

***Interactive comment on “Identify the core bacterial microbiome of hydrocarbon degradation and a shift of dominant methanogenesis pathways in oil and aqueous phases of petroleum reservoirs with different temperatures from China” by Zhichao Zhou et al.***

**Anonymous Referee #1**

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Review of manuscript bg-2018-470 Core bacterial microbiome of petroleum reservoirs in China The manuscript contains interesting data and is sufficiently well written such that it should be suitable for publication after minor modifications. The main contributions of the manuscript are to help define a common core microbial community in petroleum reservoirs and to hypothesize that the dominant methanogenic biochemical pathway and associated microorganisms shift in water versus oil phase microorganisms, and that the relative importance of hydrogenotrophic and acetoclastic pathways

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is different in low versus high temperature reservoirs. Nowhere in the text are the temperatures that correspond to low, moderate, and high petroleum reservoirs described. The revised manuscript should specify temperatures in the abstract and the introduction as a minimum. Since aqueous phase and oil phase microbes were recovered from only 7 locations consisting of 2 low, 4 moderate, and one high temperature reservoirs it is premature to state conclusions that the relative importance of hydrogenotrophic and acetoclastic pathways is different in low versus high temperature reservoirs. Rather, the revised manuscript should discuss the observations made by inspecting these data and offer a hypothesis that requires further testing. Table 1 shows that the concentration of acetic acid in the water phase of these 7 samples does not correlate with the reservoir temperature and does not support the claims made regarding the importance of acetoclastic methanogenesis derived from the genetic data. This should be discussed. Another issue is that the production of glycine betaine as an osmoprotectant in high salinity petroleum reservoirs has been shown to serve as the main source of methane, via methylotrophic methanogenesis, in several reservoirs. The reservoirs studied here are low salinity and no evidence of methylotrophic methanogenesis was found, but the discussion of a core microbial community should be improved by discussing genetic data from higher salinity reservoirs as it compares with the results of this study. Are there any prior publications describing the recovery of microbial cells from oil-phase samples, or is this a new technique reported for the first time? If this technique is new, that should be highlighted in the revised manuscript. Line 86 change pervious to previous. Line 275 replace ture with true.

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