

Interactive comment on “Interconnectivity vs. isolation of prokaryotic communities in European deep-sea mud volcanoes” by M. G. Pachiadaki and K. A. Kormas

Anonymous Referee #2

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The study offers a synthesis of the current knowledge on the microbial diversity at European deep-sea mud volcanoes based on studies that used traditional cloning/sequencing of (long) ribosomal RNA sequences. This may serve as baseline for future studies that target shorter sequences produced by NGS technologies for instance. The study identified the core phylotypes in those habitats, which are characterized by very distinct biogeochemical processes.

Main comments

-Table 1: please also indicate the total number of sequences in each study along with the number of unique OTUs. This may help understand whether large variation in

C7871

coverage effort may be expected. Indication on average sequence lengths in each case may be useful too.

- Line 183: Before comparing OTU richness between archaea and bacteria, it is important to ensure that the definition is about the same in both cases: Were the aligned rRNA gene sequences positioned at about the same nt position and covering about the same sequence length? If not, you may capture different levels of nt variability in the respective OTU definitions.

- Most of the analyses were done at the OTU level, but it may also be interesting to also provide a fuller picture of the similarity between MV communities at different taxonomic levels. This could then inform on the taxonomic levels at which endemism may be less pronounced and on the taxonomic resolution needed to either differentiate MV samples from each other or from typical deep sea sediments.

Minor comments

- Line 121-129: what is the final number of nt being retained in the final alignment?

-Line 122: "Taxonomic" not "Taxinomic"

-Line 135: against which database?

-Lines 159-162: A reference seems to lack here.

- Line 178: the highest number [...] was found

- Line 179: "deeper or fine-scaled analysis" it is not clear if you refer to spatial scale or to the resolution or diversity coverage of the techniques being used. The sentence should be clarified. In fact, when sequencing depth increases, more OTUs may be obtained, but also the chance that they differ in sequence may also increase (i.e. by going deeper in the rare biosphere). With a shallow sampling (reduced sequencing effort) you may find more shared types, because the latter would represent the dominant types.

-line 357: typo "environments"

C7872

-Line 532: typo "datasets"

- Figure 3. A legend with what the thickness and size of the points mean would be useful.

- Line 373: "the" repeated.

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C7873