically $\text{C}_{16:4\omega 1}$, $\text{C}_{20:5\omega 3}$, $\text{C}_{20:4\omega 6}$) produced by diatoms, were not detected despite sediments containing abundant preserved diatoms and HBI markers, likely due to grazing, scavenging, and degradation in surface waters and throughout the water column. *Phaeocystis antarctica* fossils are not preserved in marine sediments; however, this study shows that phytoplankton derived fatty acids (high $\text{C}_{14:0}$, $\text{C}_{18:0}$, and $\text{C}_{18:1\omega 9}$, low levels of polyunsaturated fatty acids, and a low $\text{C}_{16:1\omega 7}/\text{C}_{16:0}$ ratio) demonstrate potential to record *Phaeocystis antarctica* variability through time. Biomarkers are also influenced by downcore degradation: fatty acids in the southwestern Ross Sea demonstrate an overall exponential decay in the top ~20 cm of the sediment cores. This degradation derives from bacterial biogenesis, demonstrated by 10-20 % of branched fatty

acids sourced from bacteria. Despite the degradation process, fatty acid profiling still records the relative composition of phytoplankton groups over this period. A Principal Component Analysis of the combined biomarker and diatom dataset provides additional support for this structure, resolving three distinct groupings: a sea ice associated group (*F. curta* group, C_{24:0}, sterols), an inversely related open water and increased fast ice habitat group (*Chaetoceros* resting spores, open ocean, cold water, and sea ice diatoms), and an independent fatty acid/HBI group consistent with shared degradation processes. We propose C_{24:0} as a biomarker of sea ice change in the southwestern Ross Sea. Overall, biomarkers in the southwestern Ross Sea sediment independently distinguish between pelagic diatoms, haptophytes, and sea ice associated diatoms, offering a valuable tool for developing decadal resolution records of sea ice and phytoplankton changes in the Ross Sea over the last 2000 years and beyond.”

SPECIFIC COMMENTS

Lines 17-20: the second sentence seems a bit redundant.

Thank you for this comment, the sentence has been removed.

Line 23: reading this sentence, it seems that the coring locations are on a transect that directly includes the Terra Nova Bay polynya. But, according to Figure 1, the sampling locations are quite far from there. Possibly rewrite the sentence making this clearer.

We thank the reviewer for highlighting this ambiguity. We have revised the sentence here and, in the methods, to more accurately describe the sampling locations, replacing “spanning two seasonally recurring polynyas in McMurdo Sound and Terra Nova Bay” with “extending from McMurdo Sound coastal polynya to south of Terra Nova Bay”. This clarifies that the northern sampling locations are situated south of Terra Nova Bay rather than directly within the polynya.

Line 24: maintain the same format throughout the text, core tops or core-tops. Plus, the use of core top twice is a bit redundant.

We thank the reviewer for pointing out this inconsistency. Any reference to ‘core-top’ has been replaced with core top. In the abstract, the use of core top was reduced to avoid redundancies.

Line 26: it’s not clear what “which” refers to, is it the increase in concentration towards McMurdo Sound? This sentence is not clear.

We have revised the sentence to make the referent explicit, replacing “which is driven by” with “This increase is driven by” and splitting the sentence in two for clarity. The revised text now reads: “We find that the proportion of open-ocean diatom species and bacterial fatty acid concentrations in core top samples increases towards the southern end of the transect near McMurdo Sound. This increase is driven by lower summer sea ice extent, a phytoplankton community dominated by diatoms, and higher summer biomass in McMurdo Sound.”

Line 28: put it this way, PIPSO₂₅ seems to be one of the HBIs, while it is a proxy ratio. Maybe change it with IPSO₂₅ or remove it directly from the sentence.

PIPISO₂₅ has been removed from the sentence. The reviewer is correct that it is a proxy ratio rather than a biomarker compound.

Lines 34-35: repetition of “overall”.

Thank you, this repetition has been removed.

