

Interactive comment on “Microbial communities associated with sediments and polymetallic nodules of the Peru Basin” by Massimiliano Molari et al.

Anonymous Referee #2

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General comments to authors:

The manuscript by Molari et al. describes the microbial community structure associated with sediments and manganese nodules from 3 and 2 sites, respectively, within the Peru Basin.

The authors find that Gammaproteobacteria and Alphaproteobacteria are the dominant bacterial classes in sediments and manganese nodules while all archaeal communities investigated were dominated by Thaumarchaeota. However, sediment and nodule communities were found to differ significantly at the OTU level, as assessed by calculating Jaccard dissimilarity. The authors note differences in the nodule community

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composition (specifically, a lower relative abundance of Archaea, and a different nitrifier community) in their study in the Peru Basin as compared with communities in the Clarion-Clipperton Fracture Zone (CCZ), where previous work on microbial community composition of nodules has been done.

The strengths of the manuscript include the following:

- i. There is a lack of studies of the prokaryotic diversity in the surface sediments and nodules of the Peru Basin, which has different environmental conditions than the relatively well-studied CCZ. ii. The molecular and bioinformatic methods are well-documented and the microbial community analysis is thorough.

Weaknesses of the manuscript include the following:

- i. The lack of metadata associated with the various sites makes interpretation of the differing community structures among sites difficult.

Specific comments to the authors:

Major concerns:

1. Page 3 – 4. Somewhere in this discussion of the CCZ versus the Peru Basin I think it would be helpful to briefly let the reader know the state of hypothetical mining in each of these regions. In the CCZ, the ISA has entered into contracts with various contractors for exploration for polymetallic nodules. Is this the case in the Peru Basin as well?
2. Page 5, line 113. “Samples were collected at three sites...” For clarity I think the authors should explicitly state in the text that nodules were only collected at 2 of these 3 sites.
3. Page 5, line 115. “... called “Reference Sites.” I suggest directly listing the Reference Sites here in the text instead of making the reader consult Table 1, especially since the authors refer to Reference South later in the text. Could change to “... called

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“Reference Sites”: Reference East, Reference West, and Reference South.”

4. Page 5, line 116. Here a map of the Peru Basin (in addition to the Table already provided), with the study sites and DISCOL experiment sites marked, would be very helpful to the reader.

5. Page 8, lines 226 – 232. “...significant differences were detected in sediment microbial community structure among the different sites... “Site” defined by geographic location and “Substrate” ... explained a similar proportion of variation in bacterial community structure...” This was a bit surprising to me and this is where I think some physical/chemical/biological metadata about each site would be really helpful. If any is available, perhaps from other groups on the cruise, it would help add context to some of the observations here.

6. Page 8, lines 226 – 229. “...significant differences were detected in sediment microbial community structure ... between communities associated with nodules and sediments at Reference South.” I think it is important to state directly in the text that this site, Reference South, was the only site that had enough nodule sampling to allow the authors to do this analysis (at least I assume this is what occurred). Otherwise this sentence could be taken to mean that differences in community structure between nodules and sediments were also investigated at the other 2 sites, and no differences were found.

Minor issues to be addressed:

7. Page 8, line 238. “Aphaproteobacteria” should be “Alphaproteobacteria”.

8. Page 9, line 282. “Aphaproteobacteria” should be “Alphaproteobacteria”.

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