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The Hidden Powers - Microbial Communities in Action

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BOOK OF ABSTRACTS

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SELECTION AND CHARACTERIZATION OF AN ANAEROBIC ENRICHMENT CULTURE DECHLORINATING DIVERSE CHLORINATED AROMATIC COMPOUNDS OBTAINED FROM PADDY SOIL

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can reductively dechlorinate chlorinated compounds such as polychlorinated biphenyls (PCBs) have been receiving much attention in the environmental science and technology. In this study, a microbial dechlorinating diverse chlorinated compounds was enriched by cultivation with 4,5,6,7-tetrachlorophthalate (fthalide). Fifty paddy soil were incubated with 100 ml of a mineral medium supplemented with 20mM of acetate, formate, butyrate, or lactate and 50 μ M of fthalide at 30 °C for 2 weeks. The cultures with dechlorinating activity were serially transferred to the new medium. Dechlorination activities were also estimated for 2,3,4,5-tetrachlorobiphenyl (2,3,4,5-TeCB) and 1mM of polychlorinated biphenyl (PCE) by using the same enrichment culture. The microorganisms in the culture were characterized phylogenetically by denaturing gradient gel electrophoresis (DGGE) of partial 16S rRNA gene amplified by primers 341f and 517r targeted to domain Bacteria. All of the soil cultures supplemented with single organic acid and 50 μ M of fthalide to 4-monochlorophthalate within 2 weeks. The cultures supplemented with formate or lactate maintained fthalide-dechlorinating activity more than 10 times of the serial transfer. However, the dechlorinating activity was suddenly lost in the culture with acetate and butyrate after 3rd transfer. Only the enrichment culture with lactate maintained dechlorinating activity for 2,3,4,5-TeCB and PCE but not the culture with formate. The results of fthalide-dechlorinating culture with lactate revealed the presence of *Firmicutes* and *Bacteroidetes*.

ENRICHMENT AND SCREENING OF AEROBIC DENITRIFIERS IN ACTIVATED SLUDGE SYSTEM

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By adopting sequencing batch reactor, the different effects of selection and enrichment of aerobic denitrifiers in activated sludge system using intermittent aeration mode and continuous aeration mode were investigated. The results showed that the two domestication modes were beneficial to the enrichment of aerobic denitrifier in the sludge system. After domesticating activated sludge, 105 strains of bacteria were isolated from the sludge and 21 of the 105 strains exhibited high TN removal rates of more than 50%. Eventually, after second screening, 6 strains were confirmed capable of co-respiring by using nitrate and oxygen as electron acceptor and molecular nitrogen was the end product of denitrification. The 6 strains screened were true aerobic denitrifiers. This suggests that as soon as selective pressure is applied in the sludge system, aerobic denitrification of this metabolism is amplified.

ARCHEAL AND CYANOBACTERIAL COMMUNITIES IN HISTORICAL BUILDINGS

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The need for the preservation of cultural heritage has led to a greater interest in the biological attack on such buildings. The importance of the physical and chemical deterioration of stones has been emphasized when fed by anthropogenic pollution under moderate conditions. The presence of archaea was considered as inhabitants of hostile environments. Recent studies have shown that this group of microorganisms is also present in non-extreme environments including natural ecosystems, estuaries, freshwater. Using DGGE (Denaturing Gradient Gel Electrophoresis) analysis of PCR-amplified DNA from archaeal and cyanobacterial 16S rRNA genes, we characterized the presence of those communities in monuments of Acropolis. The results showed 11 different locations of the ancient marbles and the presence of many distinguishable bands in the separation gels. The results support the idea that these microorganisms are important members of the communities colonizing such

PHENOL REMOVAL AND MICROBIAL COMMUNITY STRUCTURE IN HIGH CONCENTRATION PHENOL-FED MEMBRANE BIOREACTOR

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"Bulking" phenomenon was observed at high concentration of phenol wastewater in conventional activated sludge processes. Very little is known about the role of "bulking" floating population in aromatic degradation. In this study we hypothesized that phenol-driven floating populations may have ability to efficiently degrade phenol. To examine this hypothesis, we used membrane bioreactor (MBR) to catch floating microorganisms, and then characterized their phenol degradation and community structures. In MBRs, phenol was fed individually as a sole carbon source in non-toxic (100mg/L) and toxic (1,000 mg/L) concentrations. DO, pH, VSS, phenol, and TOC were measured constantly. Phenol degradation by floating filamentous populations was evaluated using initial phenol degradation rate assays. For phylogenetic analysis of the filamentous populations, small subunit rRNA genes were amplified, cloned and sequenced. Initially the higher phenol concentration resulted in inhibitive effect on growth in the sludge. However, after an acclimation period, floating aggregates were formed and the fed amount of phenol was completely degraded. Microscopic investigation showed that filamentous microorganisms were dominant in the floating aggregates. The following initial degradation assays revealed that the floating filamentous populations exhibited at least five times greater rate of phenol degradation than the settling sludge populations. Phylogenetic analysis was performed to explore the community structure in the intriguing floating filamentous populations. These findings supported that the high phenol-fed floating filamentous microorganisms can efficiently degrade phenol. Unlike the conventional activated sludge processes, MBR can accumulate filamentous phenol degraders, in turn providing a suitable ecological condition for treating highly phenol-loaded wastewater.