

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

Anonymous Referee #2

Received and published: 9 December 2019

The study of Lincy and Manohar investigated the microbial community between two sediment samples under the Oxygen Minimum Zones in the Northern Indian Ocean. The authors used 16S rRNA pyrosequencing data in order to assess the diversity and infer the functional potential of the two investigated sites. First of all, I would like to point out that accurate calculations and predictions about diversity of such a highly complex ecosystem are hardly possible based on the obtained sequencing depth (10,069 reads for both samples) and sample number. The authors also only focused on the bacterial community not taking into account that archaea would play an important role for ecosystem functions in such environments. This was also not mentioned in the discussion. Furthermore, authors assessed the functional potential of the microbial commu-

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nity based on the amplified 16S rRNA genes. First of all, I see such an analysis highly critical since the 16S rRNA information cannot be translated into a functional potential. In this study the 16S rRNA genes were not extracted from a metagenome but were amplified with universal primers. Taking into account the PCR bias, the low sequencing depth and the number of samples (one for each site), the assessment of the functional potential is impossible. Also as mentioned before, assessment of the functional potential is not possible without taking into account the archaeal population. For functional potential assessments, the authors should have performed metagenome sequencing and analysis. All in all, the conclusions of this study are very farfetched based on the obtained data. I suggest to either change the scope of the study or to obtain more data (e.g. metagenomics) to assess the questions raised in this study.

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

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