Line 38: I suggest inserting as soon as possible in this chapter an introduction (a table?) about the groups of phytoplankton you are considering and what group the species you cite belong. Also, it is not clear if biogenic proxies other than diatoms (whose shells preserve in the sedimentary record) have been counted as well or entirely derived from biomarker analysis. Please specify this concept already in the introduction.

We thank the reviewer for this suggestion. We have revised the introduction to address both points. First, we have added a sentence early in the introduction explicitly stating the main phytoplankton groups considered in this study: “The main phytoplankton groups considered in this study are diatoms, haptophytes (most notably *Phaeocystis antarctica*), dinoflagellates, as well as bacteria.” Second we have clarified which groups preserve in the sedimentary record and which are inferred through biomarker analysis, further in the introduction by adding the following: “As only diatoms produce siliceous material that preserves in marine sediments, haptophytes (*P. antarctica*), bacteria, and the majority of dinoflagellates cannot be identified from microfossil assemblages and are therefore inferred indirectly through biomarker analysis.” We considered a table but felt these additions adequately addressed the concern without adding unnecessary complexity to the introduction.

Line 39: “plankton” is an uncountable noun, so I would suggest adjusting the verbs at the third person singular (Antarctic phytoplankton forms ... influences). Same thing for the following lines where phytoplankton is addressed as a plural noun, i.e. line 45 (inhabits).

Thank you. These changes have been made and the rest of the introduction was checked for instances of this.

Line 45: if available, I suggest adding some other references.

Additional references have been added to support this statement.

Line 50: *P. antarctica* needs to be spelled out as it is its first appearance in the main text. Also, briefly specify what haptophytes are and remember that both haptophytes and diatoms are part of phytoplankton.

Phaeocystis antarctica is now spelled out at its first appearance earlier in the introduction following revisions made in response to the comment at Line 38, where we have also introduced the main phytoplankton groups considered in this study: “The main phytoplankton groups considered in this study are diatoms, haptophytes (most notably *Phaeocystis antarctica*), dinoflagellates, as well as bacteria.” This also addresses the point that both haptophytes and diatoms are part of phytoplankton. We have not added a separate definition of haptophytes as we feel their introduction alongside diatoms and dinoflagellates as phytoplankton groups provides sufficient context for the reader.

Line 57: here, the name of *Phaeocystis antarctica* is expanded, but if you expand it the first time it is cited in the text, here you can use the abbreviated form.

As *Phaeocystis antarctica* begins the sentence at Line 57, it cannot be abbreviated following standard taxonomic convention. The full name has therefore been retained at this instance.

Line 67: add “communities” after phytoplankton.

Done

Line 84: change “also known as ‘diene’ is suggested to be solely sourced from the diatom *Berkeleya adeliensis*” with “also known as ‘diene’ **and** suggested to be solely sourced from the **sympagic** diatom *Berkeleya adeliensis*”.

Done

Line 88: these bacteria are intended as bacteria living in the sediments or in the water column? Please clarify this aspect and specify what type of bacteria you are referring to.⁴

We have clarified that branched fatty acids are produced by bacteria in both the water column and sediments and are used here as indicators of bacterial contribution to sedimentary organic matter, rather than as indicators of a specific bacterial community.

Line 96: change “paleo-biomarker records” with “biomarker paleorecords”.

Done

Line 111: in the table the precision of year and error does not match. I would expect to read 2007 ± 2 or, for example, 2007.5 ± 1.5 .

We have revised the age estimates and errors in the table to ensure consistent precision, removing decimal places throughout so that years and errors are reported to the nearest whole number (e.g. 1963 ± 12).

Line 117: add the location of the ESR Institute.

Done

Line 122: the table says 1856 as the lowest age of BC02, not 1857.

Thank you. This has been checked and the intext reference has been adjusted to 1856.

Line 127: change “sediment core sites” with “sampling sites”.

Done

Line 128: a bracket is missing after 2011. I would also move the details (6.25 km resolution, 2002-2011, Spreen et al. (2008)) at the end of this sentence. Also, how can the paper from Spreen et al. (2008) include information on sea ice cover up to 2011? This applies also to the other subsequent figures.

