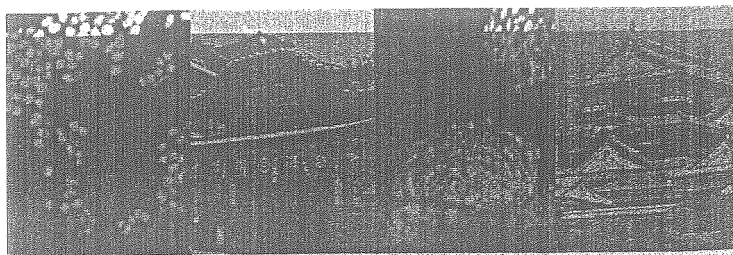




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Identification of major dechlorinating populations in multiple-permeable reactive column experiments using nested and quantitative PCR techniques

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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.