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Biogeosciences Discussions

Interactive comment on "Ecology and biogeochemistry of contrasting trophic environments in the South East Pacific by carbon isotope ratios on lipid biomarkers" *by* I. Tolosa et al.

I. Tolosa et al.

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Responses to the Anonymous Referee #1

1) **The abstract should list those biomarkers that represent the different taxa (rather than just saying; the diatom marker; etc).**
We have now specified the chemical name for the concerned lipid biomarkers in the revised abstract.

2) **In the methods section, two sizes of PM were collected, on a Nitex screen and on a microquartz filter. Were both size fractions analyzed, together or sep-**

arately? This is important since diatom aggregates might be preferentially collected on the Nitex whereas coccolithophorides and dinoflagellates (if not incorporated into large aggregates) might be enriched on the microquartz filter; same with a potential discrimination of bacterial biomarkers (preferentially on the microquartz?) and zooplankton biomarkers (preferentially on the nitex?).
We only analysed the fraction collected on the microquartz filter and we are aware of possible discrimination regarding the analysed size fraction. However, this does not fundamentally alter the outcome of this paper. A clarification has now been inserted in the revised manuscript (L 124-125 and L. 322-324).

3) **A major concern is the presentation of concentration data for the biomarker lipids, but without reference to some normalizing factor, such as POC. Are concentrations peaks shown simply because there is more biomass (or POC) at certain depths, or because certain compounds are specifically enriched in the POC?**
According to this concern, we have included a new Table (new Appendix B) that presents the concentration data for the biomarker lipids normalised to the POC. In the revised manuscript we have also addressed the POC parameter in the discussion, which follows the profile of chlorophyll a except in the gyre. The concentrations of biomarkers normalised to the POC exhibited the same enrichments in POC at certain depths as the profiles on the relative contribution of the biomarkers within the total lipids. Therefore, we keep our discussion using the relative contribution of the biomarkers within the total lipids, but we specified within the text that both approaches provided similar trends or enrichments in the water column.

4) **In addition, reference is made throughout to how a profile for a specific biomarker is related to the chlorophyll a profile, but it is not clear that the chl-a profiles are shown anywhere. Likewise, except for the 198217;-hex, what about the other diagnostic pigments that are referred to?**

We did not display the chlorophyll-a profiles, because the concentration values from the different sites at the sampled depth are already shown on Table 2. Other diagnostic

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pigments that are referred to in the text are discussed by Ras et al., (2008) in the same special issue. If necessary, this reference is mentioned. Moreover, we did not consider it necessary to include profiles for other pigments, in order to interpret our data.

5) **On p 4663, is should be made clear that C25-HBIs are not markers for all diatoms (i.e. there might be an offset between diatom sterols and the HBIs depending on the diatom species composition), nor do all haptophytes produce alkenones.**

We agree with the reviewer, and we have now inserted this statement in the revised manuscript (L 309-311 and L 315-318) as:
"We note, however, that HBIs are not markers for all diatom species since they are mainly synthesized by centric (Rhizosolenia species) and pennate diatoms (Haslea, Navicula and Pleurosigma), whereas $C_{28}\Delta^{5,24(28)}$ *sterol has also been found in some dinoflagellates and green algae (Volkman, 1986). Therefore, there might be an offset between the diatom sterols and the HBIs depending on the diatom species composition".*

6) **Relative abundances of biomarkers are used to estimate relative abundances of phytoplankton taxa. This is actually quite difficult since the origins of some biomarkers are diverse, and in fact the abundances of compounds in different algae might vary considerably. So really all one can say is that abundances of the biomarkers vary and this might suggest more or less of the source alga. For example, from alkenone abundances, can one really extrapolate to relative abundances (in the sense of more haptophytes vs fewer diatoms) of haptophytes, or really only E. huxleyi; and vice versa?**

We agree that relative abundances of biomarkers are not an ideal biomass estimator, because lipid content and composition of algae can be affected by changes in environmental conditions such as nutrient status, light intensity and temperature (e.g., Shifrin and Chrisholm, 1981, Reitan et al., 1994). However, we believe that the approach us-

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ing relative abundances of biomarkers can be used to reflect trends on their relative spatial distribution. According to this comment, we have modified the text (L. 399-404) as:

"Although the lipid content and composition of algae can be affected by changes in environmental conditions such as nutrient status, light intensity and temperature (Shifrin and Chrisholm, 1981, Reitan et al., 1994), the $C_{28}\Delta^{5,24(28)}$ sterol/alkenones ratio provides us with an overview on the relative contribution of $C_{28}\Delta^{5,24(28)}$ sterol-producing diatoms to alkenone-producing prymnesiophytes ".

7) **The conclusions (p 4673), that upwelling systems have high biomass, specialized carbon concentration mechanisms and high growth rates, in contrast to oligotrophic areas, are not novel, yet the data presented are for the most part sound and do demonstrate these features. The Summary and Conclusions needs to be strengthened what is really new and exciting?**

We have modified the conclusions to be more specific and strengthened.

"As a summary, lipid biomarker abundances together with their relative component contribution confirmed the general expectations on the predominance of diatom algae in nutrient-rich waters, and of zooplankton, bacteria and degraded material below the euphotic zone. In contrast, the hyperoligotrophic area of the Gyre was characterized by low concentrations of lipid biomarkers, and especially by unprecedented deep maxima of eukaryotic markers, and rather unexpectedly high heterotrophic activity in surface waters. Among these biomarkers, phytol and the more specific diatom sterol followed the chlorophyll profile. However, highest concentrations were measured for alkenones with maximum values above chlorophyll maximum and above the concentration peak of 19'HF, thus indicating a quite specific community of the alkenone producing prymnesiophytes. Discrepancies between the alkenone calculated and the in situ temperatures of the surface layer from the gyre seems to be caused by nutrient limitation and/or autoxidation of alkenones in the highly irradiated waters of the gyre. On the other hand, carbon isotope ratios of alkenones markers evidenced that prymnesiophytes inhabiting the depth of the chlorophyll were likely light limited.

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Our results along the different trophic systems showed also that source specific algal biomarkers and compound specific isotope analyses largely responded to the composition of the phytoplankton and to the different processes of carbon acquisition. Within a probably complex pattern of processes that link the ε_p of the different phytoplankton taxa and their environmental factors, our field study illustrates that carbon isotope fractionation values from nutrient-rich waters were much lower compared to those in nitrate limited. However, the high scatter of ε_p in the oligotrophic waters indicates that other factors than the major nutrients are probably affecting the carbon isotope fractionation. Light generally not being a limiting factor in the euphotic layer, higher growth rates and/or active uptake of HCO_3^- could explain the reduced ε_p values of the nutrient-rich waters. These relatively low and similar ε_p over the different phytoplankton taxa of the nutrient-rich waters implied non-diffusive C transport, whereas the high and dispersed ε_p values from the nutrient-poor waters might result from the lower growth rates and higher variability on the efficiency of the carbon uptake mechanism by diffusion. However, it is not possible to distinguish between the influence of growth rate and that of the use of different carbon acquisition pathways with the available data".

Interactive comment on Biogeosciences Discuss., 4, 4653, 2007.