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HYDROCARBONOCLASTIC BACTERIA ISOLATED FROM PETROLEUM CONTAMINATED SITES IN TUNISIA: ISOLATION, IDENTIFICATION AND CHARACTERIZATION OF THE BIOTECHNOLOGICAL POTENTIAL

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Abstract

Petroleum hydrocarbons are important energy resources used by industry and in our daily life, whose production contributes highly to environmental pollution. In order to control this environmental risk, bioremediation constitute an environmentally friendly alternative technology that has been established and applied. Bioremediation constitute the primary mechanism for the elimination of hydrocarbons from contaminated sites by natural existing populations of microorganisms.

In this work, a collection of 125 strains, adapted to grow in minimal medium supplemented with crude oil (as sole carbon source), was obtained from contaminated sediments and seawater from the Bizerte lagoon, a highly urbanized and industrialized water plan, subjected to various pollutants located in the North of Tunisia. The diversity of this collection was analyzed by amplification of the internal transcribed spacers between the 16S and the 23S rRNA genes (ITS-PCR) and by 16S rRNA sequencing. A total of 36 distinct ITS haplotypes were detected on agarose matrix. Partial 16S rRNA gene sequencing performed on 50 isolates showed high level of identity with known sequences. Strains were affiliated to *Ochrabactrum*, *Sphingobium*, *Acinetobacter*, *Gordonia*, *Microbacterium*, *Brevundimonas*, *Novosphingobium*, *Stenotrophomonas* and *Pseudomonas* genera. *Acinetobacter* and *Stenotrophomons* were found the most abundant species and showed an important microdiversity by ITS typing. Culture independent approach (DGGE) showed high diversity in the microbial community in all the studied samples.

The biotechnological potential of different isolates revealed a significant production of biosurfactants with important emulsification activities useful in bioremediation. The highest emulsification activity was detected in *Pseudomoans geniculata* with 52.77% of emulsification. Our overall results suggest that the obtained bacterial isolates may constitute future candidates for bioremediation and can be useful for biotechnological applications.