Sulfate-reducing bacterial community structures in sediments of Tokyo Bay, Japan.
Toshihiro Haneda, Shuichi Shikano, Shogo Sagahara, Hideaki Maki
Grad. Sch. of Life Sci., Tohoku Univ., CNRS, Tohoku Univ., Faculty of Sci. and Eng., Shimane Univ., NIES

Key word: sulfate-reducing bacteria, DGGE, sediment, Tokyo Bay

Dissimilatory sulfate reduction by sulfate-reducing bacteria (SRB) is the major anaerobic microbial respiration process in coastal sediments. SRB community structures from 3 sites in the inner Tokyo Bay were examined. We collected sediment samples from near Tokyo-light buoy, Chiba-light buoy, and Sanmaizu in 2011. After DNA extraction from sediment samples by beads beating method, PCR was performed with SRB specific primer set. PCR products were applied for denaturing gradient gel electrophoresis (DGGE) analysis and these obtained DGGE band patterns were used for comparison of similarity of SRB community structures. Many bands were common to all sites and site specific bands were relatively few. Although the sulfide concentrations changed seasonally, the seasonal variation of SRB community structures weren’t significantly large at all sites. The band patterns obtained from Tokyo-light and Chiba-light buoy showed especially high similarity, while the community structures of Sanmaizu were different from them. We are trying to identify both common and site specific SRB strains to determine the characteristics of the each site.

Indigenous soil bacterial populations harbored in quercus forest soil at different layers throughout the year by using PCR-DGGE
Song-Ih Han, Kyung-Sook Whang
Department of Microbial and Nano Materials, Mokwon University.
Institute of Microbial Ecologoy and Resources, Mokwon University.

Key word: bacterial populations, forest soil, indigenous, PCR-DGGE

Our previous study examined the vertical and season changes physicochemical and microbial populations in a quercus forest soil at different layers throughout the year. We founded the soil physicochemical characteristics from each layer are closely related to the bacterial community structure. The soil profile at the sampling site was defined as follows; the upper portion (L layer) was covered with undecomposed, newly fallen leaves. Below the old litter (F layer) and the H layer was more or less sharp, dark grey or brownish colored. Next to this A layer of 20 cm was observed. In this study we used PCR-DGGE to examine the bacterial populations in different layers throughout the year. One hundred seventy-five distinct DGGE bands were identified among the 456 bands from which 175 sequences were obtained as representative of the major groups. On the phylogenetic analysis, we confirmed six major groups in different layers of forest soil throughout the year were Rhizobiales, Rhodobacteriales, Spinkomonaoidaes, Burkholderiales, Acidobacteria and Actinobacteriales. Half of the total clones were alphaproteobacteria: Bradyrhizobiurn, Agromonas, Nitrobacter, and Alfia (BANA) cluster and were dominantly distributed from L layer to A layer throughout the year, prompted us to examine the contribution of indigenous forest soil, although it has been a subject of controversy.