The details have been moved to the end of the sentence. Spreen et al. (2008) describes the algorithm used to generate the sea ice concentration data. The 2002-2011 dataset was obtained via the Quantarctica GIS package (Matsuoka et al., 2021), which requests that Spreen et al. (2008) be cited alongside it. We have clarified this in the figure captions.

Line 140: change “was” with “were”.

Done

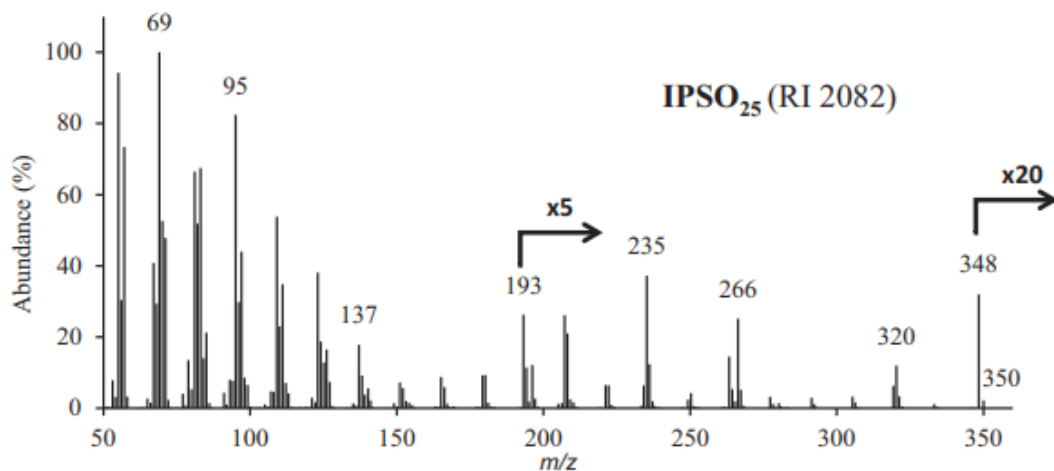
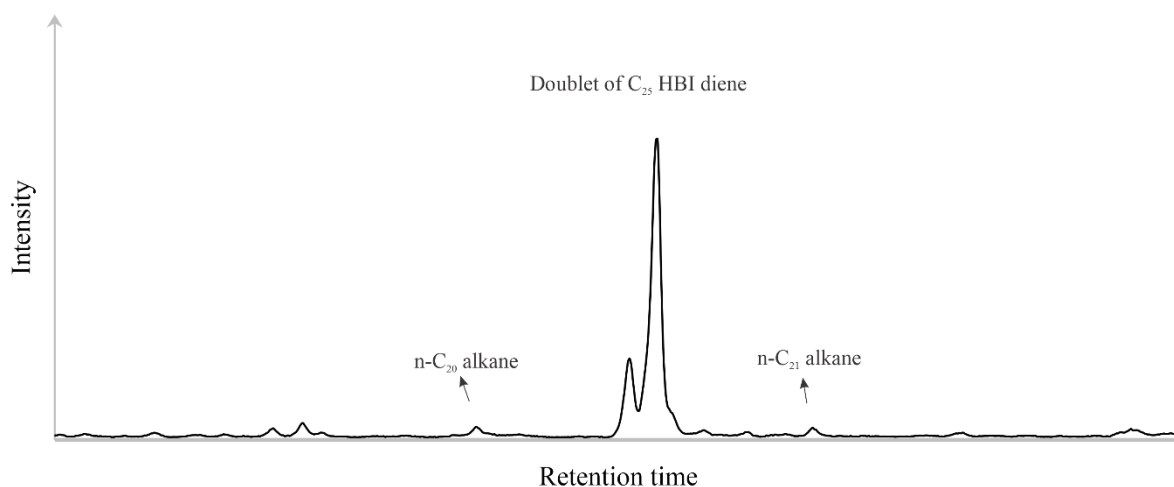
Line 144: change “factions” with “fractions”.

