PB-07

Effect of Phenol Concentration and Aeration on Phenol Degradation of *Comamonas testosteroni* TA441

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[Introduction]*Comamonas testosteroni* TA441, which was isolated from gut homogenates of termite, has a complete set of phenol degradation genes (*aph* genes) but does not grow on phenol under laboratory conditions, because the genes encoding multicomponent phenol hydroxylase (PH) are repressed by a silencer protein AphS. TA441 adapts to utilize phenol after 2~3 weeks incubation in a phenol-containing medium by spontaneous mutations that inactivate AphS. Although TA441 grew well on phenol only after the irreversible mutation, there must be physiological conditions that requires the function of intact *aph* genes. To identify the role of the *aph* genes, we examined phenol degradation by TA441 under various conditions.
[Methods]TA441 and TDS, which is a *aphS* deficient strain constructed by homologous recombination from TA441, were cultivated in jar fermenters (600ml, 30℃) under several phenol concentrations (0.5~5 mM) and aeration conditions.
[Results and Discussion]While TA441 did not degrade phenol under high concentration of phenol, degradation was observed at low phenol concentration. Although TDS grew on high concentration phenol under low oxygen tension, it did not grow under high oxygen tension despite the fact that phenol was degraded; indicating that high concentration of oxygen has toxic effect when PH is highly expressed. These results suggest that phenol degradation system of TA441 has been optimized for low phenol and low oxygen conditions where TA441 might naturally inhabit. Furthermore, AphS might control the PH level to avoid the toxic effect of oxygen.
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PB-08

Effects of temperature on sulfate-reducing consortia which degrade petroleum hydrocarbon

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In removing marine pollution by crude oil, contribution of sulfate-reducing bacteria should be important, because of limited oxygen supply and abundant sulfate in seawater. In general, marine sediment is always at low temperature. However, there are few reports on hydrocarbon-degrading sulfate-reducing bacteria under low temperature. Among various components of crude oil, mono-aromatic hydrocarbons have relatively high solubility and toxicity. In this study, sulfate-reducing enrichment cultures with petroleum hydrocarbon were established under low (8℃) and moderate (28℃) temperatures, from tidal flat sediment of Tokyo-Bay. After cell growth on the crude oil was confirmed, the each culture was transferred to the medium containing *p*-xylene, one of mono-aromatics. The total amounts of sulfide originated from sulfate reduction were significantly different between two crude oil-degrading cultures at different temperatures. Whereas, there was no significant difference between two cultures grown on *p*-xylene. The microbial communities were characterized by PCR-DGGE analyses targeting genes for 16S rRNA and dissimilatory sulfite reductase. The DGGE band profiles were significantly different depending on the temperature and substrate. These results suggest that the effects of temperature on the function and structure of sulfate-reducing consortia involved in the hydrocarbon degradation are different depending on components of utilized oil.

keywords:low temperature, sulfate-reduction, hydrocarbon-degrading bacteria
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