

Interactive comment on “Diversity and distribution of *amoA*-type nitrifying and *nirS*-type denitrifying microbial communities in the Yangtze River Estuary” by Y. Zhang et al.

Anonymous Referee #1

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The study by Zhang et al., represents an important contribution to the understanding of the nitrification and denitrification processes in river estuaries. The authors have analyzed the abundance and diversity of the bacterial and archaeal *amoA* gene, and the dissimilatory nitrite reductase *nirS* gene of denitrifiers in a transect from the Yangtze river mouth to the open water, in spring and summer, surface and bottom water and, in some cases, also differentiating between particle-associated and free-living microbial communities. In addition, they have analyzed the spatial and temporal structure of these microbial communities by clustering analysis and analyze the possible environmental factors influencing these processes. The manuscript is well-written and experimentally supported. However, I have some comments I would like to see addressed

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before recommend it for publication:

-Abstract and throughout the manuscript: The fact that the abundance of archaeal AOA *amoA* gene is higher than AOB *amoA* gene DOES NOT imply that archaea have a more dominant role than AOB in the nitrification process (see for example Mußmann et al., 2011, PNAS). I recommend addressing this possibility and reviewing what is known about it. Same thing applies for the claim that denitrification is lower than nitrification based on the lower abundance of *nirS* respect to *amoA* gene. As the authors have indeed estimated nitrification and denitrification rates it is recommended to support your statement on the rate measurements rather than on the gene abundances.

-Material and methods: What was the water depths at “surface” and “deep” samples? Why is the phylogeny of the *nirS* gene based on protein sequences?

-Results: >Page 17828 line 20: Briefly describe “water column A” and “Water column B” classification by Francis et al., 2005 >Page 17829 line 8-9: this sentence belongs to the discussion >Page 17830 line10-11: As mentioned above, higher abundance of AOA *amoA* gene does not imply higher contribution of AOA to the nitrification process. Besides, this is not part of the result section. >Page 17830 lines 18-19: Same as above regarding the *nirS* gene and the denitrification potential >Line 21-22-23: Same as above

-Discussion: >Page 17833 line 18-20: Nitrification and denitrification data should support the higher abundance of *amoA* genes vs *nirS* genes as indicators of higher nitrification potential, not the other way around. >Page 17834 lines 1-4: as mentioned above this is not always like this! In general, I think the authors should have also included some discussion on the differences between AOA/AOB ratio in the salinity transect and related to previous studies

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