Bioresource Technology 124 (2012) 129-136

Contents lists available at SciVerse ScienceDirect

Bioresource Technology

journal homepage: www.elsevier.com/locate/biortech

Biodegradation of benzene homologues in contaminated sediment of the East China Sea

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HIGHLIGHTS

- ► To enrich moderately halophilic to degrade BTEX in a wide range of salinity.
- ► The optimal degradation was 120 mg/L toluene within 5 d in the presence of 2 M NaCl.
- ▶ Marinobacter, Prolixibacter, Balneola, Zunongwangia, Halobacillus were the dominant genus.
- ▶ Ring fission was catalysed by catechol 1,2-dioxygenase and catechol 2,3-dioxygenase.
- ▶ Bacteria adjusted osmotic pressure by ectoine and hydroxyectoine as compatible solutes.

ARTICLE INFO

Article history: Received 13 May 2012 Received in revised form 8 August 2012 Accepted 10 August 2012 Available online 24 August 2012

Keywords: BTEX Biodegradation Bacterial community Metabolic pathway Compatible solutes

ABSTRACT

This study focused on acclimating a microbial enrichment to biodegrade benzene, toluene, ethylbenzene and xylenes (BTEX) in a wide range of salinity. The enrichment degraded 120 mg/L toluene within 5 d in the presence of 2 M NaCl or 150 mg/L toluene within 7 d in the presence of 1–1.5 M NaCl. PCR–DGGE (polymerase chain reaction–denatured gradient gel electrophoresis) profiles demonstrated the dominant species in the enrichments distributed between five main phyla: Gammaproteobacteria, Sphingobacteriia, Prolixibacter, Flavobacteriia and Firmicutes. The *Marinobacter*, *Prolixibacter*, *Balneola*, *Zunongwangia*, *Halobacillus* were the dominant genus. PCR detection of genotypes involved in bacterial BETX degradation revealed that the degradation pathways contained all the known initial oxidative attack of BTEX by monooxygenase and dioxygenase. And the subsequent ring fission was catalysed by catechol 1,2-dioxy-genase and catechol 2,3-dioxygenase. Nuclear magnetic resonance (NMR) spectroscopy profiles showed that the bacterial consortium adjusted the osmotic pressure by ectoine and hydroxyectoine as compatible solutes to acclimate the different salinity conditions.

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1. Introduction

BTEX contaminants have been widely detected at numerous chemical industrial facilities and oil basin, especially nearby the petroleum and related products manufacture area. As neurotoxicants BTEX was able to cause abnormality, sudden change and cancer, like leukemia (Smith et al., 2007). Recently, microbial bioremediation has been the most popular removal method which

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is environment friendly (Eldon et al., 2012). Lots of BTEX-degrading bacteria were isolated in the past few years, such as *Moraxella* sp. (Hogx and Jaenicee, 1972), *Nocarida* sp., *Alcaligenes denitrificans*, *Micrococcs* sp., *Arthrobacter* sp. (Weber and Corseuil, 1994), *Thermus* sp. (Chen and Taylor, 1997), *Rhodococcus rhodochrous* (Deeb and Alvarez-Cohen, 1999) and *Pseudomonas* spp. which were the most commonly reported bacteria to degrade BTEX compounds (Brusa et al., 2001). However, the bioremediation of the BETX contamination often met a bottleneck when the pollution occurred in the high salinity environment, because the degrading bacteria normally were not suit to the high salinity condition. Numerous oil seeps and abandoned drilling fluids from petroleum exploring procedure make serious BTEX contamination in saline-alkali soil and sea water. Industrial water also contains high salinity and BTEX,



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