

Interactive comment on “High-throughput screening of sediment bacterial communities from Oxygen Minimum Zones of the northern Indian Ocean” by Jovitha Lincy and Cathrine S. Manohar

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Review of 'High-throughput screening of sediment bacterial communities from Oxygen Minimum Zones of the northern Indian Ocean' submitted to Biogeosciences, by Jovitha Lincy V.J. and Cathrine S. Manohar

General comments:

The manuscript by Lincy and Manohar presents a study comparing one amplicon sequence dataset from the Arabian sea sediments to another amplicon dataset from the Bay of Bengal sediments. The authors performed a phylogenetic analysis and a di-

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iversity study using some of the classical indices used for community diversity studies. The manuscript is very hard to read for two reasons, the first of which is the quality of the language (see specific comments), the second of which, and this is the more severe point, it lacks a clear storyline. The authors base their analysis on two samples and come up with various claims that could possibly also just be a sequencing artifact given the difference in sequencing quality and depth of the two (!) sampling points. First, they claim a significant difference between the samples which is statistically impossible to claim, second, they claim a variability within the Indian ocean, again based on two samples, third, the diversity indices are not reliable because of the difference in sequencing quality and finally, based on this, the functional diversity model doesn't give any reliable result. Another point is that the authors constantly compare their sediment data to water column metagenomes, which just doesn't make any sense and is very confusing.

I would suggest a major rewriting of the manuscript with a clearer focus: It could be very interesting to see those sediment amplicon datasets compared to other OMZ sediment data and then to obtain information on a core benthic OMZ community versus a 'flexible' OMZ community. This, rather than a PICRUST model, could then be used to explain the differences in benthic biogeochemistry and benthic-pelagic fluxes of different OMZ regions. I would further suggest to re-run the amplicon BLAST analysis on SILVA instead of Greengenes, SILVA is the only database constantly updated which will certainly give a way more informative result.

For specific comments, please see the attached document.

Please also note the supplement to this comment:

<https://www.biogeosciences-discuss.net/bg-2019-330/bg-2019-330-RC1-supplement.pdf>

Interactive comment on Biogeosciences Discuss., <https://doi.org/10.5194/bg-2019-330>, 2019.

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