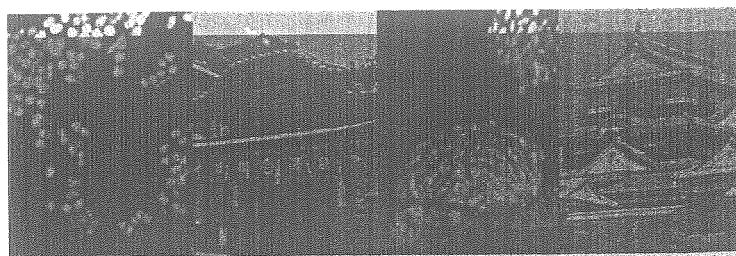




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Program and Abstracts



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Poster No.	Title	Authors	Page No.
ISME-01	Archaeal nitrification in marine sediments	Soo-Je Park, Byeong-Jun Park, Myeong-Soon Kim, Sung-Keun Rhee	22
ISME-02	Comparison of bacterial density and diversity on the Rhizosphere of halophyte <i>Phragmites communis</i> inhabited in mudflats of freshwater and seawater	Ho-Sang Moon, Suhk-Hwan Park, Geon-Hyoung Lee	22
ISME-03	Effects of concentration of coplanar PCBs on reductive dechlorination and microbial community in sediment slurries	Chuan-Hsin Ho, Chih-Hung Chen, Chin-Feng Chang, Shiu-Mei Liu	23
ISME-04	Comparison between yeast populations in sea surface microlayer and underlying water by cultivation method	Chin-Feng Chang, Shiu-Mei Liu	23
ISME-05	Uncultivated genome-probing microarrays by amplifying the genomes from a single bacterial cell using digital multiple displacement amplification	Jin-Woo Bae, Young-Do Nam, Ho-Won Chang, Kyoung-Ho Kim, Seong Woon Roh, Won-Hyung Chung, Youlboong Sung, Che Ok Jeon, Jung-Hoon Yoon, Hee-Mock Oh	24
ISME-06	Dye degrading bacteria in monoculture and consortia	Aileen C. Jalandoni, Anna Lynn A. Decena, Wilfredo L. Barraquio, Virginia L. Barraquio, Ernelea P. Cao	24
Lucky ISME-07	Identification of major dechlorinating populations in multiple-permeable reactive column experiments using nested and quantitative PCR techniques	Jaejin Lee, Joonhong Park	25
ISME-08	Microbial diversity and population structure analysis of lead-tolerant microbial communities effectively sorbing lead	Kaliannan Thamaraiselvi, Lam Pui Yeng, Shankar Congeevaram, Kangsuk Kim, Joonhong Park	25
ISME-09	Diversity of polyhydroxyalkanoate (PHA) synthase genes (phaC) of <i>Rhodocyclus</i> -related polyphosphate-accumulating organisms	Seung Hyun Ryu, Thu-Huong Thi Vu, Shipeng Lu, Qian Wang, Che Ok Jeon	26
ISME-10	Enhanced production of laccase by <i>Trametes versicolor</i> during treatment of hormone mimicking compounds	Sumin Yeo, Hong Gyu Song, Hyoung Tae Choi	26
ISME-11	Increase of laccase expression by hormone mimicking compounds in <i>Phlebia tremellosa</i> transformants that having extracopies of laccase gene	Soomin Yeo, Myung K. Kim, Hyoung Tae Choi	27
ISME-12	Degradation of hormone mimicking compounds using laccase transformants in <i>Irpeix lacteus</i>	Yun Jeong Gim, Hong Gyu Song, Hyoung Tae Choi	27
ISME-13	Molecular analysis of nitrifying bacterial community in a biofilm reactor under various operating conditions	Tae-ho Lee, Im-Gyu Byun, Jung-Jin Park, Jae-Cheul Yu, Tae-Joo Park	28
ISME-14	Microbiological risks of waste sludge used as liquid fertilizer	Young-Ok Lee, Eung-Ju Hwang, Hye-Joo Lee, Gyu-Cheol Lee, Se-Hee Nam	28

ISME-07

Identification of major dechlorinating populations in multiple-permeable reactive column experiments using nested and quantitative PCR techniques

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Key words: Dechlorination, *Clostridia*, *Dehalococcoides*, *Desulfuromonas*

Complete TCE (trichloroethene) degradation was achieved in laboratory column experiments of a dual column system in which the first column was packed with zero-valent iron, and the second column was filled with the pieces of recycled wasted tire, which was inoculated with anaerobic digestion sludge from a municipal wastewater treatment plant in Korea. In this work, we examined which dechlorinating populations were involved in dechlorination activities in the second bioreaction column. According to T-RFLP (terminal restriction fragments length polymorphism) for 16S-rRNA, the population diversity of microbial communities for the bioreactor was higher than that for the seeding microbial communities. In the bioreactor, the phylum groups of firmicutes and chloroflexi were decreased or insignificantly detected while proteobacteria phylum group was increased. For specific detection of dechlorination microbes, nested PCR analysis was performed using specific 16S-rRNA primers for known dechlorination populations from amplified 16S-rRNA PCR products. The results showed that nested PCR amplification response for *Desulfurmonas* populations was significantly increased in the bioreactor while those for *Clostridia*, *Anaerolineae*, and *Dehalococcoides* were relatively weak and unchanged. This was confirmed by the following quantitative PCR analysis. These findings suggest that *Desulfurmonas* populations were responsible for the observed dechlorination activities in the bioreactor.

ISME-08

Microbial diversity and population structure analysis of lead-tolerant microbial communities effectively sorbing lead

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Key words: Microbial diversity, heavy metal, biosorption, activated sludge

Lead is one of the most abundant toxic heavy metals to be found in the environment due to its wide applications in the manufacturing industries. Recently, a few studies suggested that heavy metal tolerant microbes can be used as biosorption materials. In the present study, comparison of the microbial diversity and population structure between original activated sludge and lead amended activated sludge have been carried out. Restriction enzyme digestion was carried out using RFLP enzymes (*HhaI* and *MspI*) and 16S rRNA amplification and sequencing was performed. Results showed a substantial variability in the response of activated sludge microbial community to lead amendment, which indicates the impact of lead exposures on community diversity and resiliency. The following sorption experiment with the lead-tolerant microbial consortium showed an effective biosorption of lead at high concentration. These findings implied that pretreatment of activated sludge with heavy metal exposure would improve the capability of biosorption of lead by activated sludge microbial communities.