The community structure of bacteria in groundwater was examined by PCR amplified 16S rDNA-denaturing gradient gel electrophoresis(DGGE). DGGE is attractive technique, as it separate same length dsDNA according to sequence variation typical 16S rDNA genes. The genetic diversity and similarity of bacterial community in groundwater was analyzed by GC341f and PRUN518r primer sets for amplification of V3 region of eubacteria 16S rDNA.

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Eubacterial Diversity as Determined by 16S rRNA Gene with Depth in Lake Soyang

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The phylogenetic relationship of the domain bacteria with the depth was investigated by performing a comparative sequence analysis of PCR-amplified 16S ribosomal DNAs. Water and sediment samples were collected with the depth (0, 10, 20, 50, 80, 100 and sediment) in front of Soyang dam. DNA extraction was performed to identify members of the domain eubacteria which inhabit such an aquatic environment, we used PCR to construct a library of 16S rDNA genes cloned from DNA extracted from the waters of Lake Soyang. The 16S rDNAs were amplified by PCR by using oligonucleotide primers (27F-1492R) complementary to 16S rRNA genes and gel-purified PCR products were cloned into vector pGEM-T. Clone libraries (501 clones) of PCR-amplified archaeal rRNA genes were constructed with samples from 0 m to 100 m depth. A restriction fragment length polymorphism (RFLP) analysis of the 16S rDNAs was performed with MspI and AluI. Partial sequencing of the cloned 16S rDNAs revealed an extensive amount of phylogenetic diversity within this system. Sixty-one 16S rDNA clones were partially sequenced. The estimated values of richness in the SY6 (14.76) clone library was much higher than other sites. By comparative sequence analyses, the majority of the examined clones could be affiliated with the Verrucomicrobiales in upper depths and Proteobacteria in lower depths.

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Relationship of the Eubacterial Communities by DGGE Profiles in Lake Soyang

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The community structure of eubacteria in mesotrophic Lake Soyang was examined by PCR amplification of the V3 region of 16S rRNA from microbial communities recovered from various depths in the water column and sediment. Amplified DNA fragments were resolved by denaturing gradient gel electrophoresis (DGGE), and the resulting profiles were reproducible and specific for the communities from different depths. Eubacterial diversity estimated from the number and intensity of specific fragments in DGGE profiles. The similarities of DGGE profiles were determined by UPGMA. SY1 and SY2 of the DGGE profiles were similar over 95%. The similarity between SY4 and SY5 of the DGGE profiles was over 82%. Several dominant fragments in the DGGE profiles were compared with environmental clones. Among the dominant populations were representatives related to methanotroph, sulfate-reducer and so on.

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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.