



“Gheorghe Asachi” Technical University of Iasi, Romania



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

Yujia Liu¹, Yuan Zhao¹, Muwang Li³, Zhibao Zhu¹, Yuting Liang²*

¹*School of Environmental & Safety Engineering, Changzhou University, Changzhou 213164, China*

²*State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science,
Chinese Academy of Sciences, Nanjing 210008, China*

³*The Sericultural Research Institute, Chinese Academy of Agricultural Sciences, Zhenjiang 212018, China*

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, Huaian, 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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*Author to whom all correspondence should be addressed: e-mail: ytliang@issas.ac.cn; Phone: +86-25-86881534; Fax: +86-25-86881000