B013

Screening for Genes Related to Oxidative Stress from The Tidal-flat Metagenome

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Reactive oxygen species (ROS) are produced as an inescapable consequence of aerobic life and affect all macromolecules (DNA, lipids, and proteins) To protect themselves against oxidative stress by ROS, living organisms build up mechanisms with enzymes such as catalase and superoxide dismutase which eliminate ROS However, this basic protection is not sufficient to cope with oxidative stress So, other global responses are induced that enable bacteria to survive the stress period by multiple means We exploited the metagenome from a tidal-flat soil to search for genes related to oxidative stress. Total genomic DNA of a tidal-flat soil was used to construct small insert (3~5kb) libraries, which were functionally searched for the genes related to oxidative stress Six clones involving genes related to oxidative stress were obtained from the metagenomic library
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B014

The Role of Chitinase of *Chromobacterium violaceum* KBC1001 in Biocontrol of Plant Pathogenic Fungi

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An extracellular chitinase-producing microbe isolated from soil was identified as a strain of *Chromobacterium violaceum* KBC1001 and its cultural condition for production of chitinase was investigated Optimum incubation condition for the highest chitinase production was colloidal chitin 0 12%, soy peptone 1 0%, malt extract 1 0% (or lactose 0 5%), K_2HPO_4 0 015%, $MgSO_4$ 0 025%, NaCl 0 1% and pH 5 0 at 30℃ for 36hours Antagonistic bacterium *Chromobacterium violaceum* KBC1001 as a potent biocontrolling agent against plant fungal disease was evaluated An extracellular chitinase, which is key enzyme for the lysis of fungal cell walls, had an inhibitory effect of fungal growth by the degradation of cell wall of plant pathogenic fungi These results suggest that chitinase produced by *Chromobacterium violaceum* KBC1001 attacks and degrades the hyphae in lytic mechanism for biological control of the plant pathogenic fungi

B015

Construction of Microbial Consortium for Bioremediation of Polycyclic Aromatic Hydrocarbons Contaminated in the Marine Sediments

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A bacterial strain, *Novosphingobium pentaromativorans* US6-1, capable of degrading various high-molecular-weight polycyclic aromatic hydrocarbons (PAHs) such as Benzo [a]pyrene, was isolated from marine sediments There are limitations to eliminate PAHs contaminated in the marine sediments. To overcome those limitations, we tried to select the best microbial consortium As a result of sequential screening from the previously isolated PAHs degrading microorganisms and resin compounds degrading microorganisms, each one strain from PAHs degraders (PAH5) and resin degraders (YSR9) was selected to construct a consortium combined with strain US6-1. The degradation rate of PAHs mixture (fluorene, phenanthrene, anthracene, pyrene, chrysene, and benzo[a]pyrene) coated on alumina was determined depending on the initial inoculation ratio of the three strains. Among the experimental set, the consortium consisted of US6-1 YSR9.PAH5 = 2 1 1 showed the highest degradation rate of PAHs. The applicability of the selected consortium will be tested in the large-scale bioslurry reactor in the future.
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B016

Lysobacter spp. Constitute Major Bacterial Populations in the Root of Sand Dune Plants.

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Bacterial community diversity associated with plants growing in four coastal sand dune areas was studied by using PCR-denaturing gradient gel electrophoresis (PCR-DGGE) technique with universal bacterial primer sets 341fGC and 518r Rhizosphere and soil samples were taken from two major sand dune plant species, namely *Calystegia soldanella* and *Elymus mollis*, and the comparative analysis indicated that root endophytic bacterial community was relatively simple and homogeneous regardless of the sampling areas and plant species, whereas no general tendency was observed in that of rhizosphere As individual bands from the gels were sequenced, the major bands were identified as species of *Lysobacter* in all of root samples examined Other minor constituents included *Pseudomonas*, *Flavobacterium* and *Arthrobacter* spp. in root The major bands in rhizosphere samples were also identifiedas *Lysobacter* sp , whereas other minor bands were as *Pseudomonas*, *Bacillus* and others The dominance of *Lysobacter* spp was also confirmed by the analysis of 16S rDNA clones derived from the same samples.