

***Interactive comment on “Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temperatures” by L.-Y. Wang et al.***

**Anonymous Referee #1**

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Wang et al. (bg-2012-148) Molecular analysis of the microbial community structures in water-flooding petroleum reservoirs with different temperatures

General comments: The article deals with a characterization of the microbial communities in water-flooding petroleum reservoirs with different temperatures. The community structure and diversity of Bacteria and Archaea in six reservoirs were elucidated via sequence analysis of 16S rRNA genes from clone libraries. The paper does not really have new findings. The solely DNA-based results do not provide information on the in situ activity of the studied microorganisms. Therefore, the study cannot draw real conclusions about the potential role of these communities. The introduction drives

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attention to the considerable potential of microorganisms in such systems in energy flow and nutrient cycling. Therefore, an RNA-based approach would have been more suitable to elucidate the active fractions of the studied communities. In addition, attempts to cultivate members of specific functional groups (e.g. methane producers, sulfate-reducers or yet not known thermophilic archaea) would have been useful.

Specific comments:

The Abstract is too descriptive. Summarizing the results is not sufficient; an abstract has to clearly state the new findings of the study as well as the conclusions drawn by the authors.

The Introduction gives an overview of studies in the field of oil reservoir microbiology. These investigations applied several (not only DNA-based molecular biological) approaches. On the contrary, the last paragraph with the aims of this study makes the reader insecure if techniques applied in this study are properly chosen to answer the questions linked to the potential role of bacteria and archaea in the petroleum reservoirs.

In the Results section it does not become clear why the physicochemical parameters were grouped before analyzing the relationships between environmental factors and microbial community structures. The following sentence (Results, section 3.3) “The physicochemical parameters of petroleum reservoirs were divided to three groups to better analyze the relationships.” does not really clarify the reason.

The Discussion interprets the results linked to sequence similarities, showing that members of the studied communities were mostly related to sequences originating from similar environments, referring to the adaptation of these microorganisms to their habitat. Furthermore, some discussion aims to support this findings based on the results of correlation analyses on environmental factors and microbial communities. However, the discussion stays speculative as the DNA-based sequence information does not allow insights into the diversity and structure of metabolically active members

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of the investigated microbial communities.

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