butane, *n*-hexane, *n*-octane, *n*-dodecane, and hexadecane. It is interesting to observe that an insertional mutant strains EK385 (*bphC*::Km) and MB1 (*bphA4* ::Cm), which lost BphA3 and BphA4 activitis, are also unable to grow on all of the alkanes tested. This observation indicates that the same ferredoxin and reductase components are associated even with the aliphatic-oxidizing oxygenase. Furthermore another mutant strain EK121 (*xylE*::Km), which lost the downstream gene activities (*xylGJQKIHCbphB*) due to polar effects, was found to be unable to grow on the alkanes tested. However, it should be noted that EK121 still grows on dodecanoic acid although it lost the ability to grow on the upstream metabolic intermediates of alkane degradation including dodecyl alcohol and dodecyl aldehyde. Complementation experiments with different subclones showed that 2.2-kb *Cla* I restriction fragment, containing only the *xylQ* gene for a putative acetaldehyde dehydrogenase, allowed EK121 to recover the ability to grow on alkanes as well as the intermediate compounds. These data suggest that XylQ converts aliphatic aldehydes to corresponding acids.

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Distribution of PAH concentrations and Degradation Potential for PAHs by Natural Microorganisms in Marine Sediments of Kwangyang Bay and Ulsan Bay

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The distribution of PAH concentrations in sediments of Kwangyang Bay and Ulsan Bay and degradation potential for PAHs by indigenous microorganisms were investigated. The concentrations of PAHs in Kwangyang Bay and Ulsan Bay were 0.11~55.1 ppm and 0.54~76.05 ppm, respectively. The evolution of carbondioxide was increased to 9.6~184.9% by the additional PAH mixture (ca. 1000 ppm) after 25 days incubation. For the evaluation of more direct evidence of degradation potential by indigenous microorganisms, we tried to measure the decrease of specific PAHs by GC. The amount of artificially added each 100 ppm of phenanthrene, pyrene and benzo[a]pyrene were checked for 2 to 4 weeks of incubation. In the sediments of Ulsan Bay, 73.8~89.8% of phenanthrene and 24.0~76.7% of pyrene were degraded by natural microorganisms at aerobic condition and ~18.1% of phenanthrene and ~6.5% of pyrene were degraded at anaerobic condition after 2 weeks of incubation. In the sediments of Kwangyang Bay, 100% of phenanthrene and 89.3~95.9% of pyrene were decreased after 4 weeks. But the benzo[a]pyrene was shown to be recalcitrant. From these results we concluded that, 1) the availability of oxygen seemed to be one of the important limiting factor in degradation of PAHs smaller than 4 ring in natural environment and 2) another remediation techniques such as bioaugmentation is required to remove large PAH molecules like as benzo[a]pyrene.

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Phylogenetic Characterization of Bacterial Isolated from Acid Mine Drainage-Contaminated of Stream and Ground water

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Twenty-six pigment forming bacteria isolated from acid mine drainage-contaminated of stream and ground water were characterized by

phylogenetic analysis of 16S ribosomal RNA gene nucleotide sequences. The isolates were found to fall within four major phylogenetic groups: the alpha-, beta-, and gamma-*Proteobacteria;* the low-G+C Gram-positive bacteria group. The alpha-group was further separated into three subclass, alpha-1, 2, and 4. Some of the isolates were not closely related to any genus in the 16S rDNA sequence databases. The genus *Sphingomonas* of alpha-4 subclass of the *Proteobacteria* was dominant group. The genus *Spingomonas* was yellow pigmented, motile rods and nonmotiles, gram-negative rods, 2-hydroxymyristic acid and isoprenoid quinone Q-10. Moreover, P5-21 and P5-11 strains within genus *Sphingomonas* appeared to be novel species, they will be discussed for new species in their taxonomic aspect.

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Molecular Ecological Study on The Distribution of *Aeromonas* Species in Rainbow Trout Fish Farm

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Aeromonas species are mesophilic motile or psychrophilic nonmotile gram-negative bacteria. They are ubiquitous and widely isolated from clinical, environmental, and food samples. Although they have been recognized as primary fish pathogens, many studies have reported that they are potential human pathogens. As they are fish pathogens and found in aquatic environments, rainbow trout fish farm may be a potential *Aeromonas* reservoir. The present study describe the seasonal and spatial distribution of *Aeromonas* species in rainbow trout fish farm. In each season samples were taken from specific sites including inflow, farming area, lagoon, the upper part of stream and the lower part of stream to join outflow and rainbow trouts. To characterize and to investigate the distribution of *Aeromonas* species, we used fatty acid methyl ester analysis to isolate *Aeromonas* species. The amplification of 16S rDNA and restriction fragment length polymorphism (RFLP) analysis were performed to isolates and samples without cultivation. In seasonal distribution, *Aeromonas* species except *A. salmonicida* showed seasonal differences. *Aeromonassalmonicida* was not detected in inflow but appeared in farming area and affected to lower part of stream showing little seasonal difference of distribution. *Aeromonas* species isolates from intestine of rainbow trout showed that most of them were *A. salmonicida*. From these results, it was supposed that rainbow trout acted as reservoir of *A. salmonicida* showing independent distribution in seasonal distribution and the distribution of other *Aeromonas* species was affected by temperature and precipitation in each season.

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Characterization of the Cell Wall Lytic Enzyme of*Anabaena cylindrica*Produced by*Aspergillus sp.*HCLF-4

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In the mixed culture of *Anabaena cylindrica* and *Aspergillus* sp. HCLF-4, the algae was lysed in 5 days. And then, in the mixture of *Anabaena cylindrica* and extracellular enzyme when the HCLF-4 was grown in a PDB media which contained 0.05% heat killed *Micrococcus luteus* cells as substrate, it was observed segmented and lysed algae on microscopy. The lytic enzyme which molecular weight was about 14kDa, have