



Impact of spent engine oil contamination on the antibiotic resistome of a tropical agricultural soil

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Abstract

Profiling of hydrocarbon-contaminated soils for antibiotic resistance genes (ARGs) is becoming increasingly important due to emerging realities of their preponderance in hydrocarbon-inundated matrices. In this study, the antibiotic resistome of an agricultural soil (1S) and agricultural soil contaminated with spent engine oil (AB1) were evaluated via functional annotation of the open reading frames (ORFs) of their metagenomes using the comprehensive antibiotic database (CARD) and KEGG KofamKOALA. CARD analysis of AB1 metagenome revealed the detection of 24 AMR (antimicrobial resistance) gene families, 66 ARGs, and the preponderance (69.7%) of ARGs responsible for antibiotic efflux in AB1 metagenome. CARD analysis of 1S metagenome revealed four AMR gene families and five ARGs. Functional annotation of the two metagenomes using KofamKOALA showed 171 ARGs in AB1 and 29 ARGs in 1S, respectively. Majority of the detected ARGs in AB1 (121; 70.8%) and 1S (16; 55.2%) using KofamKOALA are responsible for antibiotic efflux while ARGs for other resistance mechanisms were also detected. All the five major antibiotic efflux pump systems were detected in AB1 metagenome, though majority of the ARGs for antibiotic efflux belong to the RND (resistance-nodulation-cell division) and MFS (major facilitator superfamily) efflux systems. Significant differences observed in the ARGs recovered from 1S and AB1 metagenomes were statistically validated ($P < 0.05$). SEO contamination is believed to be responsible for ARGs increase in AB1 metagenome via mechanisms of cross-resistance especially with efflux pumps. The detection of these ARGs is of great public health concern in this era of multidrug resistant isolates resurgence.

Keywords Spent engine oil · Agricultural soil · Multidrug-resistant efflux pumps · Antibiotic resistance genes · Shotgun metagenomics

Introduction

The soil environment encompasses diverse population of organisms, interacting as members of communities. The balanced interaction of the abiotic and biotic components of

the soil is very crucial to soil health and its ability to provide the spatial interactions and functioning of the biota. Microorganisms, including bacteria, archaea and fungi play by far the most important role in soil health by virtue of their metabolic diversity and versatility, which makes them a major driver of biogeochemical cycling of elements between biotic and abiotic state (Aislabie and Deslippe 2013).

Microbial populations achieve sustainable existence in the soil by their ability to benefit from useful interactions, deploy arsenals of offensive and defensive mechanisms and establish enduring occupancy of their preferred niche. Production of antibiotics and other antimicrobial agents that inhibit the growth and metabolism of other organism is one of the means by which such competitive edges are achieved (Killham and Prosser 2007). However, other populations abound in the soil environment which are not perturbed by such offensive metabolites because of their ability to elicit coping strategies in the form of antibiotic resistance

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