Done

Line 169: did all biomarkers identifications happen in TIC? Usually it is extremely challenging and unlikely to identify HBIs such as IPSO₂₅ with certainty without SIM mode.

We thank the reviewer for this comment. All biomarkers were present at concentrations that could be identified using TIC mode. IPSO₂₅ identification was confirmed based on

characteristic mass spectra consistent with those described in Belt (2018). While we acknowledge that SIM mode offers greater sensitivity, concentrations of IPSO₂₅ in our samples were sufficient for confident identification and quantification by TIC. Below is an example of the doublet of diene present in a sample between the C₂₀ and C₂₁ alkanes as well as the mass spectra fragmentation pattern used to identify diene with a molecular ion (M⁺) of 348 and large 55 and 69 fragments, adapted from (Belt, 2018).



Line 188: the references listed here need to be direct, without brackets.

The sentence has been restructured so that references appear directly in the text rather than in a list.

Line 192: HBIs were already introduced and you can use the abbreviation from there on.

Done

Line 196: change "source differences" with "different sources"

Done

Line 223: "the southwestern Ross Sea is dominated by diatoms rather than (Arrigo et al., 2000; Arrigo et al., 2015; McMinn et al., 2010; Noble et al., 2013) which may lead to a larger diatom source of dinosterol". I suppose something is missing after "rather than". Please, complete the sentence.

Thank you for the helpful comment. This sentence now reads: "However, the southwestern Ross Sea is dominated by diatoms rather than dinoflagellates (Arrigo et al., 2000; Arrigo et al., 2015; McMinn et al., 2010; Noble et al., 2013) which may lead to a larger diatom source of dinosterol."

Lines 227-242: the different diatom groups must be described with the same style, otherwise it is not clear if every group is on the same importance level as the others. Also, it is not perfectly clear which conditions are reflected by each group. This paragraph needs to be adjusted.

Thank you for this comment. We have revised this paragraph so that all diatom groups are described with a consistent structure, with each group introduced in the format: "The [group name], comprising [species], [environmental conditions reflected], [presence in surface waters, and in preservation in sediment] (citation)." This ensures all groups are presented at the same level of importance and the ecological conditions reflected by each group are clearly and consistently stated.

Line 227: a part of the sentence is missing?

This sentence now reads: "To compliment biomarker analysis, we assessed diatom assemblages grouped by ecological preference..."

Line 229: change "with melting late in the year" with "with a late melting season".

Done

Line 230: *F. cryophilic* in italic everywhere in the text, tables and figures/captions.

All mentions of *F. cryophilic* group are now in italics.

Line 234: *E. antarctica* in italic everywhere in the text, tables and figures/captions.

All mentions of the *E. antarctica* group are now in italics.

Line 245: Table 2 is extremely useful and complete, but it needs an improved formatting.

Thank you for this comment. The table has been edited to fit onto one page so that it is easier to follow.

Line 251: change “fatty fraction” with “fatty acid fraction”.

Done

Line 255 and others (264, 290, 398, 403, 407, etc.): there is a space between numeric value and % symbol, then in line 259, 260, 317, 318 and others there is no space. Please uniform the style throughout the text.

A space has been added between all numbers and the % symbol throughout the manuscript, in accordance with the Copernicus journal style guidelines.

Lines 263-264: I would not call “exponential” a decrease of 50% in 30 cm, maybe a rapid decrease?

The sentence now reads: “Downcore, total fatty acid concentrations decrease rapidly by ~50 % between 1-30 cm depth before stabilising toward the base of the cores.”

Line 272: change “a typical southwestern Ross Sea sediment sample (BC02; 11-12cm)” with “a sediment sample from BC02 core (11-12 cm)”.

Done

Line 275: “IPSO25” should be IPSO₂₅ everywhere in the text, tables and figures/captions (the same holds true for C₁₅ FAs, C_{16:0}, etc), and species names must be in italic. Change “percent” with “percentage”.

