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Interactive comment on "A comparison of bacterial communities from OMZ sediments in the Arabian Sea and the Bay of Bengal reveals major differences in nitrogen turnover and carbon recycling potential" *by* Jovitha Lincy and Cathrine Sumathi Manohar

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We express our gratitude to referee #1 for correcting all grammatical errors, as well as pinpointing unclear statements.

Please find below our point-to-point response to the review of referee #1.

Referee comments are numbered; our response to each comment is posted in the next paragraph, which is differentiated with an arrow symbol. Also, changes made in the manuscript are highlighted in a double inverted “comma”, and the previous statement is shown in single inverted ‘comma.’

There are three sections: General comments, Specific comments, and Technical corrections.

General comments

1. This study describes the diversity of microbes in sediments below the OMZ of Arabian Sea and Bay of Bengal, based on V1-V3 region of the 16S rRNA gene using 454 pyrosequencing data. The phylogenetic information is interesting, and the authors have done further analysis to extrapolate the information to find the functional capability of the microbes’ present.

→Yes, we used a comparative amplicon sequencing, biogeochemical analysis and metagenomic modeling to explore the microbial communities and predict their metabolic potential.

2. The manuscript is hard to follow intermittently, however attempts have been made to correct those error which are minor in nature.

→We appreciate the efforts made by referee#1 for correcting the grammar and express our sincere gratitude.

3. The manuscript is interesting and will be of use to understand the biogeochemistry and the community composition of the sediments underlying the OMZs.

→ Thank you for the positive comments. It is highly encouraging for an Early Career Scientist like me.

Specific comments

1. Line 177-179: Any particular reason why only these pathways were chosen to study?

‘We focused on the KEGG database pathways for nitrogen (ko00910), sulfur (ko00920), and methane (ko00680) turnover, as well as on carbon metabolism (ko01200) with specific focus on fermentation and bioenergetics pathway related to carbon fixation’

→ In the OMZ, as oxygen is limiting, microbial inhabitants rely on other favorable electron acceptors for energy metabolism such as nitrogen, sulfur, and methane. Also, we assume different microbial communities could explain patterns of carbonate precipitation, hence given focus to fermentation pathways also (Fig.6).

Since the statement looks incomplete as pointed out, we modified the statement as follows.

“We focused on the KEGG database pathways for nitrogen (ko00910), sulfur (ko00920), and methane (ko00680) turnover, as well as on carbon metabolism (ko01200) with specific focus on fermentation and bioenergetics pathway related to carbon fixation, as they are reported to be prevalent in the OMZ sediment.”

2. Line 193-195: Not clear what the authors are trying to say hear?

‘The only striking difference was observed regarding TOC and TN values are in the typical range of OMZ sediments and higher than non-OMZ surface sediments with TOC and TN values as low as 0.2 and 0.02 wt. %.’

→ We are trying to tell that the obtained TOC (3.47/2.24%), and TN (0.28/0.16%) values from the AS and BoB surface sediments are within the typical range identified in similar oxygen-deficient sediments; whereas in non-OMZ surface sediments of the Indian Ocean, the TOC and TN values as low as 0.2% and 0.02% was reported (Pattan et al., 2013). However, for clarity and completeness we have re-written the statement as follows:

“The AS samples had higher TOC and TN contents than the BoB samples. The values are in the typical range of OMZ sediments and higher than non-OMZ surface sediments of the Indian Ocean, whereas the TOC and TN concentration as low as 0.2% and

0.02% reported (Pattan et al., 2013).”

3. Line 202 Not clear what the authors are trying to say here. Do they mean: While TOC values are within the ranges of values found in OMZ sediments, the TIC values are different and could be attributed to the difference in CaCO3 content?

‘While in the range of OMZ sediments and higher than the difference in TIC could be attributed to the difference in CaCO3 content caused by increased carbon sequestration.’

→ The estimated TOC proportions were 2.012% and 1.297% for the AS and BoB sediments, respectively, while TIC proportions were strikingly different with 8.11% in the AS but only 0.289% in the BoB. We are trying to tell that, though the TOC value are not much different between the two basins within the northern Indian Ocean OMZ sediments, the TIC values differed significantly and these differences could be attributed to difference in CaCO3 content caused by increased carbon sequestration (Sarma et al., 2007). Additionally, we would like to merge the paragraphs to get continuity (ln:184-201; 202-207). For clarity we have re-written the statement as follows:

“Here the TOC values fall within the range reported in similar OMZ sediments and don’t vary much between the sites. This is in sharp contrast to TIC, where the AS values were an order of magnitude higher than BoB values. This difference could be attributed to the difference in CaCO3 content caused by increased carbon sequestration (Sarma et al., 2007).”

4. Line 218: this sentence is not complete, what was the result of SILVA? the same result, if so specify that!

‘The dominant communities and their relative percentage remained the same for BLASTN searches using the EzTaxon-e 16S database, where a total of 48 phyla were identified, and pairwise alignment using the SILVA 132 database. This led to a successful in classification of 44 phyla, 27 of which were common to both sites and pairwise alignment using the SILVA 132 database.’

→Thanks for pointing out the error, the statements were combined and modified as follows.

“The dominant communities and their relative percentage remained the same for BLASTN searches using the EzTaxon-e 16S database, where a total of 48 phyla were identified, and pairwise alignment using the SILVA 132 database led to a successful classification of up to 44 phyla, of which 27 were common to both sites.”

