Isolation and Characterization of Explosive RDX-utilizing Bacterium

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The feasibility using an isolate derived from the enriched microbial consortium for explosive degradation was explored. The present study reports on the isolate which was developed to grow aerobically with RDX (hexahydro-1,3,5-trinitro-1,3,5-*s*-triazine) as the sole sources of carbon and nitrogen. Complete depletion of RDX at the initial concentration of 15 mg per liter was achieved within 24 days of incubation in bench-scale bioreactors. Addition of supplemental carbons (*e.g.*, succinate, glucose, fructose) stimulated the degradation of RDX. The isolate also could degrade structurally related explosive 2,4,6-trinitrotoluene. Degradation of RDX was verified by HPLC analysis of the residual RDX concentration in the test culture. Microscopic examination of this degrader, HK-6 revealed a Gram-negative and coccobacillus-shaped cell. Strain HK-6 was characterized by using the BIOLOG system and an analysis of the total cellular fatty acids. The strain indicated that the bacterium could be identified and designated as *Pseudomonas sp.* HK-6.

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Microbial Diversity in Marine Sediment from Sunchon Bay, Chunnam Province, by 16S rRNA Gene Analysis

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In order to investigate the diversity of microbial community in the marine sediments of Sunchon Bay, diversity of amplified 16S rDNA was examined. Total DNA was extracted from sediment soils and 16S rDNAs were amplified using PCR primers based on the universally conserved sequences in bacteria and archaea. Clonal libraries were constructed and clones were examined by amplified rDNA restriction analysis (ARDRA) using HaeIII. Clones were clustered based on restriction patterns using computer program, GelCompar II. There were very few clones which had same restriction patterns and almost all the clones were single-type clones. To investigate the relationships of clusters, serveral clones were examined by sequence analysis.

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The Effect of rpoH Gene on the Expression of virG in *Agrobacterium tumefaciens*

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The virG of Agrobacterium tumefaciens has two promoters, P1 and P2. The P2 promoter is transcriptionally induced by the treatment of acidic pH and acetosyringone. The -10 sequence of P2 promoter is similar to the consensus sequence of *E. coli* heat shock gene promoter, which is recognized by RpoH(σ 32). In this study, we used the P2 promoter deletion mutant and the rpoH deletion mutant to find out whether the rpoH gene expression is required to induce the virG P2 promoter under the conditions of acidic pH and acetosyringone treatments. The results of this study showed that the expression of P2 promoter of virG requires the rpoH gene expression.