

Characterization of bacterial community structure in a hydrocarbon-contaminated tropical African soil

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Abstract

The bacterial community structure in a hydrocarbon-contaminated Mechanical Engineering Workshop (MWO) soil was deciphered using 16S rRNA gene clone library analysis. Four hundred and thirty-seven clones cutting across 13 bacterial phyla were recovered from the soil. The representative bacterial phyla identified from MWO soil are Proteobacteria, Bacteroidetes, Chloroflexi, Acidobacteria, Firmicutes, Actinobacteria, Verrucomicrobia, Planctomycetes, Ignavibacteriae, Spirochaetes, Chlamydiae, Candidatus Saccharibacteria and Parcubacteria. Proteobacteria is preponderant in the contaminated soil (51.2%) with all classes except Epsilonproteobacteria duly represented. Rarefaction analysis indicates 42%, 52% and 77% of the clone library is covered at the species, genus and family/class delineations with Shannon diversity (H') and Chao1 richness indices of 5.59 and 1126, respectively. A sizeable number of bacterial phylotypes in the clone library shared high similarities with strains previously described to be involved in hydrocarbon biodegradation. Novel uncultured genera were identified that have not been previously reported from tropical African soil to be associated with natural attenuation of hydrocarbon pollutants. This study establishes the involvement of a wide array of physiologically diverse bacterial groups in natural attenuation of hydrocarbon pollutants in soils

Keywords: Hydrocarbons, bacteria, 16S clone library, hydrocarbon-contaminated soil

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