

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 #2

Received and published: 17 May 2016

This manuscript by Chen and co-workers describe microbial plankton community structure in a coastal bay in Eastern China (Sanggou Bay, Shandong Peninsula, Yellow Sea). They measured abundance and biomass variations of the main prokaryotic and eukaryotic groups (heterotrophic prokaryotes, *Synechococcus*, picoeukaryotes, heterotrophic nanoflagellates, pigmented nanoflagellates, and ciliates). They highlighted various correlations between abundances of some of these groups, and used these correlations as basis to describe food web structure. Although the authors' dataset certainly has some value, I do not recommend it for publication in Biogeosciences, as it shows several strong flaws.

1) Authors rely only on abundance (cell counts) to attempt a food web reconstruction.

C1

While this approach has been applied in the past, I think the present paper shows over-reliance on shortcomings that strongly reduce its value and interest. Authors highlight correlations between abundance of certain groups, use them as proof of existence of a trophic link between pairs of groups, and discuss of potential bottom-up and top-down control in these trophic processes. From a data interpretation point of view, this is quite bold (and arguably wrong), as correlation does not imply causality. From an ecological perspective, this represents an oversimplification of the reality. Authors only describe the food web as composed of separate vertical interactions between functional groups. Their food web depiction does not take potential trophic cascade effects into account. They do not even mention potential horizontal interactions between groups sharing common trophic levels. Nor do they discuss potential "intra-group" variability among the studied taxa (e.g. interspecific variability in the feeding habits), even when efforts were made to identify taxa to a generic or specific level. They only treat influence of environmental parameters on ecological interactions among pelagic microbes in a very shallow way, while it is well known to be a major driver of pelagic communities structure and function. Overall, I think their views are simplistic, and I do not feel that the presented dataset is adapted or sufficient to back up their assumptions about ecosystem functioning.

2) While authors mention that the system they study is highly variable in both physical (high thermal amplitude) and biological features, the paper is based on only 4 short (2-3 days) cruises, representing only 10 sampling days. Moreover, some of the samples were lost. This strongly questions how representative this study is. This adds to the concerns on representativity issues formulated by reviewer 1, that were, in my opinion, not correctly addressed by authors in their response (the fact that the total number of samples was higher than in previous studies does not solve problems linked with potential low replication for each of the groups taken separately).

3) Insights drawn from this study mostly have local value. The dataset presented here could be useful for depiction of plankton community structure inside the studied bay, but

C2

given the specificities and peculiarities of the studied system, I doubt that they would be of any use outside Sanggou Bay. Authors do try to give a wider scope to their article by applying their normalisation technique to another system (the Arabian Sea). However, I don't understand how this provides new insights or shed new lights on results already published over 15 years ago by Garrison et al (2000). If authors want to show that this normalisation approach is valuable and should be widely used, they need to test it in a much wider range of systems and conditions.

Overall, I encourage the authors to substantially modify their manuscript to put forward what it really is (an in-depth assessment of seasonal variability of microbial plankton communities in one given coastal bay) rather than to present it as a food web analysis (this would require a more holistic view of the system) or a methodological paper (this would require a larger, more widely applicable testing procedure). Although this decision is of course the responsibility of the editor, I don't feel this article is particularly suitable for publication in Biogeosciences, and I would recommend the authors to submit it to a more adapted (i.e. more focused on plankton community structure) journal instead. This would ensure that the paper is really broadcasted to an adequate audience and receives the attention it deserves.

Interactive comment on Biogeosciences Discuss., doi:10.5194/bg-2015-665, 2016.