B005

Nutrient Removal Efficiency and Dynamics of Denitrifying Bacterial Community Structure in a Treatment Wetland System

Keunyea Song*, Seung-Hoon Lee, and Hojeong Kang
Department of Environmental Science and Engineering, Ewha Womans University

Nutrient removal efficiencies in wetland depend on various factors such as vegetation, soil type, and microbial activities Especially, the presence and diversity of denitrifying bacteria may affect the water quality improvement. The objectives of this study were to determine the nutrient removal efficiency in wetland and to investigate the microbial diversity during the wetland operation In particular, we focused on the diversity of specific denitrifiers which play a key role in nitrite reduction For this, we operated two kinds of wetland mesocosms, pond- and marsh-types, and analyzed water and soil samples collected on a monthly basis To investigate the community structure of denitrifiers, nitrite reductase (*nirS*) genes analyzed by terminal restriction fragment length polymorphism (T-RFLP) analysis During the wetland operation, nitrate removal efficiency was continuously increased from 42 % to 86 % The pattern of T-RFs showed a high level of diversity and changes in community structure during wetland operation were also observed.

[This study is supported by Ministry of Environment as The Eco-Technopia 21 Project and Advanced Environmental Biotechnology Research Center]

B006

The Activities and Community Structure of Methanotrophs in a Temperate Forest Soils

Inyoung Jang*, Seung-Hoon Lee, and Hojeong Kang
Department of Environmental Science and Engineering, Ewha Womans University

To explore the activity of methanotrophs in forest soil, we measured methane oxidation rates on a monthly basis from May 2004 to March 2005 in a temperate forest in Korea. The community structure of methanotrophs were analyzed by using terminal restriction fragment length polymorphism (T-RFLP) analysis with methantrophs type- specific primers Natural rates varied from 0 31 to 5 41 mg CH_4 m^{-2} day^{-1} Methane oxidation rates in spring and autumn were higher than those in summer and winter. In general, species of methantroph type II group were more frequently observed than type I group The pattern of terminal restriction fragments (T-RFs) were distinguished among each analyzed samples and showed a high level of diversity Changes in community structure with seasons were also observed In conclusion, the rates of methane oxidation in a temperate forest soil in Korea are comparable to previous reports in other countries These results also indicated that the dynamics of methane flux might be related with changes of methanotroph community structure

[This study was supported by Korea Long Term Ecological Research(KLTER) and Advanced Environmental Biotechnology Research Center(AEBRC).]

B007

Analysis of Bacterial Biofilms on the Electrode of Microbial Fuel Cells using Fluorescent *In Situ* Hybridization (FISH)

Jiyoung Lee*, Kyung Shik Kim, Yeng Fung Choo, Gi Su Kang, Ho Il Park, Bor Chyan Jong, In Seop Chang, and Byung Hong Kim
Water Environment and Remediation Research Center, Korea Institute of Science and Technology

Complex microbial communities of a microbial fuel cell (MFC) were visualized by Fluorescent *in situ* hybridization (FISH) with 16S rRNA-targeted oligonucleotide probes, which is a tool for the specific and sensitive identification of target organisms within biofilms Probes were designed for detection of one domain (*Archaea*), 3 subclasses (*β proteobacteria, δ proteobacteria,* and *γ proteobactera*), and 3 single species (*Shewanella putrefaciens, Pseudomonas aeruginosa,* and *Geobacter* sp) The fluorephore such as FITC (fluorescein isothiocyanate), CY3 (cyanate 3), or CY5 (cyanate 5) was conjugated with at the 5' end of probes Confocal laser scanning microscopy (CLSM) confirmed that electrodes surfaces in MFCs fed with various substrates contained different spatial distribution of bacteria in multi-species biofilms.

[Supported by NRL(M1-0104-00-0024)]

B008

Physiological Characterization of Hdrogen-Oxidizing Denitrafication Bacterium, Pseudomonas sp. SKU

Hai-Yan Jin[1*], Yong Keun Park[1], and Doo Hyun Park[2]
[1]*Korea University, Graduate School of Life Science and Biotechnology,* [2]*Department of Biological Engineering*

A novel denitrifier was isolated from anaerobic digestive reactor of waste water treatment plant and characterized for the physiologies especially related to denitrafication. 16s rDNA sequence of isolate was identified with sulfide-oxidizing bacteria by data base analysis. When the bacteria are grown in the medium containing nitrate, acetate and hydrogen, they use hydrogen gas as electron donor, nitrate as electron acceptor, and acetate as carbon source respectively When the bacteria are grown in the medium containing sulfide, acetate and without hydrogen gas, they use sulfide as electron donor, nitrate as electron acceptor, and acetate as carbon source respectively The bacterium can not use acetate, glucose or lactate as both carbon source and electron donor, because it can not grow in the medium containing nitrate and without hydrogen gas The bacterium has nitrate assimilation ability, because it can grow when there is no other nitrogen source in the medium except nitrate The bacterium is heterotrophic, because it can not use CO_2 and H_2 to support its growth, when there are no organic carbon sources

[Supported by College of Life Science and Biotechnology, Korea Univ]