

Culture-independent-based analyses identified site-specific microbial in two oil-wells from Malaysia

ABSTRACT

Microbial communities of two oil reservoirs from Malaysia, denoted as Platform Bo and Platform Pe were studied using culture-independent approach. Environmental DNA was extracted and the universal amplified ribosomal region (UARR) was target amplified for both prokaryotes and eukaryotes. The amplified products were purified and cloned into pTZ57R/T vector to construct the 16S/18S rDNA library. Restriction endonucleases HhaI and MspI were used to screen the library. From that, 125 and 253 recombinant plasmid representative clones from Platform Bo and Platform Pe, respectively, were sent for DNA sequencing. Twenty-six operational taxonomic units (OTUs) consist of 20 genera detected at Platform Bo and 17 OTUs consist of 13 genera detected at Platform Pe. *Marinobacter* and *Acinetobacter* species co-occurred in both platforms whereas the rest are site-specific. Gammaproteobacteria accounted for 86.0% of the microbial community in Platform Bo, where OTUs affiliated to *Marinobacter*, *Pseudomonas* and *Marinobacterium* that were the most abundant. The major OTUs in the Platform Pe were with affinities to *Achromobacter*, followed by *Stenotrophomonas* and *Serratia*. The only archaeal isolates were detected in Platform Pe, which affiliated to *Thermocodium*. The singletons and doubletons accounted for about 50.0% of the OTU abundance in both platforms, which considerably significant despite their rare occurrence.

Keyword: Microbial community; Operational taxonomic unit; Petroleum reservoir; 16S/18S rRNA