B041

A Novel Canthaxanthin-Producing Bacterium Isolated from Marine Environment of Jeju Island

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An orange-colored marine bacterium, strain S76, was isolated from marine environment of Jeju Island The isolate showed gram negative, catalase positive, and oxidase negative reactions The temperature range for growth of strain S76 was from about 20℃ to 40℃, with optimal at 30℃ The range of NaCl concentration for growth of isolate was from above 0 to below 9%, with optimal 3% The major cellular fatty acids of isolate were $C_{16:0}$, $C_{18:1}\omega7C$, and $C_{14:0}$ 2-OH. Data analyses of 16S rDNA sequence and BIOLOG test for isolate revealed that strain S76 shows very close phylogenetic association to *Erythrobacter* spp. And strain S76 exhibited 16S rDNA similarities of 99 2% and 97 7% to the species of *Erythrobacter vulgaris* and *Erythrobacter longus*, respectively. Pigment extracted from cell of strain S76 showed the identical retention time in reverse-phase HPLC and a similar Rf value in TLC with standard canthaxanthin. On the basis of phenotypic and molecular properties, strain S76 seems to be a new canthaxanthin-producing bacterium in the genus *Erythrobacter.*

B042

Metabolic Characterization of Microbial Communities in the Forest Soils After a Fire

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To investigate changes of microbial metabolic activities at the community level in the forest soils after a fire, soil samples, which were collected from the sites near Gangnung area where a forest fire was broken out four years ago, were analyzed for the patterns of the sole carbon source utilization using Biolog GN2 microplate and a statistic process Two soil samples were from the burnt area, one from the naturally restoring soil (NRS) and the other from the artificially restoring soil (ARS) For a comparison, a normal soil sample (NS) near the same area, which was not burnt, was included Each sample was also divided into surface (top soil) and subsurface (sub soil) portion, and each portion was analyzed for the community-level physiological profiles (CLPPs) after 45, 96 and 192 hours incubation in GN2 microplate Among the samples tested, top soils of NS and NRS, and sub soil of NRS showed higher metabolic activities Sub soil of ARS showed the lowest metabolic activity. Other characterizations on the metabolic and physiological properties in the soil microbial communities affected by a forest fire was also revealed in this study

B043

Biochemical and Genetic Diversity of Microbial Communities in the Soil Affected by a Forest Fire

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Changes of biochemical and genetic diversity of microbial communities in the soil affected by a forest fire were analyzed Soil samples were collected from Gangnung area where a forest fire was broken out in 2000 Two soil samples were from the burnt area, one from the naturally restoring soil (NS) and the other from the artificially restoring soil (AS). A normal, unaffected soil sample (US) was also included as a control For the biochemical diversity, each sample was directly applied to the Biolog system, and the cluster analysis through a statistic process (SSCP) were performed Genetic diversity was analyzed through DGGE using 16S-rDNA amplified from soil DNA Among the samples tested, top soils of US and NS, and sub soil of NS revealed more than 70% of the similarity value in biochemical diversity In case of genetic diversity, however, the similarity value was found to be in the range of 53% to 68% in all samples The number of DNA bands was also similar in all samples in about 30 to 40. This result indicates that the biochemical diversity is not always correlated with the genetic diversity in the analysis of microbial communities.

B044

Design of Long Oligonucleotide Probes for Detection of Highly Conserved Genes in the Environmental Genome

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Analysis of functional diversity and its dynamics in environment is essential for understanding microbial ecology Molecular ecology techniques such as DNA microarray could be successfully adapted for massive monitoring of functional gene diversity One of the biggest challenges of this analysis is the selection of optimal oligonucleotide probes from highly conserved functional gene set in high throughput mode In previous studies, design of probes has been focused long oligonucleotide probes (50~70-mer) for genes from single genome To apply previous works to design long oligonucleotide probes from highly conserved genes, a serious limitation exists Here, we propose a program, named HPD, designing probes from several hundreds of conserved genes for widely applying to the detection of functional genes in the environment with DNA microarrays