Response (in blue) to Reviewer

Manuscript Title: Diatom community assemblages and microbial degradation resistance modulate local heterogeneity in diatom contribution to carbon export in the western North Pacific Subtropical Gyre

Journal: Biogeosciences

Authors: Feng Li, Hongzhen Jiang, et al.

Dear Editor and Reviewer,

We thank the reviewer for the thorough re-evaluation of our revised manuscript and for the constructive comments. We have carefully addressed each of the technical and editorial points raised. Below we provide point-by-point responses.

Comments

This article is substantially improved from its prior version. Most critically, the limited dataset now matches the conclusions of the paper. The manuscript now reads as an exploration of the effects of depth structure in diatom populations on export flux. There is an additional component of degradable compounds which is interesting. I am not in a good position to judge the metagenomic work in the manuscript but am not opposed to its conclusions. I am comfortable with the manuscript being published. I wish that the authors had a better set of figures to explain their work, but this is not imperative. I recommend major revisions due to the technical points that I will enumerate below along with a few editorial issues.

Response: Thanks for your comments.

I am concerned about some of the statistics in the paper:

Line 357-358: These values cannot go below 0 yet the error bars all include 0. How were your error ranges calculated?

Response: We thank the reviewer for this observation. The standard deviations were calculated using the STDEV.S function in Excel based on raw cell abundance

and carbon biomass data across different sampling sites. Due to substantial inter-site variability in cell abundance and carbon content, the resulting standard deviations occasionally exceeded the mean values, producing negative lower bounds when expressed as mean ± SD. This reflects high data dispersion rather than biologically meaningful negative values. In the revised manuscript, we have therefore removed these mean ± SD values to avoid misleading interpretation.

Lines 431, 435, 437: Please explain why r=1? Please put the number of samples down. Are you correlating the depth profiles? If this is valid, it needs to be discussed.

Response: We thank the reviewer for this comment. Spearman's r = 1 indicates a perfect monotonic positive correlation, meaning that all paired samples share identical rank orders. In the surface mixed layer, *Thalassiosira* and *Thalassionema* occupy equivalent nitrate niches; their abundances fluctuate in complete synchrony with subtle variations in nitrate concentrations, resulting in perfectly aligned rank values for both genera relative to nitrate pools and to each other. Within the DCM, *Nitzschia* constitutes the overwhelming majority of the diatom assemblage, such that the rank order of total diatom abundance matches that of *Nitzschia* abundance exactly.

We emphasize that all correlation analyses were conducted separately on surface mixed layer and DCM datasets from five independent sampling stations (n = 5 for each layer), rather than on sequential depth points within a single vertical profile. Each station yielded one discrete sample for the surface mixed layer and one for the DCM, with concurrent matched measurements of environmental variables and diatom abundances collected for each layer. We have added this clarification to the Methods section (Section 2.10) and briefly discuss the ecological interpretation in the Results (Section 3.4).

General Line by Line:

Line 131: Please put in a citation here.

Response: Thanks for your comment. We have added the citation accordingly.

Line 162: Please summarize the environmental data available.

Response: Thank you for comment. The environmental data collected during sampling were obtained by the research group led by Du (Du et al., 2024). In situ measurements of temperature and salinity were performed using a Seabird SBE 911 conductivity-temperature-depth (CTD) sensor. Nutrient concentrations were determined onboard immediately after collection, using 500 mL seawater samples analyzed with a Technicon AA3 Auto-Analyzer (Bran-Luebbe, GmbH, Germany). For chlorophyll a analysis, an aliquot of the 8 L seawater subsample was filtered through a Whatman GF/F glass-fiber filter, and the retained pigments were extracted with 2 mL of N,N-dimethylformamide (Huang et al., 2010). The extracted pigments were subsequently quantified using an Agilent 1100 Series High-Performance Liquid Chromatograph (HPLC) (Agilent Technologies, USA). We have incorporated this summary into the revised Methods section.

Line 236: What is '1-D'?

Response: We thank the reviewer for this question. In the context of the Simpson index, "1-D" is a commonly used transformation where D represents the probability that two randomly selected individuals belong to the same species. The transformation "1-D" yields a value that increases with community diversity, making interpretation more intuitive: higher values indicate higher diversity, and lower values indicate lower diversity. To improve clarity, we have now supplemented the interpretation for "1-D" in the revised Methods section (Section 2.6)

Line 239-240: It is not at all clear why 'higher J suggests more stable export potential'. Please explain.

Response: We thank the reviewer for this observation. This sentence was included inadvertently and does not accurately represent our findings. We have removed it

from the revised manuscript.

Fig. 2: It looks like Station K8a is different than the others as Salinity and Chla appear very correlated. Does this matter to your results?

Response: We thank the reviewer for this observation. No significant correlation was found between salinity and Chla at Station K8a in our dataset. In the upper 200 m, the salinity maximum was observed at 150 m, while the Chla maximum was located shallower at 125 m. The higher Chla levels and shallower fluorescence peak at K8a, compared to Station M22, are attributed to the elevated upper nutricline within the North Equatorial Current (NEC) region. This regional hydrographic feature does not compromise our comparative analyses, as our study focuses on differences in diatom community composition and export contribution across stations rather than on salinity–chlorophyll relationships.

Fig 3: Please put an axis label on the colorbar for panel e.

Response: Thanks for your comment. We have added the axis label on the colorbar in Fig. 3e in the revised figure.

Line 376: What is a 'within-lay' comparison'?

Response: We thank the reviewer for identifying this typographical error. The term "lay" was intended to refer to "layer" (i.e., sampling depth layer). We have replaced "within-lay" with "within-layer" throughout the revised manuscript.

Line 473-481: How can you determine where the flux comes from? Are you assuming that flux is proportional to the abundances of each type?

Response: We thank the reviewer for this important question. Yes, we infer the source depth of exported diatoms by matching the dominant taxa in sediment traps with their peak occurrence depths in the water column (surface mixed layer vs. DCM). This approach is based on the widely used assumption that the relative contribution of each taxon to export flux is proportional to its abundance in the

source layer (Scharek et al., 1999a). We acknowledge that this assumption, while widely used, may not fully account for species-specific differences in sinking rates or grazing pressure. To address this, we have added a clarification in Section 3.5 of the revised manuscript.

Line 496: How are you splitting primary production between groups? I can not find it in the methods and am unsure how this works.

Response: We thank the reviewer for this question. The estimation of primary production for total phytoplankton groups was based on carbon biomass calculated from chlorophyll a (Chl a), as described in Section 2.5. Specifically, total phytoplankton carbon biomass was obtained by converting Chl a concentration into carbon equivalents using a carbon-to- Chl a ratio (C: Chl a) derived from in situ measurements at Station ALOHA at corresponding depths.

For diatoms, carbon biomass was estimated from cell size measurements via SEM, biovolume calculations, and subsequent conversion to carbon content using established formulae.-Deuer & Lessard, 2000).

The production proportion for diatom was then calculated based on its respective carbon biomass contribution.

We acknowledge that the original Methods section lacked clarity on this point; therefore, we have revised Section 2.5 to explicitly describe the calculation of diatom production proportions (DPP) based on carbon biomass contributions.

Line 665: Typo - 'This This'

Response: Thanks for your comment. We have corrected the duplication and revised the sentence accordingly.