B001

Bacteriocidal Activity of *Lactobacillus* sp. JK-11 against Pathogenic Bacteria

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The purpose of this work was evaluated for anti-bacterial activity of bacteriocin derived from *Lactobacillus* sp JK-11 Strain JK-11 was isolated from marine environment, and was developed to grow on MRS media. On the basis of BIOLOG test, JK-11 could be assigned to *Lactobacillus hilgardii* JK-11, and designated as *Lactobacillus* sp JK-11. JK-11 was tested for the changes in the optical density associated with cell growth and production of organic acids The stain produced only small amount of organic acids, and pH was changed 7.0 to 5 4 In pH-adjusted and pH-nonadjusted cultures of JK-11, growth inhibition around soaked filter discs were shown on *Vibrio harveyi, V parahemolyticus*, and *Edwardsiella tarda*. SEM revealed irregular rod shapes with punctured surfaces Bacteriocidal activity derived from JK-11 was determined by radial diffusion assay. Among 72 fractions collected from RP-HPLC, the first fraction showed the strongest bacteriocidal activity in this experiment Molecular mass of bacteriocidal substance was measured by Tricine SDS-PAGE and determined as approx 4 kDa.

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B002

Microbial Clean-up of Contaminated Sea Water in Bench-top Scale Cistern: Removal of Nitrogens and Phosphorus

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The feasibility of using bacterial cultures with the ultimate aim for the marine environmental clean-up was explored The present study reports on the elimination of nitrogens (N) and phosphorus (P) by strains CK-10 and CK-13 isolated from shrimp farming pond The strains were identified as genus *Bacillus* on the basis of BIOLOG test and 16S rDNA, and designated as *Bacillus* sp CK-10 and *Bacillus* sp CK-13, respectively Simultaneously removal of nitrogens or phosphorus was studied with co-cultures under aerobic conditions in bench-scale scale cistern. 0 01% (w/v) Farming feed contained approx 13 2 μM NH_4^+, 14 7 μM NO_2^-, 66.3 μM NO_3^-, and 40 1 μM PO_4^{-3} which could dissolved within 120 hrs of leaching in aqueous solution followed by bacterial removal Complete bacterial removal of NO_2^- leached from 0 01% feed was achieved within 72 hrs, and NH_4^+ and PO_4^{-3} were removed to completion within 120 hrs, respectively Co-cultures displayed only a partial removal of NO_3^- (~90%) during the given period The work demonstrated that co-cultures, CK-10 and CK-13 showed simultaneously effective removal of N/P

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B003

Fabrication of Subspecies-Level Specific Microbial Diagnostic Microarrays by Using the Genes Amplified from Subtractive Suppression Hybridization as Microarray Probes

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Fabrication of microarray probes with higher specificity below the species level is a long-term question since the high throughput detection of microorganism is an efficient means of identifying the microbes that may play an important role in ecosystems Here we describe the application of a genomic DNA coupled with suppression subtractive hybridization (SSH) as a microarray probe for the differentiation of the subspecies level SSH was used for initial isolation of different part of genomes of 9 *Salmonella* strains, quadraplicate validations of which was accomplished by microarray analysis. The data reveals a large group of genes subtracted by SSH could serve together as one probe for detecting a subspecies while not subtracted whole microbial genome played a species-specific probe. The detailed methods described herein could be useful and adaptable to the estimation of any cultivable bacteria from different environments

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B004

Molecular Analysis of Bacterial Community Structure in Rice Field Soil

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The bacterial community structure in rice field soil planted with genetically-modified(GM) and non-GM rice plants was monitored by analysis of denaturing gradient gel electrophoresis (DGGE) profiles and 16S rDNA sequences obtained from clones and cultivated dominant isolates The DGGE analysis revealed that the bacterial community structures were quite similar to each other in a given month, indicating that there were no significant differences in the structure of the soil microbial populations between GM rice and non-GM rice over the experiment However, the DGGE profiles of June soil after a sudden flooding indicated that the selective growth of some indigenous microorganisms occurred Phylogenetic analysis of 16S rDNA sequences from clones and isolates showed that the microbial diversity of June soil reduced compared to the other months The results indicated that flooding of rice field gave a significant impact on indigenous microbial structure, but that the initial structure was gradually recovered over time

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