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Biogeosciences Discussions

Interactive comment on "Diversity, distribution and nitrogen use strategies of bacteria in the South China Sea basin" *by* Yuan-Yuan Li et al.

Anonymous Referee #2

Received and published: 8 April 2019

This study focuses on the 16S and nifH community structure of the South China Sea. It is a description study with a few sampling points at various depths. The main problem of this paper, is the lack of a narrative. The reader will not be sure what is the main finding of this study against already acquired knowledge. The nifH amplicon approach could be mentioned, but as the nifH primers can only capture a small proportion of the community, the findings could be used in support of other results, rather than forming the main findings narrative.

In general, the study is worth publishing as it describes the community snapshot of the SCS. However, this paper needs re-writing in order to better show the importance of the findings.

Introduction: Could you add a few a paragraph about how does the SCS microbiome

structure, N-fixation and nutrient limitation etc. compares with other seas. As a reader I would like to know either SCS is an anomaly or does it represent a typical coastal microbiome.

Results: I find the use of percentage values almost irrelevant considering that you have a single biological replicate per sampling site/depth. I can agree that there is a pattern of depth vs surface vs location at the global community level (the whole community pattern as represented on PCoA), but the percentage differences would definetely change with more replications. Please, add that the single replicate does not allow for any statistical analysis to be conducted and instead of using numbers, please just state either some phyla/genera seem to be more/less abundant for a specific sampling point.

Results: I would like to see a PCA or similar analysis linkning nutrient, salinity, temperature with the community structure. Is the influence of the nutrients, salinity etc. smaller or greater than the location? Can you separate them? What I am asking, is the knowledge about salinity and nutrients status of the sampling location enough to predict the likely microbial community structure?

(a small remark) please use 100,000 instead of 100, 000 in your sequencing number reports

For the nifH part, please clearly state that no nifH primers are able to provide a comprehensive nifH community profile. Different studies chose different primers. You are unravelling a part of nifH community. While the comparisons between sites are valid, please remember that this is just a part of the community, and quite likely most of this community is still our of our reach.

Figure 1, please add a legend, what depth does the colour signify

Figure 2a-d please increase the font size of the labels (graph bottoms)

Figure 3cd plase correct *Bacteira to Bacteria, please explain, which groups are included in this category in the figure legend.

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