

Original Article

Molecular Identification of Oil-Utilizing Bacteria Isolated From Oil Contaminated Soils in Basrah City

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Abstract

The main objective of this study was to isolate and identify native hydrocarbon-utilizing bacteria from oil-contaminated soils and to investigate their genetic relatedness. Mineral salt medium broth was used as an enrichment medium supplemented with crude oil as the sole source of carbon to isolate the requested microorganisms. Fifteen isolates have been discovered based on biochemical and molecular criteria. Due to its conservative over generations, 16S rRNA was used for molecular identification. The identified genera were as *Acintobacter radioresistens*, *Pseudomonas aeruginosa*, *Pseudomonas oryzihabitans*, *Enterobacter* sp., *Klebsiella* sp., *Aeromonas* sp., *pseudomonas putida*, *Pseudomonas guariconensis*, *Achromobacter xylosoxidans*, *Staphylococcus* sp., *Bacillus thuringiensis*, *Bacillus* sp., *Bacillus cereus*, *Pseudomonas stutzeri*, and *Exiguobacterium* sp.. All obtained sequences were having Expected (E) value 0.0, indicating the matches were meaningful.

Keywords: Molecular Identification, Oil Utilizing Bacteria, Soil

1. Introduction

Even though crude oil is the most significant source of energy in the world, the frequent drilling, extraction, transporting, storing, refining of this fossil fuel seriously harm the environment (Akpe et al., 2015, Hamoudi-Belarbi et al., 2018). Crude oil comprises a wide range of compounds that pose a significant threat to the environment and human health, as well as having cytotoxic, mutagenic, and carcinogenic effects on cells and tissues (Ramirez et al., 2017). Petroleum hydrocarbon biodegradation could be accomplished using a variety of microorganisms like bacteria, fungi, yeast and microalgae. However, bacteria are key microorganisms that play an important role in hydrocarbon breakdown (Al-Dhabaan, 2019). As a result, research is being conducted to identify microbes with catabolic potential to digest these contaminants (Chaillan et al., 2004). Microorganisms make a wide range of metabolic enzymes that can be used to get rid of harmful substances in the environment in a safe way. This can be accomplished either by direct destruction of the chemical or by transformation of the contaminants into a safer or less toxic intermediate product or by a combination of both (Dash and Das, 2012). Bacteria play a major role in oil biodegradation. The use of bacteria for biodegradation of numerous natural and industrial compounds, and thereby lowering the degree of risks, is gaining popularity (Karigar and Rao, 2011). Bacteria have a wide range of bioremediation potentials that are advantageous. Most of petroleum hydrocarbons present in the environment are finally decomposed or metabolized by native bacteria because of their vitality and carbon needs for growth and reproduction coupled with the requirement to reduce physiological stress caused by the presence of hydrocarbons (Xu et al., 2018a). Traditional methods to identify bacteria, such as biochemical tests and phenotypic classification methods, are no longer sufficient, requiring the employment of molecular techniques that are rapid and more precise. The current study comprises molecular identification of oil-degrading bacteria isolated from oil contaminated soils as well as the creation of a Phylogenetic tree to demonstrate the scope of their biodiversity and the evolutionary relationship between them.

Because it is highly conserved amongst bacteria and archaea species, the 16S rRNA gene is employed for phylogenetic investigations. For a variety of reasons, the use of 16S rRNA gene sequences to investigate bacterial phylogeny and taxonomy has been by far the most prevalent housekeeping genetic marker used. The 16S rRNA gene is amplified using universal PCR primers to yield phylogenetic data (Azizan et al., 2018). Mineral salt medium was used as enrichment media for isolating of oil degrading bacteria from oil polluted soils. Branching tree-like diagrams generated by phylogenetic analysis are used to show the inherited associations among molecules, organisms, or both. Evolutionary phylogenetic trees are a visual representation of how families have evolved over time

This study was carried out to identify the indigenous oil degrading bacteria at some polluted soils in Basra city. The biodiversity of oil-degrading bacteria changes dramatically over time due to anthropogenic activities related to oil production.

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