**PE-09**

**Community structure analysis of nitrite-oxidizing bacteria in nitrite-oxidizing cultures obtained from sandy sediment of eelgrass zone.**

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Little study on nitrite-oxidizing bacteria (NOB) in the eelgrass zone is reported. The purposes of this study are to attempt incubating nitrite-oxidizing bacteria at different temperatures, and investigate the community structures of NOB in the cultures obtained from the sand of the eelgrass zone. Sand for inoculum was collected from eelgrass zone at the Tanoura Bay, Shimoda, Shizuoka on July 16, 2009. The 10 g of sand were incubated in 30 ml of medium containing 0.5 mM nitrite for NOB at 10°C, 20°C and 30°C, respectively. The DNA was extracted from cells after collection from each culture. The PCR was performed with the specific primer for 16S rRNA genes of NOB, Nitrobacter, Nitrospira, Nitrosospira, and Nitrotricha. The PCR product was sequenced for identification. Nitrite consumption was observed in culture at all of the temperature. 16S rRNA genes of the genus Nitrosospira was detected from NOB incubated at both 20°C, 30°C. On the other hand, 16S rRNA gene of the genus Nitrotricha was detected from incubated culture at 10°C. These results suggest the possibility that the NOB within the genera Nitrospira and Nitrotricha are responsible for oxidizing of nitrite in sandy sediment of eelgrass zone.

**Key word:** nitrite-oxidizing bacteria, Nitrotricha, Nitrospira, eelgrass zone

**PE-10**

**Stable isotope probing analysis of anaerobic CO₂-fixing bacteria in the meromictic Lake Suigosetsu.**

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Microbial populations of anaerobic CO₂ fixation were investigated in the chemocline of the meromictic Lake Suigosetsu using DNA-stable isotope probing technique. Water samples collected from the chemocline were incubated in anaerobic bottles with 13C-labelled sodium bicarbonate at in-situ temperature in the dark. Most of 16S rRNA sequences amplified from 13C-DNA under light condition were related to the genera Chlorobium and Desulfovibrio, suggesting that green sulfur bacteria (GSB) and sulfur-disproportionating bacteria assimilate CO₂ in the light. This result suggests that GSB assimilate CO₂ and supply elemental sulfur or sulfur oxanions for Desulfovibrio in the chemocline of Lake Suigosetsu. Desulfovibrio can grow chemolithotrophically and may contribute to anaerobic CO₂ fixation in the chemocline. Clone sequences related to the genera ThiKomicrospira and Chlorobium were frequently recovered from 13C-DNA fraction library under dark condition, suggesting that chemolithotrophic sulfur-oxidizing bacteria and GSB assimilate CO₂ in the dark. Our results suggest that GSB play a significant role in the anaerobic CO₂ fixation in the chemocline of Lake Suigosetsu even under dark condition and that chemolithotrophic sulfur-oxidizing and sulfur-disproportionating bacteria contribute to the anaerobic CO₂ fixation using sulfur oxanions during the sulfate oxidation by GSB.

**Key word:** phototrophic sulfur bacteria, Anaerobic CO₂ fixation, DNA-stable isotope probing

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**PE-11**

**Microbial community structure on tree leaves.**

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**Key word:** phyllosphere, leaf surface, bacterial community composition, forest tree

The phyllosphere is a hostile environment for the survival of microbes, because the leaf surface is exposed to dry conditions and strong ultraviolet radiation, and is sparse in nutrients. Nevertheless, many bacteria exist in such extreme environments (10⁹ to 10³ cells cm⁻²). Terrestrial leaf surface area is estimated to be about 6.4 x 10⁹ km², which is comparable to the earth's surface area. Thus, the phyllosphere microbes play an important role in terrestrial ecosystems. In this study, the bacterial community composition (BCC) and the bacterial number on leaf surface of forest trees were determined using clone libraries of 16S rRNA genes and DAPI-staining. The phyllosphere microbial samples were collected from the evergreen tree leaves of Japanese cedar and cypress which were most typical forest trees in Japan. The phyllosphere BCC on Japanese cedar and cypress were mainly composed of phyla Proteobacteria and Acidobacteria. Especially, a specific characteristic was observed in the relative contribution of phylum Acidobacteria. Subdivision 1 acidobacteria were most abundant (average >90%) in the acidobacterial communities. The phyllosphere bacterial number of Japanese cedar and cypress were average 4.0 x 10⁶ and 1.6 x 10⁷ cells cm⁻², respectively. To our knowledge, these are the first comparable analysis of phyllosphere microbial communities of the Japanese cedar and cypress.

**PE-12**

**Effect of chlorine to microbial community structures in seawater desalination process by reverse osmosis under different conditions.**

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**Key word:** microbial community, desalination process, chlorine, biofouling

Membrane fouling in desalination plants is major problem affecting water production. Although biofilm formation and microbial diversity have been investigated by many researchers, an appropriate operation depends on mostly empirical knowledge. In this study, we examined the variations of microbial cell density and community structure in pilot-plants to clarify the effect of chemicals addition for biofouling formation. In order to compare the microbial community structure associated with fouling formation, three series of ultrafiltration plus reverse osmosis test plants with different water supply and/or chemicals were operated and water samples were obtained from each processing step in the plants. A plant using surface seawater with different pressure indicating that the biofouling would be affected in the addition of chlorine to seawater failed to completely kill microorganisms. It is assumed that resistant bacterial groups proliferate by utilizing organic compounds originating from killed cells, that would lead to establish new microbial communities in the plant. Functional gene analysis in relation to the biofouling is in progress.