

Biogeosciences Discuss., referee comment RC1
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Comment on bg-2022-43

Anonymous Referee #1

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-RC1>, 2022

Dai et al. investigated the distribution of six key genes and transcripts related to N₂O production and consumption in four main estuaries in China. The authors analyzed the correlation between these genes and N₂O fluxes or concentrations obtained from previous literature and discussed what environmental factors might control the gene distribution pattern. This work implies denitrification might be essential for N₂O emissions in these estuaries. This study provides new insight into microbial divers of N₂O cycling in estuaries in China.

Here are some minor suggestions:

Line 70: cite (Frey et al., 2020 Biogeosciences) for the dominance of nitrate derived N₂O in OMZs.

Lines 75-79: cite (Ji et al. 2018 Biogeosciences) for N₂O production from denitrification in the Chesapeake Bay.

Line 82: cite Figure 1 for the location of the four estuaries.

Line 126: What were the minor modifications? Please elaborate.

Line 145: What kind of alpha diversity? (e.g. Shannon alpha diversity?)

Line 148: 'The top 10 most similar sequences of each OTU were used as references.' It is not clear how the taxonomy of the OTU was assigned. Did you use the taxonomy of the top 1 reference as the taxonomy of the OTU or the dominant taxonomy among all 10 references? Please explain this.

Line 235: accounting for % and % of N₂O production-related gene abundance

Line 240: I believe you meant to say 'one to two orders of magnitudes'.

Line 291: should be (Figure 4b). Abundance was not reflected in Figure 4a.

Line 376: need to tune down this sentence here since N₂O emission is controlled by both N₂O production and consumption. You could say 'suggesting that acidification of the ocean may decrease N₂O consumption potential.'

Line 345: Since the four estuaries were sampled in different seasons, it would be useful to see some discussion about how different seasons might affect the distribution of genes and transcripts.

Lines 388-404: nosZ clade I was transcribed more even though nosZ clade II genes were more abundant (Figure 3 i). The discrepancy between nosZ DNA and transcripts is worth discussing.

Lines 415-416: (a) are these datasets measured from the same months or years as the microbial samples? Or they are mean values of some sort? Please provide a little more detail here. (b) why use gene abundance as indicators but not transcripts? The latter shows 'activity' in some sense. Could you present the transcript data in Figure 6 or the supplement?

Line 456: additional citations should be included here: (Bertagnolli et al., 2020 Environmental Microbiology reports) and (Sun et al., 2017 Frontiers in Microbiology).

Figure 1: I suggest adding sampling time for each estuary in the figure.

Figure 2: please label the four estuaries (maybe as row names for all subplots). Latitudes and longitudes for the first few plots were missing. Please add latitudes and longitudes for all subplots. It is hard to tell ammonia, nitrite, and nitrate concentrations in three out of the four estuaries. You could use a different scale bar for PRE, so the other three plots could have a better resolution.

Figure S2: red and orange in the plots were too similar to each other, please choose another color to distinguish the two better.