The manuscript has been revised to adjust any discrepancies in subscript, species names and percentages.

Line 276: in the caption of figure 3 change “Fatty acid concentrations of saturated and unsaturated fatty acids” with “Concentrations of saturated and unsaturated fatty acids”.

Done

Line 277: in the caption of figure 4 change "select" with "selected".

Done

Line 280: change "ranged between 19 and 182" with "ranged from 19 to 182".

Done

Line 284: the description of downcore trends does not reflect the data precisely. Sterols trends differ from one core to the other and do not seem to be consistent.

We thank the reviewer for this comment and agree that the current description does not accurately reflect the data. The description has been updated to: "Downcore concentrations of the two sterols do not follow the same decreasing trend as fatty acids (Figure 7). Brassicasterol remains relatively stable in all three cores, except for an increased concentration in the BC04 core top. Dinosterol is relatively stable in BC03 and BC04, except the BC04 core top. However, dinosterol shows a decrease with depth in BC02."

Line 290: change "northern" with "northernmost".

Done

Line 292: asymptotes in this case should be represented by the biomarker value, not the core depth. I would rephrase "below which it remains constant. The asymptote of IPSO₂₅ diene is ~20-30 cm in all three sediment cores (Figure 5)" as "below which it remains constant in all three sediment cores (Figure 5)".

Done

Line 298: change "per cent" with "percentage".

Done

Line 297: in figure 5 the unit of IPSO₂₅ should be $\mu\text{g g}^{-1}$ TOC. Add the name of the cores in these images.

The unit has been corrected (Figure 5). The name of the cores are in the legend on the right side of the plot.

