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Comment

Interactive comment on “Paleoenvironmental imprint on subseafloor microbial communities in Western Mediterranean Sea Quaternary sediments” by M.-C. Ciobanu et al.

Anonymous Referee #2

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This paper reports on an interdisciplinary study of two sediment cores from the Western Mediterranean. Both cores exhibit a different sedimentation history due to different locations at the continental slope and different exposure to riverine input. The cores were analyzed and compared in terms of their sedimentological, chemical and microbiological composition. The authors try to correlate the physicochemical settings with the microbial diversity identified by both, molecular and cultivation-based analyses. This kind of interdisciplinary approach is highly appreciated, usually shows synergistic effects and fits nicely to the scope of the journal.

However, such an approach leads to a high amount of data that have to be presented

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in a condensed way to guide the reader through the main findings of the manuscript. For instance, I would concentrate on a few figures that indicate the correlation of geochemistry and microbiology. The age model in figure 2 is nice, but should be shifted to the supplementary section as the age is sufficiently indicated in figures 3 and 6. The same is true for most of the data of figures 4 and 5. The microbiologically important values of sulfate and salinity can be integrated in figure 3 while the calcium profile can be removed from this figure. On the other hand, some of the data that were shifted to the supplementary section can easily be integrated in the main text. The methods for example are described twice. It would be better to combine the description of methods in the supplementary material and in the methods section in a condensed way. If standard techniques were used that were published elsewhere, please just cite them.

My major methodological concern is the application of a nested PCR ahead of the DGGE analysis. Normally, there is no need for this. There are protocols for DNA extraction available to gain enough nucleic acids for a single-step PCR, even from much deeper subsurface samples. A nested PCR can dramatically change the DGGE profiles. A slightly preferential amplification might explain the high amount of Betaproteobacteria in the molecular analysis in comparison to the cultivation study. I can not understand why the DNA of Betaproteobacteria should be preserved in the "paleome" better than the DNA of other microorganisms. Also, a quantitative analysis based on a nested PCR is highly questionable.

In the canonical correspondence analysis, the authors have identified environmental parameters that influence the microbial community structures. The availability of electron acceptors (sulfate and metal oxides) and the quality of electron donors (indicated by age?) strongly influence the community structure. However, other trace elements are probably proxies for the origin of the sedimentary material (fluvial, marine) and should only be interpreted that way. Please make this point more clear.

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Abstract: The statement, that the two cores can be calibrated with previously analyzed reference cores is at a relatively prominent position. However, except for the age determination, this is not really done in the paper.

Introduction: What do you mean by "microbial effectiveness"? Please explain.

Methods section: Chapters 2.9.1 and 2.9.2: It is rather unusual to use bullet points here. Please describe the media composition in a "normal" text.

Results section: Both cores have a rather complicated name and it would help to follow the results if the authors would refer the names to their origin a few times in the results section (e.g. "The Gulf of Lion core RHS-KS-33" and "The Ligurian Sea core KESC9-30").

References: Too many. If you cite other publications, please focus on the most important ones and avoid long listings.

Figures: Figure 6: Please explain the line in the right part of the diagrams.

Figure 7: Showing a cluster analysis of DGGE profiles as a dendrogram only makes sense if defined clusters are visible.

Figure 8. This figure can be removed. The quantification of Betaproteobacteria and the Chloroflexi can be integrated into Figure 6.

Supplementary material: I am not sure if this material will be formatted by the production editor. If not, please number the figures and write the captions directly under the figures.

Interactive comment on Biogeosciences Discuss., 9, 253, 2012.

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