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Cometabolism of o-Xylene by BTEX Degrader, *Burkholderia* sp. SCU1 Isolated from a Reed Rhizosphere of Suncheon Bay

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Strain SCU1 from reed rhizosphere of Suncheon Bay was capable of growth on a medium containing all six BTEX components (benzene, toluene, ethylbenzene, and the xylene isomers). The alkylated mono-hydrocarbons (toluene, ethylbenzene, and xylenes) as well as benzene were degraded by a combination of assimilation and cometabolism. Benzene, toluene, ethylbenzene, the xylene isomers, m-xylene and p-xylene were used as sources of carbon and energy, whereas o-xylene was cometabolized. o-xylene was not used as a carbon source, but in combination with toluene, it appeared to be mineralized. Identification of the isolate based on analysis of 16S rRNA gene sequences revealed that SCU1 was *Burkholderia* sp. with over 95% confidence. Monooxygenase genes for initial catabolism of aromatic hydrocarbons in *Burkholderia* sp. SCU1 were found by PCR of Rieseke type iron-sulfur protein and determination of amino acid sequences, indicating most identified genes are the enzymes for degradation of BTEX.

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B054

Taxonomical Study of Heterotrophic Bacteria in the Rhizosphere of Halophytes in Western and Southern Coastal area of Korea

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This study was carried out to investigate the population densities and R/S ratio of heterotrophic bacteria in the rhizosphere soil of halophytes found on the western and southern coastal area of Korea. The population densities of aerobic and anaerobic heterotrophic bacteria in the rhizosphere soil of halophytes were in the range of $2.9 \pm 0.6 \times 10^6$ – $3.7 \pm 0.9 \times 10^8$ and $4.1 \pm 2.0 \times 10^4$ – $6.3 \pm 3.3 \times 10^7$ cfu g⁻¹ d wt, respectively. Population density of aerobic heterotrophic bacteria on the rhizosphere of *Suaeda maritima* and that of anaerobic heterotrophic bacteria on the rhizosphere of *Suaeda japonica* showed the highest value among sampled halophytes. The R/S ratios ranged from 1.11 ~ 8.50, which showed lower value compared with those of rhizosphere found on common terrestrial environment, which indicated that coastal sediment environment was less favorable than common terrestrial environment to the microbial communities of rhizosphere. Dominant strains were Proteobacteria γ (6 strains) group for *Suaeda japonica*, Fimicutes group (5 strains) for *Suaeda maritima*, Proteobacteria γ (6 strains) group for *Phragmites communis*.

B055

Distribution and Characteristics of Airborne Microorganisms in Indoor Environment of Schools

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To assess microbiological indoor air quality in schools, concentrations of viable airborne microorganisms were monitored at classrooms and corridors of 3 middle or high schools in Ulsan. Airborne microorganisms were sampled at various situations (class-hour, lunchtime, after school, during vacation) with an impacton-type air sampler. During the semester, the numbers of bacteria were highest at lunchtime in corridor with an average of 1,111 MPN/m³ and lowest at class-hour in corridor with an average of 132 MPN/m³. During the vacation, the bacterial concentrations at classrooms and corridors were only 5% and 27% of the values during the semester, respectively. Among the colonies tested, 60% were identified as *Micrococcus* species. During the semester, the average values of fungal concentrations at each situation ranged from 105 to 213 MPN/m³, and the values during the vacation were 32 MPN/m³ at classrooms and 83 in corridors. *Cladosporium* species, *Penicillium* species and *Aspergillus* species were identified from the colonies. The obtained data can be considered as a step to set the guideline for bioaerosols in indoor environment of schools.

B056

Diversity and Characterization of Moderately Halophilic Bacteria from Seashores and Solar Salterns in Anmyeondo

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Ten bacterial samples were collected from seashores and solar salterns in Anmyeondo. Both culture-independent and culture-dependent approaches were used to characterize the diversity of moderately halophilic bacteria taken from enrichment cultures. The bacterial diversity was monitored using DGGE (denaturing gradient gel electrophoresis) and T-RFLP (terminal restriction fragment length polymorphism) techniques. Bacterial 16S rDNA fragments were amplified using a set of two primers, namely 341F-GC and 536R for DGGE, and Fluorescein-9F and 926R for T-RFLP, respectively. The DGGE band profiles showed no clear difference between seashore samples and those of solar saltern, while the T-RFLP peak profiles showed clear differences between seashore samples and those of solar saltern. Totally seventy bacterial strains were isolated from ten bacterial samples. The 16S rDNA sequences of the isolates were assigned to six bacterial genera including *Chromohalobacter*, *Halomonas*, *Idiomarina*, *Pseudomonas*, *Salinivibrio* and *Halobacillus*, which belongs to γ -Proteobacteria except *Halobacillus*.

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