PHYSIOLOGICAL, PHYLOGENETIC AND FUNCTIONAL IDENTIFICATION OF CRUDE OIL-DEGRADING MICROBIAL POPULATIONS

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Abstract

In this study, nine microbial strains with oil-degrading function were isolated from oil-contaminated soil near four oil wells in the 0.6 km² area of the Jinnan Oil Field, Huai’an, Jiangsu, China (32°57’ N, 119°02’ E). Based on morphological observations, physiological and biochemical responses, and molecular identification, we confirmed that the nine strains belong to five genera: Pseudomonas, Raoultella, Lysinibacillus, Escherichia, and Klebsiella. The degradation capacity of the nine strains in crude oil medium ranged from 2.43% to 32.63% with an average rate of 21.64%. Further plasmid and chromosome analyses on the oil-degrading genes of the nine microbial strains were conducted. The GST gene (degradable polycyclic aromatics) was widely distributed in the chromosomes of eight strains and the plasmids of three strains. The alkB gene was detected in the chromosomes of seven strains and the plasmids of two strains. The LmPH gene (degradable phenolic substances) was only detected in the chromosome of one strain. Molecular biological analyses on the isolation, identification, and degradation characteristics of oil-degrading microbial strains provide a foundation for microbial remediation in oil-polluted environments.

Key words: biodegradation, functional gene analysis, molecular identification, oil pollution

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