

Comment on bg-2022-43

Anonymous Referee #2

Referee comment on "Potential contributions of nitrifiers and denitrifiers to nitrous oxide sources and sinks in China's estuarine and coastal areas" by Xiaofeng Dai et al., Biogeosciences Discuss., <https://doi.org/10.5194/bg-2022-43-RC2>, 2022

I have carefully read the manuscript "Potential contributions of nitrifiers and denitrifiers to nitrous oxide sources and sinks in China's estuarine and coastal areas" by Dai et al. The manuscript describes the spatial distribution and abundance of marker genes and transcripts related to the production and consumption of nitrous oxide in four estuaries in coastal China. Moreover, the diversity of the clade II-type *nosZ* gene was further investigated along the same four estuaries. The manuscript is nicely written and provides valuable information on the potential mechanisms controlling nitrous oxide consumption/production in coastal China. Furthermore, the results are put in context by using water column physicochemical data and by previously published measurements of nitrous oxide fluxes in the same four estuaries. I have, however, the following minor comments on this manuscript:

- Line 39: add "the" before nitrification.
- In the introduction, between lines 52-59 the authors describe the physiology/ecology of microorganism possessing the clade II-type *nosZ*. How is that different from microbes containing the clade I-type?
- Check verb tense in the introduction. Usually, present tense is used.
- In material and methods please provide the depths from which samples were collected.
- Lines 125-126. What minor modifications?
- Was the same qPCR program (lines 178-180) used for all primer sets?
- Line 199: What characteristic of the community? (i.e., community assembly or structure?)
- Please add units to salinity values (ppt, I guess?)
- When reporting the qPCR/RT-qPCR copy numbers, it is nice that the authors provided the range for each site. However, the median could also be informative, since the extremes may be outliers.
- Line 241: Orders of magnitude?
- Line 283: It was not clear to me what did the authors mean by "sequencing coverage"?
- Line 311-313. NMDS is only a visualization approach, I think the authors measured the similarity level by performing pairwise comparisons of the Bray Curtis dissimilarity index.

- In the discussion, as well as in the introduction, when describing previous literature, the present tense is usually preferred.
- Lines 374-376: Authors mention that the *nosZ* gene/transcript abundance was correlated with pH. Could it also be a confounding effect of DIN concentration, since pH seems to have a similar spatial gradient as DIN, with higher pH and lower DIN in the open ocean (Fig. 2).
- As I mentioned above, it is a strength of the manuscript to use N₂O flux, and deltaN₂O data to put in context the results. However, greater background/information on where, when, and how that data was collected would be helpful to the reader.
- As reviewer 1 mentioned, I also wonder why the authors decided to use the gene abundance, and not the transcript abundance to correlate it with N₂O flux and deltaN₂O.
- Figure 2: What were the depth layers? Adding a label explaining which panel corresponds to which estuary may be helpful for the reader (same for Fig 3).
- Figure 6: Could it help to log transform the qPCR/RT-qPCR data to plot it in order to avoid breaking the y-axis?