

Interactive comment on “The pelagic microbial food web structure in Sanggou Bay, Yellow Sea: Spatial variation over four successive seasons” by X. Chen et al.

Anonymous Referee #1

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Comments on the manuscript "The pelagic microbial food web structure in the Sanggou Bay, Yellow: spatial variation over four successive seasons" submitted to Biogeosciences by Xue Chen et al.

General This manuscript reports on microbial food web (MFW) structure in a relatively large (144 km²) semi-enclosed Bay, the Sanggou Bay (Yellow Sea, China). The authors collected samples at 19 sites in this Bay and analyzed the abundance and the biomass of heterotrophic prokaryotes (HP), *Synechococcus* (SYN), picoeucaryotes (PEUK) heterotrophic and pigmented nanoflagellates (HNF and PNF) and ciliates. The authors examined the structure of MFW using cluster analysis and regressions analyses. They found significant relationships between members of the MFW and observed

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seasonal variation in the structure of MFW, which they interpreted as the results of top-down or bottom-up structuring the studied communities. Based on the positive relationships and the upper and the lower boundaries that they found in their regressions analyses, the authors concluded that they have extended the relationship that has been found by previous works between HNF and HP to the other members of the MFW.

The manuscript is well written and easy to read. However I have two main problems:

1 – I have difficulties in understanding in this study what is new and what is its ecological significance compared to previous works, especially since early ecological studies have shown that comparison of the relative biomass of the components in a food web provides insights into the structure of this food web. The authors stated that by applying the normalization method (they normalized the biomasses of other microbial communities to that of HP) on the data of Garrison et al (2000), they confirmed the results of these latter authors. I therefore wonder where the added value of this normalization method is, since this manuscript only confirmed the results of Garrison et al which did not use normalization.

2 – The dataset used in the study to compute the boundaries is from a single aquatic area. In my opinion, this dataset ($n = 72 - 76$) is not sufficiently large (and also might not cover a wide range of environmental conditions) to allow for generalization such as those performed by Sanders et al (1992) and Gasol (1994) when they analyzed the HNF-bacteria relationships in aquatic systems ($n > 250$). In addition, Gasol (1994) provided a model to explore whether Bacteria (or HP) are controlled mainly by top-down or by bottom-up factors. Based on this, it is unclear to me what is the ecological meaning of the relationships they authors have constructed in attempts to extend the relationships that have been found by previous studies between HNF and bacteria to the other members of MFW (e.g. between SYN and HP or between PNF and HP, Are they not simply equivalent to the positive relationships that are commonly found between phytoplankton and heterotrophic prokaryotes in aquatic systems?)

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Specific comments p.6 line. How was the biovolume estimated ? How many individuals were analyzed for this estimation? p. 12 line 21. Are these ranges really similar ? p 14. lines 16-18. Could correlations be interpreted as indicators of strong grazing pressure? lines 19-20. Are there data supporting these statements? p. 15 line 13 – 15. It is necessary to have similar sampling dates to apply this approach? ./.

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