

Metagenomic insights into effects of spent engine oil perturbation on the microbial community composition and function in a tropical agricultural soil

[Lateef B. Salam](#), [Sunday O. Obayori](#), [Francisca O. Nwaokorie](#), [Aisha Suleiman](#) & [Raheemat Mustapha](#)

Abstract

Analyzing the microbial community structure and functions become imperative for ecological processes. To understand the impact of spent engine oil (SEO) contamination on microbial community structure of an agricultural soil, soil microcosms designated 1S (agricultural soil) and AB1 (agricultural soil polluted with SEO) were set up. Metagenomic DNA extracted from the soil microcosms and sequenced using Miseq Illumina sequencing were analyzed for their taxonomic and functional properties. Taxonomic profiling of the two microcosms by MG-RAST revealed the dominance of *Actinobacteria* (23.36%) and *Proteobacteria* (52.46%) phyla in 1S and AB1 with preponderance of *Streptomyces* (12.83%) and *Gemmatimonas* (10.20%) in 1S and *Geodermatophilus* (26.24%), *Burkholderia* (15.40%), and *Pseudomonas* (12.72%) in AB1, respectively. Our results showed that soil microbial diversity significantly decreased in AB1. Further assignment of the metagenomic reads to MG-RAST, Cluster of Orthologous Groups (COG) of proteins, Kyoto Encyclopedia of Genes and Genomes (KEGG), GhostKOALA, and NCBI's CDD hits revealed diverse metabolic potentials of the autochthonous microbial community. It also revealed the adaptation of the community to various environmental stressors such as hydrocarbon hydrophobicity, heavy metal toxicity, oxidative stress, nutrient starvation, and C/N/P imbalance. To the best of our knowledge, this is the first study that investigates the effect of SEO perturbation on soil microbial communities through Illumina sequencing. The results indicated that SEO contamination significantly affects soil microbial community structure and functions leading to massive loss of nonhydrocarbon degrading indigenous microbiota and enrichment of hydrocarbonoclastic organisms such as members of *Proteobacteria* and *Actinobacteria*.

Keywords: Spent engine oil ; Agricultural soil ; Soil microcosm ; Illumina sequencing ; Microbial community structure

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