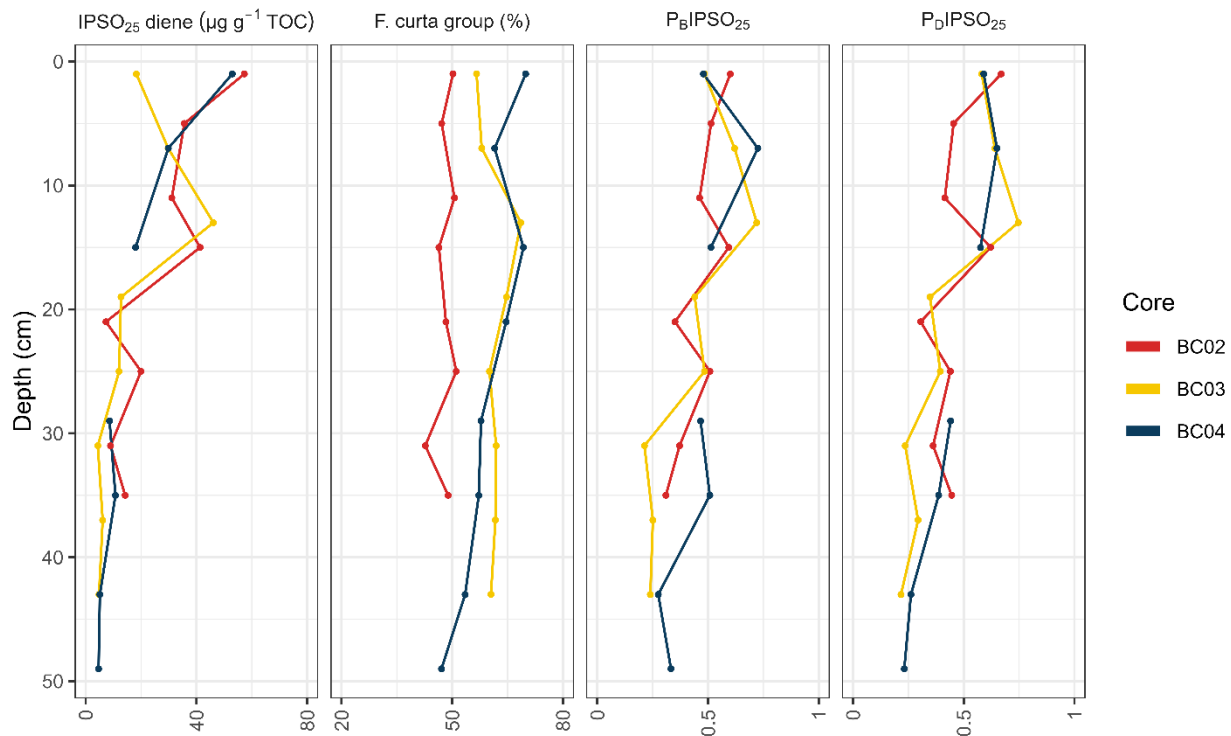


Figure 5: IPSO₂₅ diene concentrations relative to total organic carbon (TOC), percentage of *Fragilariopsis curta* (*F. curta*) group, and PIPSO ratios (P_BIPSO₂₅ and P_DIPSO₂₅) in RS14-BC02, RS14-BC03, and RS14-BC04 vs depth.

Lines 313-315: these 2 sentences are repeated.

The repeated sentence has been removed.

Line 316: the decrease of *F. curta* group % is clear only for BC04 looking at the graph, the other trends are quite obscure.

Thank you for this comment. We have changed the manuscript to reflect this, and the sentence now states that "The *F. curta* group dominates the diatom assemblage across the record and ranges from 42 % to 70 % of all diatoms counted and decreases downcore in BC04".

Line 317: the increase of CRS % does not seem true for BC03 judging from the graph.

The sentence has been adjusted to reflect the increase in CRS in BC02 and BC04.

Line 318: change "represent" with "represents".

Done

Line 319: change "do no" with "do not".

Done

Line 325: in the caption of figure 6 change “select” with “selected”.

Done

Lines 346, 365 and 383: titles here are followed by a colon, while in line 397, which I assume has the same hierarchy, the title is not followed by the colon. I would delete the colon from all the titles, possibly enhancing the four titles through the italics text rather than bold text.

We thank the reviewer for this suggestion. The colons have been removed and the bold text has been changed to italics.

Line 353: remove the first “the” from “in the any of the studied”.

Done

Line 358: “First, show a strong affinity to particles and are efficiently scavenged from surface waters (REF)”. I suppose here a reference is missing. Please provide a reference. I suggest also to revise and rewrite the sentence in a more fluid way, adding the subject for the first part, for example: “First, PUFAs show a strong affinity to particles and are efficiently scavenged from surface waters (missing reference here); second, PUFAs are highly sensitive to microbial remineralization in the water column and sediments (Wakeham et al., 1997) and finally, they also undergo intense photo and autooxidation in the water column before reaching the seafloor (Rontani et al., 2019).”

Thank you for this comment. The sentence now reads: “First, PUFAs are preferentially assimilated by zooplankton from their phytoplankton diet and are incorporated into zooplankton tissues before reaching the seafloor (Dalsgaard et al., 2003); second, PUFAs are highly sensitive to microbial remineralisation in the water column and sediments (Wakeham et al., 1997), and finally, they also undergo intense photo and autooxidation in the water column before reaching the seafloor (Rontani et al., 2019).”

Line 346: sterols are not mentioned as indicators of pelagic diatoms in this chapter, despite being listed as such in Table 2.

We thank the reviewer for this comment and we have added a section to this section to strengthen the argument for pelagic diatoms as a source of biomarkers. The following section has been added: “C₁₆ fatty acid compounds were broadly similar across core tops, with the exception of lower values in the southernmost core (GC72), suggesting a potentially reduced contribution from pelagic diatoms (Nichols et al., 1993; Nichols et al., 1986; Skerratt et al., 1995; Wing et al., 2012). This interpretation is supported by the low abundance of dinosterol at GC72, further indicating diminished pelagic diatom input at this site (Rampen et al., 2010). In contrast, brassicasterol did not exhibit a clear spatial trend

across the core tops and instead showed substantial variability along the transect. This variability may reflect additional sources, as brassicasterol has been identified as a stronger signal of haptophytes, particularly *P. antarctica* (Rampen et al., 2010; Nichols et al., 1991; Skerratt et al., 1995)."

