

Biogeosciences Discuss., referee comment RC2
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Comment on bg-2022-45

Anonymous Referee #2

Referee comment on "First phytoplankton community assessment of the Kong Håkon VII Hav, Southern Ocean, during austral autumn" by Hanna M. Kauko et al., Biogeosciences Discuss., <https://doi.org/10.5194/bg-2022-45-RC2>, 2022

The *Biogeosciences* submission 'First phytoplankton community assessment of the Kong Håkon VII Hav, Southern Ocean during austral autumn' by Kauko et al. shows a lot of potential. The authors have collected a nice dataset about the taxonomy and distribution of the phytoplankton in three distinct regions of the Kong Håkon VII Hav – Southern Ocean. However, the data analysis is very basic and could be greatly improved with the introduction of statistical approaches that allow linking the structure of phytoplankton communities and the environment. The presentation and discussion of results is a simple description (very subjective) of the patterns found in the study region. For example, the separation of sub regions is a great idea, but it comes across very subjective and not quantitatively based at all. How are these phytoplankton-dominated regions determined? I want to see a statistical determination of subregions. In fact, why don't you use a multi-parameter analysis and use the ancillary data, nutrients, mixed layer depth, temperature, salinity, Chl a, phytoplankton assemblage and properly determine these phytoplankton niches? These also need to be clearly mapped out – I want to exactly see these subregions and the conditions that the phytoplankton exist in.

I would encourage the authors to revise the manuscript and submit it again. At its present state, however, I do not feel I can recommend its publication.

Specific comments

- line 143 'two types of diatoms...' The HPLC method used cannot separate chlorophyll c1 from c2, so this separation into two types of diatoms becomes difficult and arbitrary. Furthermore, chlorophyll c2 is a poor taxonomic biomarker as it is present in most marine phytoplanktonic groups (red lineage).

- The chemotaxonomic characterization of dinoflagellates-2 and haptophytes-6 is also complicated by the biomarkers (ratios) used – very similar. This separation is only

effectively possible if some specific biomarker pigments from each group are used (e.g., gyroxanthin diester; 4-keto-Hex-fuco; Chl c2-MGDG [14/14] and Chl c2-MGDG [18/14] – see Wright & Jeffrey 2006 [https://link.springer.com/chapter/10.1007/698_2_003] or Mendes et al. 2018 [<https://doi.org/10.1016/j.dsr2.2017.12.003>]).

- line 435 'Cryptophytes, ... also contain similar pigments to haptophytes' This is not true, right? ... and your table 1 makes that clear.

- lines 437-439 'The discrepancies might be partly explained with the relatively small volume filtered (typically 1 L) for HPLC samples...' This is also a flawed argument, because for microscopy the volume used is much smaller than for HPLC. In fact, the higher volume used for pigment samples (HPLC) is an advantage of chemotaxonomic methods.

- line 195 'Two of the sampling locations had an active diatom bloom...' For me, characterizing a bloom situation with chlorophyll-a values below $1 \text{ mg}\cdot\text{m}^{-3}$ is quite strange. I understand that it is a predominantly oligotrophic region, but this delimitation of what is (or is not) a bloom will have to be better defined/discussed.

- The results section will have to be restructured and, essentially, reduced. There is redundant information that does not add content to the discussion of the data presented. I speak, for example, of the graphs with the pigmentary ratios (Figs. 8 and 9) and NMDS analyses (Fig. 5). For this, authors first need to define very well the focus they want to give to the work, as it cannot simply be an unbridled compilation of hard-to-connect data.