

Journal of Chemical, Biological and Physical Sciences



An International Peer Review E-3 Journal of Sciences

Available online at www.jcbpsc.org

Section B: Environmental Biotechnology

CODEN (USA): JCBPAT

Abstract

Microbial Diversity Shifts During the Bioremediation of a Heavy Crude Oil-contaminated Soil at Microcosm

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Abstract: In this study we analyzed by a metagenomic approach some of the effects (e.g. displacement, permanence, disappearance) produced between native microbiota and a hydrocarbon-degrading microbial consortium during the bioremediation of a soil polluted with hydrocarbons. Microcosm systems were prepared using a non-sterile heavy crude oil-contaminated soil, inoculated with a fungal/bacterial degrading consortium and biostimulated with sterile corn stover for 30 days under aerobic conditions. Paired-end whole genome sequencing was performed using an Illumina MiSeq platform. Metagenomic unassembled reads were analyzed and annotated in MG-RAST. Results were visualized with both the MG-RAST and MEGAN5 platforms. Taxonomic analysis of metagenomic data showed a predominance at the domain level of Bacteria and a lesser portion of Eukaryotic and Archaeal sequences. Soil inoculation with the microbial consortium resulted in appreciable shifts in microbial communities when compared to uninoculated controls. The largest differences were observed in hydrocarbon-degrading bacterial communities (Firmicutes, Actinobacteria, Proteobacteria), particularly by day 30. Fungal communities were more stable with Ascomycota being the dominant phyla, although differences with respect to controls were also observed. In conclusion, Inoculation with a degrading consortium produced appreciable changes on the microbial diversity of hydrocarbon-contaminated soils, shifting some native microbial communities to favor hydrocarbon-degrading populations.

Keywords: Metagenomics, hydrocarbon, microbial diversity, soil contamination, bioremediation.

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