

**Interactive comment on “Latitudinal distribution of biomarkers across the western Arctic Ocean and the Bering Sea: an approach to assess sympagic and pelagic algal production” by Youcheng Bai et al.**

**Reply to review #1 Author’s replies are in Blue.**

Bai et al. have analyzed a new set of sediments (2008, 2009, 2012, 2014) and filtered seawater SPM across the Pacific Arctic region using HBI biomarkers, sterols and *n*-alkanes. The findings of this study are consistent with other similar studies in this particular region and within similar years. These new data points and additional markers do not significantly advance our understanding of HBI synthesis or dynamics in the region, but do validate previously reported observations by Bai (2019) and Koch (2020). However, a notable contribution of this study to the existing body of knowledge is the inclusion of well-defined end members for the H-print index with respect to sea ice conditions, including ice free waters in the Bering Sea near the Aleutians up through perennial ice cover in the Chukchi borderlands and analysing alongside additional sterol biomarkers.

While the results are relatively straightforward, there are a few issues or suggestions to consider further:

In the Introduction, perhaps it is no longer necessary to provide the extensive explanation of HBIs as it is rather well established in the growing body of literature on HBIs (lines 77-91). Perhaps this could be more consider by simply refer to the sea ice HBIs (IP25 and HBI-II) and the pelagic HBI III, and exclude the information about the history of the biomarker (e.g., initially proposed by Belt in 2007, used in paleo studies by Masse).

**This section in the introduction has been rephrased in the revised version (Lines 78-95).**

It is unclear why the HBI data needs to be presented twice (once without the Bai et al. 2019 data points and this study). They don’t appear to be all that different. I suggest using the one map to show the different data sources (as done in Fig 1) and only report the whole dataset (n=88) in a figure (Fig 8). A comparison of the two could be better served in a table – and if not that different, perhaps just in the supplemental data?

**The reason why we opted for this format is that new data are to be presented in the result section. The discussion section allow to compared with other result and since these new data were acquired following the same procedure it made sense to have figures combining older and new data and used this exercise as a sensitivity test.**

Major issue – In reviewing the supplemental data, I fear the H-print has been calculated incorrectly. The “relative abundance” of HBIs is not the value quantified against the standard – which is the absolute abundance. It is the raw data from the SIM chromatograms. It is these relative abundance values that should be used in the H-print calculation. I am happy to connect with the authors to advise on this. I believe this is why the H-print values are much lower than expected in Figs. 4d and 8d for the Bering Sea up through Bering Strait, indicating a dominant sympagic source. Figure 9 will also need to be revised with the new values.

Thanks for your raising this issue. The relative abundances of IP<sub>25</sub>, HBI II and HBI III in the supplemental Table 2, reported as  $\mu\text{g g}^{-1}$  TOC, are based on the area of individual HBIs obtained from SIM by GC-MS relative to the internal standard. They are not corrected by the response factors (RF) as in the original paper of Belt et al. (2012). To clarify the confusion: our data are indeed relative abundances because they are calculated relative to the internal standard, while those corrected with the RF are absolute abundances.

H-Print was originally defined as the ratio of HBIs from sympagic and pelagic diatoms by Brown et al. (2014) and Brown & Belt (2017). We used HBI relative concentrations derive H-Print index as in Koch et al. (2020, 2021) using Eq. (1), where H-Print does not refer to RF-corrected values as in our case.

$$\text{H-Print (\%)} = [\text{HBI III} / (\text{IP}_{25} + \text{HBI II} + \text{HBI III})] \times 100 \quad (1)$$

We thus compared our data to those from other authors who calculated it the same way.

For Figure 9, there does not appear to be a significant difference between the means of the Chukchi Shelf and slope regions which the authors indicate are distinct.

Indeed, the Chukchi Shelf and slope regions have similar means but different spread (standard deviation) highlighting lower variability in sea ice cover to the North reflecting extended sea ice cover. This is the point we want to make in figure 10.

In this discussion section, I also recommend looking at and comparing with the Koch et al. 2020 paper from Marine Ecology Progress Series which expands the sediment dataset into 2018 and is presented similarly.

In the revised version, this remark has been considered in Section 5.1(Lines 413-416).

I like how the biomarkers are presented with sea ice data in Figure 10.

Sea ice concentration data used in the final version were obtained for the interval 1994-2014 as reviewer 2# suggestion.

Line 461 – this was also reported by Koch et al. 2020 through the sediment trap data linking HBI III with the mentioned genera. Apologies for repeatedly referring to this paper but there is a great deal of overlap.

We added Koch et al. (2020) there as well (Lines 462-466).

Line 552 suggests weak benthic-pelagic coupling based on the sterol ratios in SPM versus sediment. I'm not convinced by this and the region is known for having strong B-P coupling. Is the use of sterol ratios in this way based on previous work?

We rephrased this part of the discussion to clarify (Lines 555-559). Differences between SPM and surface sediments involves other mechanisms than vertical transport, such as grazing. The time span of each sample type may also account for the observed differences.

Line 615 in the conclusion states the influence of PDO rather than global warming. This was not tested in this study.

Here, we suggest based on previous discussion (Lines 425-429) that refers to the findings of Wash et al. (2017), that since 1850 despite global warming PDO variability was dominant in shaping the phytoplankton community in this region of the North Pacific, which is also consistent with the absence of a long-term reduction of sea ice there.

Other editorial suggestions include:

Line 49-50: change to “at the onset of the spring bloom”; remove “still”

Done.

Line 52: change “is” to “are”

Done.

Line 62: change to “mixotrophic”

Done.

Line 78: remove “indeed”

Done.

Line 108: suggest using “community composition” rather than phytoplankton structure

Done.

Line 283: change to “higher” rather than “high”

Corrected.

Line 294: suggest including Koch et al 2020 a & b (PLOS One and MEPS papers)

Done. See Lines 294.

Line 310: an issue with the symbol character displaying as a square

Corrected. The symbol should be displayed as  $\alpha$  isomer.

Line 515: should be primary production, not primarily

Corrected.

Line 552: change to benthic-pelagic

Done.