B332 Molecular microbial diversity based on 16S rDNA analysis in aquifers within a stockfarming area

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Bacterial communities of two confined aquifers within a stockfarming area were characterized by 16S rDNA-based analysis. Groundwater samples were collected from the boreholes located in the upstream(W3) and downstream(W1) region to pig barns, and livestock wastewater samples(LW) were collected from the wastewater dumping sites. Universal 16S rDNA primers(27F-1492R) were used to amplify DNA extracted from groundwater and livestock wastewater. The purified PCR products were cloned into pGEM-T, and resulting clones(1160 clones) were characterized by *Hae*III RFLPs. Among the 222 clones that had unique RFLP patterns, 42 abundant clones were chosen for partial sequencing. The most common clones, RFLP types 1 and 2, were epsilon group of Proteobacteria and beta subclass of proteobacteria, respectively. The frequently occurring clone types were related to *Janthinobacterium*, *Pseudomonas*, *Zoogloea*, *Flexibacter*, *Flavobacterium*, and *Clostridium*. Clonal diversity of W-1 and LW samples by RFLP types was higher than that of W-3 samples. From the distance and similarity matrices calculated by RFLP types, it was found that livestock wastewater highly influenced bacterial communities of confined aquifer.

B333 Comparative Analysis of Bioremediation Potential in Different Soil Types : weathered and freshly Petroleum Hydrocarbon Contaminated Soil

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Soil microcosm studies were performed in order to investigate the effectiveness of bioremediational treatment of different soil samples. The influences of the contamination history and microbial characteristics on biodegradation were analyzed. Comtaminated soils were treated as follows : abiotic control, deionezed H_2O, N P supplement and addition of TPH(total petroleun hydrocarbon) degrader. Residual concentrations of TPH, abundance of petroleum degrading bacteria(PDB), bacterial activity, CO_2 evolution and O_2 consumption were analyzed for 10 weeks on different soil types. PDB numbers were $10^7 \sim 10^8$ MPN g^{-1} in weathered soil and $10^3 \sim 10^5$ MPN g^{-1} in freshly contaminated soil and 10% of them were alkane degraders. In each soil, bacterial activity was determined to be in the range of 4.5~59.4 μgINT-formazan $g^{-1}day^{-1}$. In the first 3 weeks initial microbial activity had correlation with CO_2 evolution(R^2=0.96, $p<0.01$), O_2 consumption(R^2=0.92, $p<0.01$) and TPH reduction (R^2=0.91, $p<0.01$). Eighty percent of TPH was reduced in this period. In weathered soils, the most effective treatment to enhance the TPH biodegradation was N,P supplement. However, in freshly contaminated soils, bioaugmentation was more efficacious than N,P supplement to remove petroleum hydrocarbon from soil. These results indicate that the number of PDBs and bacterial activity in samples before treatment should be considered in predicting the feasibility for bioremediation.