Line 369: change "with high sources of" with "with an important contribution from".

Done

Line 372: change "evidence for" with "indicating".

Done

Lines 378-380: I suggest to rewrite the sentence to avoid the repetition of *Berkeleya adeliensis* as follows: "IPSO₂₅ is dominantly sourced by the sea ice diatom *Berkeleya adeliensis* (Belt et al., 2016), which was not identified in any of the three cores studied here despite the presence of IPSO₂₅, consistently with other studies around Antarctica (Tesi et al., 2020)."

Done

Line 392: change "have a varied phytoplankton community spatially and temporally" with "have a variable phytoplankton community, both spatially and temporally".

Done

Lines 403-404: references are needed for this; it is not straightforward that bacteria communities respond to the same productivity changes as phytoplankton communities. Some studies have been made, especially for Archaea (<https://onlinelibrary.wiley.com/doi/10.1155/2019/3717239>), but clear evidence is still missing.

We agree with the reviewer that the relationship between bacterial communities and primary productivity is not straightforward and that clear evidence is still missing in this study. We have revised the sentence to remove the supported claim, instead noting the spatial variability in bacterial contributions to sedimentary organic matter while acknowledging that the relationship between bacterial community abundance and primary productivity in Antarctic sediments remains poorly constrained. The text is modified to "This suggests spatial variability in bacterial contributions to sedimentary organic matter across the transect, though the relationship between bacterial community abundance and primary productivity in Antarctic sediments remains poorly constrained."

Line 407: change "which is covered" with "an area covered".

Done

Line 408: add “of the year” after 40%.

Done

Line 409: change “spring/summer” with “warm season”.

Done

Line 410: BC02 is THE closest site to McMurdo Sound without considering GC72.

We thank the reviewer for this comment and have adjusted the 4.1.2 section to reflect all of the core tops rather than just the box cores.

Line 411: sea ice duration? I guess you mean the site with less average sea ice concentration? Or do you mean the site where sea ice melts, on average, later during the year? Please clarify.

We agree that the language used in this section was confusing and have changed all instances of ‘sea ice duration’ to ‘sea ice concentration’ for clarity.

Line 433: as per a previous comment, the use of the term asymptote here is a bit misinterpreted, I suggest rephrasing. Maybe you could say that the asymptote starts at around 20 cm of depth?

We have revised the wording to “concentrations approaching an asymptote at ~20 cm depth” to more accurately describe the degradation pattern, following the reviewer’s suggestion.

Line 452-453: “The detection of unsaturated and branched fatty acids is consistent with another southwestern Ross Sea (Smith et al., 1986), where a range of unsaturated fatty acids were detected...”. I suppose there is a missing word, possibly “consistent with another southwestern Ross Sea site/location/study (Smith et al., 1986)”?

The word ‘study’ has been added to the sentence. Thank you for this comment.

Line 465: change “relative abundance *F. curta*” with “relative abundance of *F. curta*”. From figure 8 it is not possible to appreciate the increasing trend of this group in BC03.

The sentence at line 465 has been changed. We thank the reviewer for highlighting the *F. curta* trend in BC03. Upon reflection, the text incorrectly described BC03 as showing an increasing trend in the *F. curta* group. We have revised the text to more accurately

described BC03 as remaining relatively stable throughout the record, which is consistent with what is shown in Figure 8.

Line 466: change "*F. curta* is a well-established sea ice diatom proxy" with "*F. curta* relative abundance is a well-established sea ice diatom proxy".

Done

Line 470: "Here, the *F. curta* group suggests an overall increase in sea ice activity in the southwestern Ross Sea between 1900 CE to present. from 1900 to present". This sentence contains some typos. Please rewrite as follows: "Here, the *F. curta* group suggests an overall increase in sea ice activity in the southwestern Ross Sea from 1900 CE to the present time".

