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Analysis of Bacterial Communities in Marine Biofilms

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We investigated the bacterial communities in marine biofilms by terminal restriction fragment length polymorphism (T-RFLP) and amplified ribosomal DNA restriction analysis (ARDRA) of 16S rRNA gene For the substratum of biofilm development, acryl, glass, and steel coupons were submerged in seawater. T-RFLP profiles of microcosm experiments showed that the bands of gamma-proteobacteria were predominant. In the case of a field study, the band of Bacteroidetes group was predominant ARDRA with HhaI digestion showed 19, 26, and 31 clusters from the acryl, glass, and steel coupons, respectively Although the steel coupon showed a high diversity, bacterial communities of 3 substrates were similar. The nucleotide sequences of 16S rRNA clone libraries and the major fragments in T-RFLP profiles were similar to those of Flavobacteriaceae, Rhodobacteraceae, Alteromonadaceae, and Vibrionaceae family Our result suggests that Bacteroidetes, alpha-proteobacteria, and gamma-proteobacteria play an important role in the initial stage of biofilm formation in marine environment.

[Supported by grants from Marine BIO 21 Program]

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Analysis of Bacterial Communities in Wastewater Treatment Systems using Bacillus Biofilm

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The bacterial communities of the wastewater treatment systems using Rotating Activated Bacillus Contactor (RABC) were investigated by T-RFLP and FISH methods The RABC process utilizes Bacillus biofilm and has high removal efficiencies of organic pollutants from a food factory Bacillus was detected from the all samples of RABC process with the exception of influent water The major bacterial groups of the return sludge were also detected from the whole process The predominant groups of domestic samples were Latobacillus, Pectinastus, Acrobacter, Cytophaga, and Bacteroides Otherwise, Mycobacterium, Pseudomonas, Lactobacillus, Eubacterium, and Clostridium were predominant in the samples from a RABC system in Japan

[Supported by grants from Eco-STAR Project]

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Analysis by cDNA Microarrays of Altered Gene Expression in Human Intestinal Epithelial Cells in Response to Infection with *Aeromonas*

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Many clinically important enteric pathogens initiate disease by adhering the intestinal epithelium As an initial step in the infectious process, many bacterial pathogens adhere to cell adhesion molecules as a means of exploiting the underlying signaling pathwas, entering into host cells or establishing extracellular persistence To further define the role intestinal epithelial cells play in initiating and modulation the host response to infection with bacteria, hybrid selection on cDNA microarrays was used to characterize the mRNA expression profile of ~8,000 genes in human intestinal epithelial cells after infection with *Aeromonas*. Selected findings were further evaluated by reverse transcription-polymerase chain reaction The results also show that evaluation of mRNA expression profiles by cDNA array analysis is a powerful approach to characterizing and understanding host-pathogen interactions.

[Supported by grants from Hankuk University fo Foreign Studies Reserch Fund]

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Two-electrode System Oxidizing Organic Materials in Sediment

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We investigated the possibility of stimulating the oxidation of organic materials in lake sediments through a microbial fuel cell (MFC) system Sediment collected from river bed was placed MFC-type bioreactors with graphite anode at bottom graphite cathode at surface without proton exchange membrane. A set of 3 reactors were operated with closed circuit connecting the anode and cathode through a resistor of 10 ohm, and another set of 3 reactors were operated under open circuit conditions as control They were operated over a year with monitoring potential between the anode and cathode and change in COD, pH and DO The current of reactors with closed circuit increased continuously and reached to 2 1 mA in 6 months Control reactors showed a potential over 0 8 V After 1 year operation, we analyzed the organics content of sediments Analyses showed that the closed circuit MFC consumed more organic materials than that of control. These results indicate that microcosm (electrochemically active consortia) was developed in the anode compartment of MFCs

[Supported partly by MOST (NRL program) and partly by KIST]