Biogeosciences
Discussions

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Interactive comment on "Archive of bacterial community in anhydrite crystals from a deep-sea basin provides evidence of past oil-spilling in a benthic environment in the Red Sea" *by* Yong Wang et al.

Yong Wang et al.

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Reviewer 1: The paper by Wang et al describes the microbial community associated with anhydrite crystals in a deep sea sediment basin located at more than 2 km depth in the Red Sea. According to the authors the microbial communities detected could verify past oil-spilling events to a relatively good accuracy. The microbial communities were investigated using metagenomic tools and the authors found that alkane-degrading Alcanivorax species were dominant in the metagenomes coinciding with the past oil-spill. Several metabolic alkane-degradation pathways were detected. The microbial commu-

nity of the anhydrite crystals were investigated using fluorescent in situ hybridization for identification of Alcanivorax cells that contained alkB genes. The chemistry and biological parameters of the sediment core from which the anhydrite crystals originated, differed with depth. A clear peak in organic carbon content and a significant peak at specific depth corresponding to the oil-spill. The authors conclude that the organic carbon stored in the sediments, e.g. as anhydrite crystals, is slowly released for the benefit of the whole sediment microbial community. The text as a whole is quite clear and the subject is interesting. The materials and methods could benefit from more information. I would also like to see some mote of the genome of the Alcanvorax and some metabolic pathway maps. The fact that a new uncultured Alcanivorax has been detected could be discussed more as well as its role in carbon cycling in deep sediments. Response: Thanks for the comments. We have put more details in the MM. In the Results, we made a schematic map for the Alkanivorax bacteria. Regarding the role of Alcanivorax, we put several lines in Discussion, lines 451-453.

Specific comments; L115, how did you get the supernatant? Did you let the solids sedimentate first or did you use centrifugation? Response: we put the sample for 30 min and did not centrifuge. We modified the corresponding place. L175, give more information about what you did with R and which packages you used. Response: yes, we inserted the linkage of the R scripts. L178, what is HMM Response: HMM means hidden markov model. We have deleted it. L203, what label did you use? Did you have a nonsense probe to check for unspecific labeling? Response: actually we used E. coli to examine the probe as a negative control. We have inserted this in the new version. L223, MQ water? Response: we have spelled out. L234-251, check the figures. I thing the reference to Fig 2 should be Fig 3 and vice versa. Response: yes, modified. L255 ->, did you get any sequences from the blanks and if so, Response: The sequences in blanks were dimers of the primers for the amplification, which can be justified from the size of the smear. There were not any long amplified sequences from contaminated DNA. ResultsDiscussion, I would like to see some figures with the Alcanivorax genome and relevant metabolic maps. How does the Alcanivorax interact
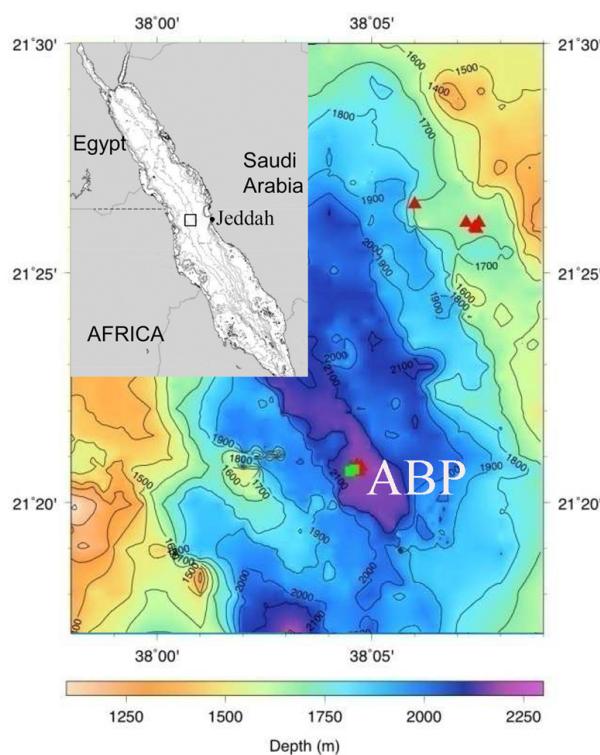
with the rest of the microbial community? Response: yes, we inserted a metabolic map for the Alcanivorax bacterium. Regarding the interaction, we inserted lines in Discussion, (lines 451-454). They are supposed to a convertor between alkanes and organic carbons and nitrogen. Typos; L58, change 'were' to 'are' L81, do you mean 'found', not 'located'? L137, correct 'grounded' to 'ground' or 'homogenized' Response: yes, all are corrected.

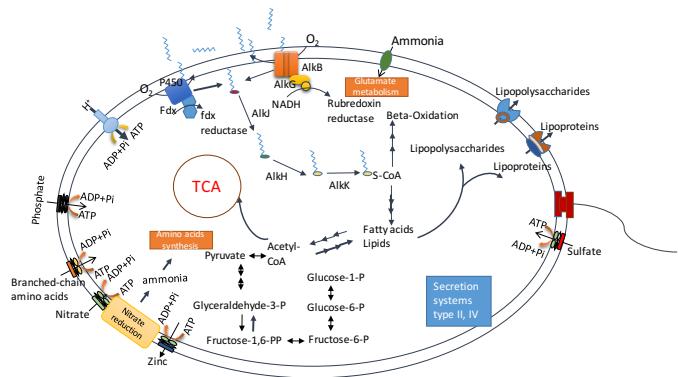Please also note the supplement to this comment:
http://www.biogeosciences-discuss.net/bg-2016-204/bg-2016-204-AC1-supplement.pdf

Fig. 1.

Fig. 2.

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