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Review

Microbiota and their affiliation with physiochemical characteristics of different subsurface petroleum reservoirs



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ABSTRACT

Microbial communities and their functions in subsurface petroleum reservoirs are crucially important for better understanding of biogeochemical processes and life forms in extreme environment, and developing new strategies and technologies for microbial enhanced energy recovery (MEER) and control of reservoir souring and corrosion in oil production systems as well as bioremediation of contaminated sites. Over the last decades, broad phylogenetic and functional diverse microbial communities of different subsurface oil reservoirs have been described by using the newly available molecular techniques, but the information has been scattered in individual publications. In this review, we present a synthesis on critical analysis of the bacterial and archaeal composition and diversity in oil reservoir systems for a more comprehensive understanding of microbiota and their affiliation to specific oil reservoir conditions, including temperature, salinity and production practices. In particular the frequently reported core and common species of microorganisms with specific characteristics of oil reservoirs including temperature, water flooding, oil and water phases were identified. This review gives an up-to-date information synthesis of the current data available and also a discussion on the challenging questions and the future research needs.

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1. Introduction

Petroleum reservoirs are generally characterized by high-temperature, high pressure, high salinity and anoxic conditions, representing an extreme environment to life. Knowledge about microbial communities in deep subsurface oil reservoirs is important and informative for better understanding the life forms in extreme environment and roles of them in enhanced energy recovery and corrosion control as well as degradation mechanisms for cleaning up. The activities of microorganisms may be beneficial for enhanced energy recovery and bioremediation or detrimental consequences for reservoir souring and pipeline corrosion to industrial applications (Augustinovic et al., 2012; Kaster et al., 2009). In order to augment these microorganisms for energy recovery and conversion or management and control of reservoir souring and biocorrosion, it is fundamental and important knowledge to know the key microorganisms present in both oil reservoirs and production system, and also their physiological and biochemical functions to allow for utilization or control of them.

Microbial communities in oil reservoirs and relevant systems thrive in micro-environments including water, oil and biofilms. Many reports on microbial ecology of petroleum reservoirs using culture-dependent and more recently culture-independent methods have been published since 1926 (Mbadanga et al., 2012; Ren et al., 2011). The ecological significance and extent of microbial activity in the subsurface oil reservoirs have been recognized further in recently years with the new molecular analysis tools available for culture-independent and metagenomics analysis. It revealed much higher diversity of microorganisms inhabiting the oil reservoirs in terms of physiology, biochemistry and phylogenetics (Tang et al., 2012). Moreover, the discovery of novel bacterial and archaeal taxa in oil reservoirs indicated a much rich undetected microbial community in petroleum reservoirs for new discoveries of microorganisms and novel biochemical processes to obtain new knowledge. Unfortunately, most studies only covered microbial communities from several oil wells of specific temperature and production management condition, e.g., water flooding vs. without flooding in restricted region. A systematic and comprehensive understanding on the distribution of the microbial communities in oil reservoirs, especially in light of the core species is still not available. It is much more informative and conclusive if microbial community of petroleum reservoirs regarding temperature, water-flooding and additional factors can be synthesized and presented to benefit the scientific community as a baseline information.

In this review, published information accessible through Web of Science database and Google Scholar using the relevant search terms (oil reservoirs or oil field and microbial community) was retrieved and reviewed for molecular inventories of 16S rRNA gene library to understand microbial communities in natural oil reservoirs and associated environments. Nucleotide sequences from

artificial and semi-artificial environments, such as enrichments, bioreactors, were excluded from the metadata of this analysis. In total, 101 and 62 clone libraries of bacterial and archaeal 16S rRNA genes were obtained for further analysis (Jan 23, 2016 [data of the date accessed]). Efforts were made to synthesize current knowledge of bacterial and archaeal composition and diversity in oil reservoirs systems known to date, and provided a systematic and extensive analysis and synthesis on the current understanding of the microbial communities in petroleum reservoirs.

2. Bacterial community and diversity

The oil reservoirs and relevant samples for in this analysis were from accessible published sources as shown in Table 1. The primary bacterial lineages detected in *in situ* oil reservoirs included Proteobacteria, Firmicutes, Deferribacteres, Bacteroidetes, Actinobacteria and Thermotogae. Other phyla, namely Spirochaetes, Synergistetes, Thermodesulfobacteria, Chloroflexi, Nitrospira, Atribacteria, Acidobacteria, Fusobacteria and Planctomycetes were also detected much less extent in oil reservoirs (Fig. 1). Dominant bacterial lineages were the main foci of majority of the research conducted and reported. While minor of the community, such as Spirochaetes and Chloroflexi were comparatively less investigated.

2.1. Proteobacteria

Proteobacteria including Gamma-proteobacteria, Epsilon-proteobacteria, Beta-proteobacteria, Alpha-proteobacteria and Delta-proteobacteria were widely distributed in oil production ecosystems. The common genera such as *Pseudomonas*, *Marinobacter* (Gamma-proteobacteria), *Thauera* (Beta-proteobacteria), *Sphingomonas* (Alpha-proteobacteria), *Arcobacter*, *Sulfurospirillum* (Epsilon-proteobacteria), *Desulfovibrio* and *Desulfomicrobium* (Delta-proteobacteria) were the most frequently detected among all petroleum reservoirs investigated. Mesophilic *Pseudomonas* species, which were not believed to originate from oil reservoirs were also detected increasingly from high-temperature oil reservoirs (Korenblum et al., 2012; Li et al., 2006; Mnif et al., 2013; Orphan et al., 2000; Tang et al., 2012). It maybe a result of that many high temperature oil wells were water-flooded for a long time, and *Pseudomonas* spp. as a very versatile heterotroph have competitive capability to survive including formation of biofilms in oil/water mixture (Cai et al., 2015; Klausen et al., 2006), thus they can be detected and even grow in thermophilic environments. In addition, *Pseudomonas* spp. has the ability to degrade a large fraction of the crude oil components and prefer high concentration of nutrients when oxygen is available (Abbasnezhad et al., 2011; Mukherjee et al., 2010; Obuekwe et al., 2008). Most *Marinobacter* species are aerobic, although some members can denitrify. As oil reservoirs are considered generally under anoxic conditions, the

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