

Reviewer1#

Microeukaryotes are wide distribution and play importance role in aquatic ecosystem. Diversity and assembly processes of microeukaryotes should be paid more attention. Antarctic freshwater lakes are a kind of non-pollution freshwater ecosystem and Microeukaryotes are important contributor of primary producer. Diversity and assemblage of microeukaryotes would give us a clue to get insight into the whole ecosystem. Five freshwater lakes' microeukaryotic communities on the Fildes Peninsula were screened in this manuscript, sample data were provided, diversity, co-occurrence patterns and assembly processes have been analyzed. In my opinion, this work is very interesting and provided a better understanding of the dynamic patterns and ecological processes of microeukaryotic community structure in oligotrophic lakes. I recommend it is worthy to be published after minor revision.

General Response to Reviewer 1 Comments

Thanks a lot for your comments and suggestions. We are very appreciated with your helpful advice and have made our efforts to revise the manuscript with clarifications/elaborations as following.

Our response is in **normal font** and colored in **blue**, and the *revised text* is in italic font and colored in **blue**.

General comments

1. As parameter of diversity, Shannon index should be mentioned in the abstract.

Response: Thanks for your advice. Revised as “Alpha diversity varied among lakes, with...” to “*Richness (113~268) and Shannon index (1.70~3.50) varied among lakes, with...*” in the abstract part.

2. WT and PO₄-P should be mentioned in the abstract, but not the “Environmental factors”.

Response: Agreed with you. We have revised in the abstract. “Environmental variables only explained 39% of the variation in community structure, *with the water temperature and orthophosphate being identified as the important driving factors (P<0.05).*”

3. In the discussion, dominant taxa and keystone species were mentioned, is there any difference between the two? If there is no difference, please use the same one.

Response: There are differences between the dominant taxa and keystone species. Dominant taxa are considered absolutely dominant (abundant), determined by their relative abundance, which are regarded to have significant control on community structure. The keystone species may be abundant or rare, not depending on their relative abundance, and their disappearance or weakening is thought to lead to the fracturing of microbial community networks (Banerjee et al., 2018).

In our study, the dominant taxa and keystone species are not identical and are therefore discussed separately.

- (1) Banerjee, S., Schlaeppi, K. and van der Heijden, M.G.A. (2018). Keystone taxa as drivers of microbiome structure and functioning. *Nature Reviews Microbiology*, 16(9), 567-576. <https://doi.org/10.1038/s41579-018-0024-1>.

4. The conclusion is too long and should be shortened.

Response: Shortened as “*The unique microbial eukaryotic community structure and low alpha diversity (richness and Shannon index) was demonstrated in five freshwater lakes on the Fildes Peninsula, Antarctic. The importance of stochastic processes and co-occurrence patterns in shaping the microbial eukaryotic community of this area was proved. Water temperature and orthophosphate were identified as important driving factors for driving variation of community structure (P<0.05). Stochastic processes played a prominent role in community assembly. This study provides a better understanding of the dynamic patterns and assembly processes of microbial eukaryotic*

community structure in Antarctic oligotrophic lakes (Fildes Peninsula)."