Done

Line 471: if you intend later melting with "increased sea ice duration", IPSO₂₅ concentrations cannot be put directly in relation with that. Sympagic diatoms production can increase independently from sea ice melting season, and it's mainly associated with nutrient and light availability. Besides, as you also stated earlier in this manuscript, IPSO₂₅ seems to be mainly associated with fast ice and platelet ice, so it is not directly showing seasonal sea ice extension, even though the two things are related (see for example Belt 2018).

We thank the reviewer for this comment and have adjusted the section so as not to overstate the ability of IPSO₂₅ to recreate sea ice on its own. "IPSO₂₅ trends indicate an increased signal of fast and platelet ice (Belt, 2018), potentially reflecting greater sea ice presence or duration. The PIPSO₂₅ index integrates IPSO₂₅ diene with open-water sterols, dinosterol and brassicasterol, and is considered a more robust measure of sea ice influence than IPSO₂₅ diene alone (Lamping et al., 2021; Vorrath et al., 2023; Vorrath et al., 2020)."

Line 478: what do you mean by "off the Ross Sea"?

The phrase has been replaced with "in the Ross Sea".

Line 492: delete "across the Ross Sea".

Done

Line 496: add a comma after "coverage": "Despite these differences in metric and spatial coverage, all records presented in Figure 8..."

Done

Lines 500-501: change “After this degradation fatty acid concentrations remain relatively stable” with “Proceeding downcore, after the degradation, fatty acid concentrations remain relatively stable”.

Done

Lines 501-502: as already said in a general comment, this seems a bit far-fetched. You cannot know if the decrease in the topmost sediments is only due to degradation or if there are other factors at play.

We thank the reviewer for this comment and agree that it is highly unlikely that degradation is the only factor causing the changes in fatty acid concentrations. We have revised this section as mentioned in the general comment section.

Line 504: in the text, when indicating stratigraphic intervals, the hyphen (short dash, -) is used. This time, it is used the longer dash (–). I suggest changing this with the shorter one and generally applying this correction everywhere in the text.

Thank you for this comment. All longer dashes have been replaced with hyphens throughout the manuscript.

Line 507: in the text you suggest that PIPSO₂₅ calculated with dinosterol might be a better pick over the one calculated with brassicasterol and I quite agree, but why then only the latter is shown in figure 8? In panel e, the curve is not black as stated in the caption.

Thank you for this comment. We agree that dinosterol might produce a better reconstruction and have replaced the PIPSO₂₅ calculated with Brassicasterol with the dinosterol values. The curve in panel e has been stated as being purple in the caption.

Line 518: please rewrite as follows “Spatial variations in biomarker composition were primarily driven by sea ice conditions and associated phytoplankton habitats, while pelagic diatoms, *Phaeocystis antarctica*, and sea ice diatoms exhibit distinctive biomarker signatures.”.

Done

Line 519: remove the comma after “While”.

Done

Line 520: remove the commas after specifically and after the closing bracket.

Done

Line 522: rewrite and unite the sentences as follows: “*Phaeocystis antarctica* fossils are not preserved in marine sediments; however, ...”

Done

Line 526: rewrite the sentence as follows: “Biomarkers are also influenced by downcore degradation: fatty acids in the southwestern Ross Sea demonstrate an overall exponential decay in the top ~20 cm of the sediment cores. This degradation derives from bacterial biogenesis, demonstrated by 10-20% of branched fatty acids sourced from bacteria. Despite the degradation process, biomarkers still record the relative composition of phytoplankton groups over this period”.

Done

Lines 529-532: rewrite as follows: “Trends in sea ice diatoms such as *Fragilariopsis curta*, sea ice diatom markers of HBIs and PIPSO₂₅, reveal a 200-year trend toward increasing sea ice extent in the southwestern Ross Sea. This reconstruction is aligned with existing regional sea ice extent reconstructions derived both from sediment cores and ice cores, which show stability in the rime frame spanning from 1900 to 1950, followed by an increase in sea ice towards the present”.

Done

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