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Chapter

Microbial Remediation Approaches for PAH Degradation

May 2022
DOI: 10.1002/9781119827665.ch8
In book: Sustainable Solutions for Environmental Pollution

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Abstract

Polycyclic aromatic hydrocarbons (PAHs) are ubiquitous pollutants that are harmful products of incomplete combustion of organic matter. PAH and their derivatives possess toxic, carcinogenic, and mutagenic effects in nearly all living organisms, which are further enhanced due to bioaccumulation and biomagnification. Thus, their detrimental effects generated the need for their mitigation in a sustainable manner. Among various remediation strategies, microbial remediation is increasingly gaining interest as economically justified and effective cleanup approach, because many microbial species use PAH as their energy source. These microbes possess various PAH degrading genes such as ndoB, nidA, pdoB, nahAc, and cytochrome P450, which also make them perfect tools for genetic engineering. Bacterial species such as Pseudomonas, Comamonas, Mycobacterium, Rhodococcus, and Sphingomonas may aerobically or anaerobically use various metabolic pathways to degrade PAH. Both ligninolytic and non-ligninolytic fungi are well known for either co-metabolizing or completely metabolizing PAH. Moreover, some algal and microalgal species such as Scenedesmus acutus, Selanastum capricornutum, and Ankistrodesmus braunii have the ability to either transform or co-metabolize PAH. Microbial remediation depends on various factors such as microbial activity, bioavailability of PAH, and environmental factors such as