Optimization of a bacterial consortium for nitrobenzene degradation

IDENTIFICATION OF THE STRAINS

The colony morphology of the isolated strains was observed on agar plates after being cultured at 30 °C for 2 d. The cell morphology of the strains was examined under an optical microscope (×1,600 magnification). The physiological and biochemical characteristics were examined by using microbiochemical tubes and drug sensitivity test papers (Hangzhou Tianhe Microorganism Reagent Co. Ltd, Zhejiang, China). Oxidase, hydrolase and decarboxylase activities, antibiotic sensitivity, utilization of sundry carbon and nitrogen were investigated. The utilization of some substrates as carbon sources and nitrogen sources by the isolates were performed based on Bergey's Manual of Determinative Bacteriology, ninth edition.

The 16S rDNAs of these strains were amplified by using primers 27F (5′-GAGTTGTACMTGGCTCAG-3′) and 1492R (5′-TACGGYTACCTGTTACGACTT-3′) (Gurtler & Stanisich 1996). Polymerase Chain reaction (PCR) was conducted with the cycling regime as follows: 94 °C for 3 min, 30 cycles of 94 °C for 30 s, 54 °C for 30 s, 72 °C for 90 s, and a final extension at 72 °C for 5 min. The obtained 16S rDNA sequences were compared with the sequences in GenBank using the BLAST program.

REFERENCE


doi: 10.2166/wst.2012.692Supplement