5. Line 244: Hard to understand what the authors are saying here!

‘Interestingly, only 28.48% of the identified OTUs were shared between the AS and the BoB on the genus level were between (64.29% on the phylum level), leaving 53.10% of unique OTUs in the BoB and 18.42% in the AS (Fig. 2). This suggests that the two sediments, while biogeochemically similar, harbor a largely different bacterial community.’

→We compared the bacterial groups at different taxonomic level. At 97% clustering, only 28.48% OTUs were shared between the sites, while 53.10% unique OTUs were identified in BoB, and remaining 18.42% were unique to AS. However, at phyla level 64.29% similarity was observed. We have also analyzed certain physio-chemical characteristics (please refer Table-1), and these were comparable between the sites, though taxonomy studies reveal huge difference in microbial community structure, which could explain why these two basins differ in nutrient cycling. As pointed out, the statement looks confusing, hence some revisions are made as shown below.

“Interestingly, only 28.48% of the identified OTUs were shared between the AS and the BoB on the genus level, leaving 53.10% of unique OTUs in the BoB and 18.42% in the AS (Fig. 2). This suggests that the two sediments, while biogeochemically similar with comparable water-column and sediment nutrient concentrations (table-1), harbor largely different bacterial communities.”

6. Line 360: Are you saying this is a nitrogen fixer? What is the relevance? 'It's interesting to note that around 68 Cyanobacterial sequences were retrieved from BoB sediment, where water column depth was ∼245m, but only one representative from the AS sediment, which was located at ∼200m depth. In addition, in the AS sediment, we observed Chroococcales, which are assumed to be a low-light adapted group (West et al., 2001).'

→It is slightly contradictory to note that sequence corresponding to primary producers like Cyanobacteria were retrieved more in 245m deep site than 200m water-column depth. As per literature it is suggested that the obtained groups were low light adapted, justifying their occurrence in deeper sites were light penetration is negligible.

As rightly pointed out by referee, Chlorococcales are well known nitrogen fixers as well, and hence we would like to add one additional statement in this aspect in accordance with our observation.

"The Chlorococcales members are known to fix nitrogen (Van Goethem, Marc W., et al. 2017); this could explain the differential abundance of nifH genes in the two sites (Fig.7)."

Technical corrections

1. Ln 56: removed 'in' and added "to be" "In contrast, the BoB-OMZ has been reported to be less intense than the AS-OMZ.

2. Ln 68: 'have' replaced with "have been" "aerobic communities have been identified to coexist. . ..

3. Ln 80: removed chiefly from the sentence ". . ...techniques has been limited to the pelagic realm."

4. Ln 95-96: Sentence modified as per suggestions. "A profile of nutrient and DO distribution is presented from the AS and BoB, respectively. These profiles represent. . .. ."

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5. Ln 111: ‘sediments’ replaced with “sediment”, and also added suffix “samples” “The sediment samples were freeze-dried,. . . ..”

6. Ln 150: ‘which’ replaced with “that” “. . .. .sequences that . . .. . .”

7. Ln 175: Added “on” “The information extracted was based on a small fraction. . .. . .”

8. Ln 190-191: Revised the sentence as suggested. “total organic carbon was slightly higher in the AS, than BoB, with 3.47% and 2.24% respectively, TN values were 0.28% and 0.16% in the AS and BoB, respectively.

9. Ln 197: Removed ‘typical’ “Our data is in line with those OMZ ranges,. . ...”

10. Ln 201: Replaced ‘with’ with “at”. Also merged the paragraph. “which was substantially higher in the AS at ?8.11%, compared to the BoB with only 0.29%.

11. Ln 204: Replaced ‘shelled meiobenthic fauna’ to “meiobenthic fauna with shells” “. . ..meiobenthic fauna with shells may. . .. .”

12. Ln 210: Replaced ‘studied’ with “study” “Between the study site,. . .”

13. Ln 221: Comma added “. . .Firmicutes (5.5%), . . .”

14. Ln 222: Removed ‘with’ and “to” “Those abundant taxa contributed >85% to the total bacterial community.”

15. Ln 225: Removed ‘determine’ “. . ..the availability of nutrients or organic carbon.”

16. Ln 243: Comma added “. . .and the BoB, . . .”

17. Ln 252: Combined the sentence by adding “followed by” “. . ... majorly Planococcaceae (26.06%) followed by Flavobacteriales (17.14%), and Oceanospirillales (12.85%).

18. Ln 261: Replaced ‘firstly’ with “first” “. . .. mostly of Pseudomonadaceae first described. . .. .”

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19. Ln 263: Additionally added “as” “. . ..which are described as denitrifier groups.”

20. Ln 269: Replaced ‘those’ with “these”; and ‘closer’ with “further” “. . .as per EzTaxon-e database these were further identified. . .”

21. Ln 272: Replaced ‘those’ with “these”; and ‘were’ with “are” “. . ...these clades are unique to AS. . ..”

22. Ln 274: Replaced ‘were’ with “are” “. . ..abundant taxa are Woeseia (6.98%). . ..”

23. Ln 280: Replaced ‘have’ with “were”; ‘which’ with “that”; and ‘have’ with “play” “. . .. . .JTB38 were identified that might play a similar role.”

24. Ln 288: Removed ‘are’ “. . .anoxic shelf sediments and were reported. . ...”

25. Ln 308: Removed ‘active’ “. . .denitrification could not be detected (Bristow et al., 2017).”

26. Ln 353: Are you saying ‘07’ or “0.7” →Thanks for pointing the error, it is 0.7.

27. Ln 368: Replaced ‘is’ with “in” “. . .. with a prime role in remineralization. . ...”

28. Ln 399: Replaced ‘work’ with “function” “. . .. . .how these basins function.”

x——————-x

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