

Interactive comment on “Nitrogen fixation in sediments along a depth transect through the Peruvian oxygen minimum zone” by J. Gier et al.

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Review of Gier et al. 2015. The paper concerns N₂ fixation and sulfate reduction (SR) in sediments below OMZ waters off Peru. The work demonstrates an interesting coupling between N₂ fixation and SR, as also suggested by nifH gene analyses. Moreover, the study indicates that organic matter load and sulfide are major drivers of N₂ fixation. The paper contributes to the compiling data on factors regulating diazotrophy and specifically to the rather limited number of studies from sediments. The paper is generally well written, clear, and to the point. My points of criticism are overall minor, but should improve the readability and clarity of the paper.

1. The wording should be changed at several places in the abstract. The current version seems to indicate that rates were measured in water, and not just in sediments.

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For instance line 6: “measured in OMZ mid-waters”; line 8: “Benthic N₂ fixation profiles” etc. Please, make sure the reader cannot be misled to believe that water samples were analyzed.

2. P1, l. 11. Define nifH genes

3. P1, l14. Delete “various”

4. P6, l1. “These bacteria. . .”

5. P6,l10-14. Unclear where this information comes from

6. P7, l16-22. It would be good to reduce the overall length of the manuscript. This section could be easily reduced. Most readers will know the principle of acetylene reduction.

7. p8, l5. Specify whether samples were analyzed onboard or stored somehow.

8. P8, l13. OK, but why were they expressed as NA. Isn't that just confusing? If keeping it as NA, then please explain why.

9. P10, l2. Please, specify how many sequences were obtained per sample. Also, describe negative controls and whether they were blank.

10. P10, l14. How can you in the description of your sediments cite literature which is published before this sampling was carried out? This is your Results section – you should describe your results, not those of others.

11. P10, l18. Redundant, described 3-4 lines higher up.

12. P13. It should be evident from the text why the authors are interested in looking at C/N ratios. It is not enough to address that later in the discussion. Likewise, it should be explained why data on DIC flux are reported (Fig. 4), also how this was measured is unclear to me.

13. P14, l8. Rephrase. A novel clade cannot belong to anything. It may be related to

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something. . .

14. P15, L5-6. Again, this sounds like water samples. Please, rephrase
15. P15, l6. “Sometimes both depth profiles revealed similar trends”. Clarify what is meant by depth profiles.
16. P15, l8. “were”
17. P15, l21. What does “this study” refer to?
18. P. 15, l28. “SR bacteria were. . .”
19. P16, l11-15. Needs work. That samples have a “certain diversity” is not informative. Unclear what “these results” refer to (line 13). Farnelid et al. did not sample an OMZ (line 15).
20. P17, l10-11. Weird and unclear sentence. Please, revise or remove.
21. P17, l20-28. I have not understood the point with the DIC fluxes. Please, make this clearer here as well as earlier in the manuscript.
22. P20, l7-8. Sentence is out of context. Please, clarify the point or remove.
23. Figure 1, text. Please, define MUC.
24. Figure 6, text. Delete “expressed”. Clarify whether the sizes of the triangles are proportional to the number of sequences within each triangle. Moreover, indicate on the figure how many clones the triangles etc represent.

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