

B309

**Increase of Bacterial Community Diversity in the Subsurface
Aquifers by Livestock Wastewater Input**

Jang-Cheon Cho* and Sang-Jong Kim

Department of Microbiology, Seoul National University

Despite intensive studies on the bacterial community structure, the questions of which kinds of bacterial populations are associated with the change of community structure have not yet been fully solved by molecular approaches. In this study, to investigate the impact of livestock wastewater on the qualitative and quantitative changes in the bacterial communities in groundwater, the bacterial communities in the subsurface aquifers were analyzed by characterizing their 16S rDNA sequences. The similarity coefficients of restriction fragment length polymorphism (RFLP) phlotypes of the cloned 16S rDNAs showed that the bacterial communities in livestock wastewater samples were more closely related to those in contaminated aquifer samples. In addition, calculated community diversity clearly showed that bacterial communities of the livestock wastewater and the contaminated aquifer were much more diverse than those of the uncontaminated aquifer. Phylogenetic analysis of the sequences from a subset of the phlotypes showed that the *Bacteroides-Cytophaga-Flexibacter* and the low G+C gram positive groups originating from livestock wastewater were responsible for the change of bacterial community in groundwater. This was evidenced from the occurrence of rumen-related sequences not only in the livestock wastewater samples but also in the contaminated groundwater samples. Rumen-related sequences, therefore, can be used as indicator sequences for fecal contamination of groundwater, particularly from livestock.

B310

Isolation of BTEX Degrading Bacteria and Their Degradation Activity

In Sook Ahn* and Sang-Jong Kim

Department of microbiology, Seoul National University

Three strains of bacteria were isolated from hydrocarbon contaminated soil based on their ability to utilize BTEX as a sole carbon and energy source, and their degradation activity were tested in liquid and soil microcosm. Two of these strains, m9 and 2p7, were identified as *Pseudomonas mendocina* and C6T was identified as *P. putida* by FAME analyses. When each BTEX compound was added to broth culture of these strains at a concentration of 100mg/l, C6T degraded more than 90% of toluene within 18hr, m9 degraded 90% of m-xylene within 24hr, and 2p7 also degraded more than 90% of p-xylene within 24hr. When they were incubated with 300mg/l BTEX mixture, they degraded 80%, 70%, and 60% of BTEX mixture in 24hr, respectively. When they were incubated in consortium, C6T and m9 degraded 87% of BTEX mixture, C6T and 2p7 degraded 75% BTEX mixture. These results show that their biodegradation activity were increased in consortium. The biodegradation activity of these strains were confirmed in soil microcosm experiment.