PB-03

Petroleum hydrocarbon-degrading bacterial communities in tropical marine environment

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Key words: crude oil, biodegradation, tropical marine environment

Petroleum hydrocarbon-degrading bacterial communities enriched from Indonesian seawater were characterized by combining culture-independent and culture-dependent approaches. Seawater and tar balls remaining on a beach in Indonesia were collected, and a tar-ball sample was used to inoculate artificial seawater supplemented with nitrogen and phosphorus sources to enrich hydrocarbon-degrading bacteria. Bacterial community structures in the seawater, the tar ball and the enrichment culture were analyzed by constructing clone libraries of 16S rRNA genes. The results showed that, after the enrichment for 7-days, bacteria closely related to the genus *Alcanivorax* became predominant in the tar-ball enrichment culture. To further characterize the bacterial communities, bacterial strains were isolated from the seawater, the tar ball and the tar-ball enrichment culture using crude-oil as sole sources of carbon and energy. The isolates were characterized based on 16S rRNA gene sequences. Some of them were related to bacterial groups already known for their capacity to degrade hydrocarbons (such as *Alcanivorax*, *Marinobacter*, *Oleiphilus* and *Gordonia* groups). The 16S rRNA gene sequences of 13 strains show less than 97 % similarity to the sequences in the public DNA databases. Growth and biochemical tests showed that these isolates are capable of degrading crude-oil.

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Isolation and physiological characterization of novel petroleum-hydrocarbon-degrading bacteria from tropical sea

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Key words: Petroleum, Crude oil, Tropical sea

[Objectives] The objective of this study is to survey petroleum-hydrocarbon-degrading bacteria in tropical seas. This will provide rational strategies required for the bioremediation in tropical seawater.

[Materials and Methods] Petroleum-hydrocarbon-degrading bacteria were enriched on crude oil in a continuous supply of Indonesian seawater supplemented with nitrogen, phosphorus and iron, and the bacteria contained in the system were isolated. The isolates were grown in “seawater medium” containing 1,000ppm crude oil, and the biodegradation of crude oil components was determined by using GC/MS.

[Results and Discussion] In addition to *Alcanivorax* and *Marinobacter* which are ubiquitous petroleum-hydrocarbon-degrading bacteria in marine environments, strains related to *Oceanobacter kriegii* (96.4-96.5% similarities by partial 16S rRNA gene sequences), *Rhodovulum iodosum* (96.3%) and *Erythrobacter luteolus* (97.4%) were obtained; petroleum-hydrocarbon-degrading activities in the last three genera have not been reported previously. *Oceanobacter*-related bacteria, which were suggested to be tropical-seawater-specific, showed high n-alkane-degrading activity similarly to SK2-type *Alcanivorax*, which appeared to be temperate-seawater-specific. On the other hand, although *Alcanivorax* strains obtained in this study, which were thought to be tropical-seawater-specific, showed lower activity for n-alkane and branched-alkane degradation than the SK2-type *Alcanivorax*, they were still considered to be important for branched-alkane degradation in the tropical sea. The bacteria related to *Erythrobacter* and *Rhodovulum* were specialists for polycyclic aromatic hydrocarbon degradation.

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