

能源和环境工程

焦化厂污染土壤中多环芳烃降解菌群解析

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收稿日期 2009-7-24 修回日期 2009-9-29 网络版发布日期 2010-3-2 接受日期

摘要

以苯并[a]芘、苯并[a]蒽、苯并[b]荧蒽、苯并[k]荧蒽、茚并[1,2,3-cd]芘5种较难降解的多环芳烃为碳源和能源,采用富集培养的方法从焦化厂污染的土壤中筛选分离得到50株PAHs降解菌。通过对其16S rRNA基因序列分析,将这些PAHs降解菌分为15个种群,分别属于Sphingomonas(鞘氨醇单胞菌属)、Methylobacterium(甲基杆菌属)、Burkholderia(伯克霍尔德氏菌属)、Rhodococcus(红球菌属)、Bradyrhizobium(慢生根瘤菌属)、Phyllobacterium(叶杆菌属)、Chryseobacterium(金黄杆菌属)、Microbacterium(微杆菌属)8个属,其中优势菌为鞘氨醇单胞菌属。纯菌株降解能力测试表明,培养12 d后,菌株3-6-12降解效果要优于其他菌株,对苯并[a]蒽、苯并[a]芘、苯并[b]荧蒽、苯并[k]荧蒽、茚并[1,2,3-cd]芘的降解率分别可达39.64%、33.52%、38.57%、25.37%、31.17%。实验结果可为多环芳烃污染土壤的生物修复提供高效的降解菌源。

关键词

[多环芳烃](#) [菌株筛选](#) [16S rRNA基因](#) [生物降解](#)

分类号

Analysis of PAHs-degrading bacteria from contaminated soil at a coking plant

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Abstract

Microbes play an important role in bioremediation technologies,the aim of this article was to investigate functional strains for soil bio-remediation.In this study benzo [a] pyrene(BaP),benzo [a] anthracene(BaA),benzo [b] fluoranthene (BbF),benzo [k] fluoranthene(BkF),indeno [1,2,3-cd] pyrene(IPY) were used as carbon and energy sources and 50 strains were isolated by steps including enrichment culture and plate cultivation from the contaminated soil at a coking plant in Beijing.The result of 16S rRNA gene sequencing analysis revealed that these strains were clustered into 15 groups and belonged to genera Sphingomonas, Methylobacterium, Burkholderia, Rhodococcus, Bradyrhizobium, Phyllobacterium, Chryseobacterium, Microbacterium, of which Sphingomonas was the dominant species.The highest degradation rates of BaA, BaP, BbF, BkF, IPY were 39.64%, 33.52%, 38.57%, 25.37% and 31.17% respectively when tested with strain 3-6-12.The experimental results will be useful for bioremediation of PAHs-contaminated soil.

Key words

[PAHs](#) [strain screening](#) [16S rRNA gene](#) [biodegradation](#)

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