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Benzo(a)pyrene degradation and microbial community responses in composted soil

By: [Zhu, FX](#) (Zhu, Fengxiao)^[1,2]; [Storey, S](#) (Storey, Sean)^[1,2]; [Ashaari, MM](#) (Ashaari, Mardiana Mohd)^[3]; [Clipson, N](#) (Clipson, Nicholas)^[1,2]; [Doyle, E](#) (Doyle, Evelyn)^[1,2]

ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH

Volume: 24 Issue: 6 Pages: 5404-5414

DOI: 10.1007/s11356-016-8251-3

Published: FEB 2017

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Abstract

Benzo(a)pyrene degradation was compared in soil that was either composted, incubated at a constant temperature of 22 degrees C, or incubated under a temperature regime typical of a composting process. After 84 days, significantly more (61%) benzo(a) pyrene was removed from composted soil compared to soils incubated at a constant temperature (29%) or at composting temperatures (46%). Molecular fingerprinting approaches indicated that in composted soils, bacterial community changes were driven by both temperature and organic amendment, while fungal community changes were primarily driven by temperature. Next-generation sequencing data revealed that the bacterial community in composted soil was dominated by Actinobacteria (order Actinomycetales), Firmicutes (class Bacilli), and Proteobacteria (classes Gammaproteobacteria and Alphaproteobacteria), regardless of whether benzo(a) pyrene was present or not. The relative abundance of unclassified Actinomycetales (Actinobacteria) was significantly higher in composted soil when degradation was occurring, indicating a potential role for these organisms in benzo(a) pyrene metabolism. This study provides baseline data for employing straw-based composting strategies for the removal of high molecular weight PAHs from soil and contributes to the knowledge of how microbial communities respond to incubation conditions and pollutant degradation.

Keywords

Author Keywords: [Benzo\(a\)pyrene](#); [Soil](#); [Composting](#); [Bioremediation](#); [Microbial community](#); [PAH](#); [Amplicon sequencing](#)

KeyWords Plus: [POLYCYCLIC AROMATIC-HYDROCARBONS](#); [16S RIBOSOMAL-RNA](#); [CONTAMINATED SOIL](#); [PHENANTHRENE DEGRADATION](#); [BACTERIAL COMMUNITIES](#); [DIVERSITY](#); [BIOREMEDIATION](#); [FUNGAL](#); [BIODEGRADATION](#); [ENVIRONMENTS](#)

Author Information

Reprint Address: Doyle, E (reprint author)

+ Univ Coll Dublin, Sch Biol & Environm Sci, Dublin, Ireland.

Reprint Address: Doyle, E (reprint author)

+ Univ Coll Dublin, Earth Inst, Dublin, Ireland.

Addresses:

+ [1] Univ Coll Dublin, Sch Biol & Environm Sci, Dublin, Ireland

+ [2] Univ Coll Dublin, Earth Inst, Dublin, Ireland

+ [3] Int Islamic Univ Malaysia, Dept Biotechnol Kulliyah Sci, Kuantan, Malaysia

E-mail Addresses: evelyn.doyle@ucd.ie

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Funding

Funding Agency	Grant Number
UCD China Scholarship Scheme	
SLAB scholarship program of the Malaysian Ministry of Higher Education	
International Islamic University Malaysia	
Ireland Wales Programme	

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Publisher

SPRINGER HEIDELBERG, TIERGARTENSTRASSE 17, D-69121 HEIDELBERG, GERMANY

Categories / Classification

Research Areas: Environmental Sciences & Ecology

Web of Science Categories: Environmental Sciences

Document Information

Document Type: Article

Language: English

Accession Number: WOS:000397013000031

PubMed ID: 28025788

ISSN: 0944-1344

eISSN: 1614-7499

Journal Information

Impact Factor: [Journal Citation Reports](#)

Other Information

IDS Number: EO9MO

Cited References in Web of Science Core Collection: **63**

Times Cited in Web of Science Core Collection: **0**