Efficient PAHs biodegradation by a bacterial consortium at flask and bioreactor scale

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HIGHLIGHTS

▶ *Bacillus pumilus* and *Staphylococcus warneri* are efficient PAHs biodegraders.
▶ Operation in stirred tank bioreactor led to 100% of PHE, PYR and BaA removal.
▶ Metabolic route to degrade PHE, PYR and BaA was elucidated.
▶ Logistic and Luedeking and Piret equations were used to suitably model the process.

ARTICLE INFO

ABSTRACT

In this work, the biodegradation of three polycyclic aromatic hydrocarbons (PAHs) such as Phenanthrene (PHE), Pyrene (PYR) and Benzo[a]anthracene (BaA) has been investigated. A bacterial consortium consisting of two strains was used for the first time based on preliminary promising biodegradation data. They were tentatively identified as *Staphylococcus warneri* and *Bacillus pumilus*. Degradation values higher than 85% were obtained for each single PAH when operating at flask scale, whereas minimum levels of 90% of PAHs removal were obtained after just 3 days of cultivation at bioreactor scale. The operation in cometabolic conditions led to maximum levels about 75% and 100% at flask and bioreactor scale, respectively. All the experimental data were analyzed in the light of logistic and Luedeking and Piret type models, with the purpose to better characterize the biodegradation process by *S. warneri* and *B. pumilus*. Finally, the metabolic pathway followed to degrade each PAH was ascertained.

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1. Introduction

Contamination by polycyclic aromatic hydrocarbons (PAHs) is a global concern in the limelight, due to their negative health and environmental consequences, such as their persistence, their known toxic effects and mutagenic and carcinogenic properties (Cao et al., 2009). Hitherto, one of the most promising technologies to remove and clean up PAHs from natural environments is bioremediation, which can be defined as an environmentally safe technology that seeks the attenuation or transformation of polluting compounds by the use of microbial communities (yeast, fungi or bacteria) (Lebkowska et al., 2011).

Although PAHs are recalcitrant hydrophobic compounds with poor solubility in water, which limits their availability to microorganisms, literature data indicates that a large number of bacteria capable of degrading a wide range of PAHs have been isolated from contaminated sites (Mrozik, 2003; Zhong et al., 2011; Janbandhu and Fulekar, 2011) and they belong to different genera such as

Burkholderia, *Pseudomonas*, *Rhodococcus* and *Sphingomonas* among others (Moscoso et al., 2012a).

Some recent studies have converged upon the idea that increased biodegradation efficiency can be reached when a mixed bacterial culture is used (Mrozik, 2003; Zhong et al., 2011; Janbandhu and Fulekar, 2011). Grounded on this fact, metabolic cooperation is gaining further momentum to explain an enhanced PAHs assimilation, since metabolic intermediates produced by some microorganisms can act as substrates for others. Following this trend, Janbandhu and Fulekar (2011) reported that the use of a single strain is a proper approach to understand bioprocess performance but does not reflect at all the situation that take place during a real bioremediation case in natural environments, where it is almost impossible that a pure strain can exist alone. Moreover, as reported Chávez et al. (2004), PAHs are usually present in the environment as a mixture of several aromatic compounds, thus standing for more difficulties in biodegradation by microorganisms. In this situation, each PAH has the capacity to influence the others, affecting their biodegradation rate. Although PAHs are typically found in soils and sediments due to their physical properties such as high hydrophobicity, several remediation methods like soil washing or electrokinetic treatment lead the contaminants from

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