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Opportunistic bacteria dominate the soil microbiome response to phenanthrene in a microcosm-based study
(2018) *Frontiers in Microbiology*, 9 (NOV), art. no. 02815, .

DOI: 10.3389/fmicb.2018.02815

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Abstract

Bioremediation offers a sustainable approach for removal of polycyclic aromatic hydrocarbons (PAHs) from the environment; however, information regarding the microbial communities involved remains limited. In this study, microbial community dynamics and the abundance of the key gene (PAH-RHD α) encoding a ring hydroxylating dioxygenase involved in PAH degradation were examined during degradation of phenanthrene in a podzolic soil from the site of a former timber treatment facility. The 10,000-fold greater abundance of this gene associated with Gram-positive bacteria found in phenanthrene-amended soil compared to unamended soil indicated the likely role of Gram-positive bacteria in PAH degradation. In contrast, the abundance of the Gram-negative PAHs-RHD α gene was very low throughout the experiment. While phenanthrene induced increases in the abundance of a small number of OTUs from the Actinomycetales and Sphingomonadales, most of the remainder of the community remained stable. A single unclassified OTU from the Micrococcaceae family increased ~20-fold in relative abundance, reaching 32% of the total sequences in amended microcosms on day 7 of the experiment. The relative abundance of this same OTU increased 4.5-fold in unamended soils, and a similar pattern was observed for the second most abundant PAH-responsive OTU, classified into the Sphingomonas genus. Furthermore, the relative abundance of both of these OTUs decreased substantially between days 7 and 17 in the phenanthrene-amended and control microcosms. This suggests that their opportunistic phenotype, in addition to likely PAH-degrading ability, was determinant in the vigorous growth of dominant PAH-responsive OTUs following phenanthrene amendment. This study provides new information on the temporal response of soil microbial communities to the presence and degradation of a significant environmental pollutant, and as such has the potential to inform the design of PAH bioremediation protocols. © 2007 - 2018 Frontiers Media S.A.

Author Keywords

Bioremediation; Microbiome; Phenanthrene; Polycyclic aromatic hydrocarbons; Soil

Funding details

2008-PhD-WRM-1

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Publisher: Frontiers Media S.A.

ISSN: 1664302X

Language of Original Document: English

Abbreviated Source Title: Front. Microbiol.
2-s2.0-85057761407

Document Type: Article

Publication Stage: Final

Source: Scopus

Access Type: Open Access