

Interactive comment on “Diversity and abundance of *n*-alkane degrading bacteria in the near surface soils of a Chinese onshore oil and gas field” by K. Xu et al.

Anonymous Referee #1

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In their study, the authors used the *alkB* gene as marker for alkane degrading microorganisms in the environment. They compared the communities in soils above an oil and gas field to the surrounding soils to evaluate the potential of *alkB* as indicator for oil and gas prospecting.

In general, it is a well conducted study and a well written manuscript which shows that the abundance of proteobacterial alkane degraders might be indicative for the presence of an oil or gas field. Nevertheless, I have some minor comments:

Many alkane degraders have several different enzyme systems to catalyse the first oxidation step. Is there anything known if the Actinobacteria or the Proteobacteria

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have several *AlkB*-like monooxygenases? This should be considered when deducing abundance from gene copy numbers. Is there anything known on horizontal gene transfer of *alkB*, or how well does it reflect the 16S rRNA phylogeny?

I think the manuscript could be improved by combining data and removing some of the figures such as Figure 3 or Table S1 (see below). Further comments:

Page 14869 Line 5: full stop after bacteria

Page 14870 Line 2: van Beilen and Funhoff

Page 14870 Line 4: full stop after reference

Page 14874 Line 26: remove the listed T-RF sizes, the link to Figure 2 is sufficient

Page 14875 Line 16-20: The T-RFLP data only represents relative abundance. Comparing the T-RFLP results to the qPCR, the total abundance of alkane oxidizers seems to increase in the oil and gas field (if the total bacteria stay the same). It would be actually helpful to not only plot the ration of *alkB* to 16S, but also to give the absolute numbers. To me, it rather seems like the Actinobacteria do not change, whereas the Proteobacteria are becoming more frequent

Page 14880 Line 12: please correct the reference: the authors are Matthias Noll, Diethart Matthies, Peter Frenzel, Manigee Derakshani, Werner Liesack

Figure 3: I do not understand this figure. Which are the sites used for this graph? Just a random subset of sites plotted in the ordination? Or the three sites from which the clone libraries were constructed? I think it would make more sense to include this information into the ordination and remove this figure. The ordination gives a better overview of the data structure, and also points out that T-RF74 is indicative for oil and gas field sites.

Table S1: the OTU definition for representative OTUs is not explained. Is it based on identity or a similarity cutoff (e.g. 95%)? It is furthermore redundant as most infor-

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mation is shown in the phylogenetic tree in Figure 2. The number of clones for each representative OTU could be included within the tree and the table could be removed.

Figure S1 is not well described and labeled. It consists of 3 sub-parts of which each includes four graphs. These graphs are all labeled Fig.1 to Fig.4. Please remove. Also, the labels for the x-axes are missing. Although the shapes of the curves have meaning in these figures, in my opinion, it would be enough to condense the information to one overview table. It is also not explained what definition is used for phylotype

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