

Authors' Response ('AR') to the Associate Editor comment on “The contribution of microbial communities in polymetallic nodules to the diversity of the deep-sea microbiome of the Peru Basin (4130 – 4198 meter depth)” by Massimiliano Molari et al.

Associate Editor Dr. Denise Akob ('AE') Comments

AE> I believe this should be the GenBank Database and please provide a reference for both BLASTn and GenBank

AR> we corrected the text and add the following reference for BLATS: “Altschul, S. F., Gish, W., Miller, W., Myers, E.W. and Lipman, D. J.: Basic local alignment search tool. J. Mol. Biol. 215:403–410, 1990.” [Lines 172-175 and 515-516]

AE> change to OTU

AR> Thanks. We corrected this. [Line 215]

AE> change to OTUs

AR> Thanks. We corrected this. [Line 216]

AE> do you mean Gemmatimonadetes?

AR> yes. We thank Editor for highlighting this typo. We corrected with “Gemmatimonadetes” [Line 302].

AE> I suggest changing "no cultivates" to "no cultured relatives"

AR> We thank the Editor for the suggestion and we modified the text accordingly. [Line 314]

AE> I don't agree with the use of the word turnover as you didn't look at changes over time. I suggest changing to shift or differ.

AR> We thank the Editor for suggestion. However we believe that “turnover” here is appropriate to describe spatial shift in OUTs composition between microbial communities, and compared to beta-diversity values reported in literature. In order to clarify that we refer to spatial and NOT temporal turnover, we reformulate the sentence as follow:

“Beta-diversity of microbial community structure in the Peru Basin sediments showed remarkable spatial OTU turnover already on a local scale (<60 km; Figure S2), which is at the higher end of previous microbial beta-diversity estimates for bathyal and abyssal seafloor assemblages (Jacob et al., 2013; Ruff et al., 2015; Bienhold et al., 2016; Walsh et al., 2016; Varliero et al., 2019).” [Lines 372-375]