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Identification and Characterization of Oil-Degrading Bacteria from Crude Oil-Contaminated Desert Soil in Northeastern Jordan

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Abstract : Bioremediation aspects of crude oil-polluted fields can be achieved by isolation and identification of bacterial species from oil-contaminated soil in order to choose the most active isolates and increase the strength of others. In this study, oil-degrading bacteria were isolated and identified from oil-contaminated soil samples in northeastern Jordan. The bacterial growth count (CFU/g) was between 1.06×10^5 and 0.75×10^9. Eighty-two bacterial isolates were characterized by their morphology and biochemical tests. The identified bacterial genera included: Klebsiella, Staphylococcus, Citrobacter, Lactobacillus, Alcaligenes, Pseudomonas, Hafnia, Micrococcus, Rhodococcus, Serratia, Enterobacter, Bacillus, Salmonella, Mycobacterium, Corynebacterium, and Acetobacter. Molecular identification of a universal primer 16S rDNA gene was used to identify four bacterial isolates: Microbacterium esteraromaticum strain L20, Pseudomonas stutzeri strain 13636M, Klebsilla pneumoniae, and uncultured Klebsilla sp., known as new strains. Our results indicate that their specific oil-degrading bacteria isolates might have a high strength of oil degradation from oil-contaminated sites. Staphylococcus intermedius (75%), Corynebacterium xerosis (75%), and Pseudomonas fluorescens (50%) showed a high growth rate on different types of hydrocarbons, such as crude oil, toluene, naphthalene, and hexane. In addition, monooxygenase and catechol 2,3-dioxygenase were detected in 17 bacterial isolates, indicating their superior hydrocarbon degradation potential. Total petroleum hydrocarbons were analyzed using gas chromatography for soil samples. Soil samples M5, M7, and M8 showed the highest levels (43,645, 47,805, and 45,991 ppm, respectively), and M4 had the lowest level (7,514 ppm). All soil samples were analyzed for heavy metal contamination (Cu, Cd, Mn, Zn, and Pb). Site M7 contains the highest levels of Cu, Mn, and Pb, while Site M8 contains the highest levels of Mn and Zn. In the future, these isolates of bacteria can be used for the cleanup of oil-contaminated soil.

Keywords : bioremediation, 16S rDNA gene, oil-degrading bacteria, hydrocarbons
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