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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 #1

Received and published: 18 January 2013

This is a nice study, which, for the first time, examines trends in microbial community composition across European deep-sea mud volcanoes, with aim to identify key community members of mud volcano sediment. Only a small number of OTUs is found across all mud volcanoes studied (please state which ones in the abstract).

I have a few suggestions, which mainly pertain to the mode of presentation, which could be more clear and simple, and (I hope) not to the way the data was analyzed.

(1) Why was a cut-off of 700 bp chosen for the analyses? Does this reduce the data set substantially? How does it affect the diversity that is actually studied?

(2) The way the important data is presented in the text, i.e. the groups that are shared

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by different locations, is cumbersome to read. Please provide a table with an overview of this, e.g. sites as columns, OTUs that occur across two or more sites as rows, each OTU (e.g. representative accession number) with info on which group it belongs to (e.g. ANME-1, Marine Benthic Group D (MBG-D), etc.) in parentheses. Of this table, part (a) could be on Archaea, part (b) on Bacteria. Table 2 can provide an overview of it, if still useful, and otherwise removed.

(3) Phylogenetic trees, displaying all OTUs, or if this is too crowded, representative OTUs for each group/cluster, would be extremely helpful. Please provide one for Bacteria and one for Archaea.

(4) As supplementary material, provide a table with clone and nucleotide accession numbers of all sequences that were included in this study. Within this table, please indicate the phylogenetic group each clone/nucleotide accession number has been assigned to (e.g. ANME-1), which site it is from, and which article it is from.

(5) Figs. 3 and 4 look nice, but I am not sure how useful they actually are in explaining the data. Either explain these better, ideally so the reader can get the key message from looking at them and reading the figure caption alone - or remove.

(6) I think it would be important to explicitly state which of the groups that are shared between mud volcanoes have only been found in mud volcano sediments (or methane seeps). I know this is not true for any of the ANMEs, MBG-D, MBG-B, or MG-1 Archaea. At least for the ANMEs, this is not surprising, since anaerobic methanotrophy is a widespread process, simply because methane is produced and consumed in many places in marine sediments. But are there any groups that are truly unique to mud volcano (methane seep) sediments, based on existing data? If not, could it be that mud volcanoes are not unique/distinct microbial habitats, and thus there is no evolutionary benefit of specialization/endemicity to this particular habitat?

(7) Along the same lines as (6), are any of the OTUs, e.g. within the different ANME groups, shared between European mud volcanoes, but not found anywhere else? This

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would help address the question of interconnectivity vs. isolation, which is mentioned in the title, but then not really addressed in the manuscript.

(8) In general, please be more specific about what you are looking for in the data, and then state whether or not the observed trends confirm your hypotheses/anticipated result. This will help add structure to the manuscript and make the implications more clear to the reader.

Interactive comment on Biogeosciences Discuss., 9, 17377, 2012.

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