

Diversity of bacteria in oil reservoirs-associated environment worldwide: A systematic review and meta-analysis

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Subsurface oil reservoirs have become a focus of intense research because of the presence of metabolically active microorganisms within the oil rich environment. Microbial communities and their associated metabolic activity in petroleum reservoirs have a fundamental importance for developing new technologies for microbial enhanced oil recovery. A global understanding of the pattern of oil reservoirs-associated environment microbial communities has not been systematically investigated, and it is not clear whether there are significant differences between water-flooded and non-water-flooded petroleum reservoirs. Here we present the first meta-analysis of the bacteria in oil reservoirs, using 16S rRNA gene sequences obtained from a range of publicly available clone-library and amplicon pyrosequencing data. Our results show that *Gammaproteobacteria*, *Firmicutes* and *Epsilonproteobacteria* are predominant in the samples. Furthermore, in *Gammaproteobacteria* and *Epsilonproteobacteria*, *Pseudomonas* and *Arcobacter* are the most frequently reported bacteria genus, respectively. Grouping previous studies from different oil fields according to low temperature low-temperature (<50°C) and high-temperature (>50°C) reveals that in high-temperature systems, *Firmicutes*, *Thermotogae*, *Thermodesulfobacteria*, *Nitrospira* and *Atribacteria* are more abundance. Bacteria in water-flooded oil reservoirs demonstrates a similar phylum-level composition (p>0.05) to that of non-water-flooded petroleum reservoirs. However, *Bacteroidetes*, *Alphaproteobacteria*, *Gammaproteobacteria* and *Betaproteobacteria* (p<0.05) existed significant differences among oil and water phase samples, which means that they are significantly affecting the overall bacterial community structure between the two groups. These analyses should be significant for well-understanding the bacteria diversity involved in worldwide oil reservoirs.