



Marine Science Center-University of Basrah

Mesopotamian Journal of Marine Sciences

Print ISSN: 2073-6428

E- ISSN: 2708-6097

[www.mjms.uobasrah.edu.iq/index.php/mjms](http://www.mjms.uobasrah.edu.iq/index.php/mjms)



## New GeneBank records of oil degrading bacteria isolated from polluted soil

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### Article info.

- ✓ Received: 4 October 2022
- ✓ Accepted: 1 November 2022
- ✓ Published: 29 December 2022

### Key Words:

Oil degrading bacteria,  
Polluted soil,  
New records,  
Local strains

**Abstract** -This work aim at isolation and identification of the dominant bacteria present in the oil polluted soil, as well as deposited the new isolates in the GeneBank. Some chemical parameters of contaminated soil were measured. Ten isolates were identified and characterized depending on the biochemical tests, as well as genetic characteristics using 16S rRNA gene comparing with reference isolates in the GeneBank, and through the detection of base pair sequence variations. These new local isolates were deposited in a GenBank under a new accession numbers; (OK576381.1, OK662612, OK662613, OK662614, OK662615, OK662616, OK662617, OK662618, OK662619, OK662620). Mineral salts medium (MSM) broth supported with crude oil as only source of carbon was adopted to isolate the bacteria. Culture media were supported with the same chemical parameters as the soil samples in order to simulate the physiochemical criteria of the environment. The successfully identified and recorded genera related to the above accession numbers were; *Pseudomonas aeruginosa*, *Acinetobacter radioresistens*, *Pseudomonas oryzihabitans*, *Aeromonas hydrophila*, *Pseudomonas putida*, *Micrococcus luteus*, *Pseudomonas guariconensis*, *Achromobacter xylosoxidans*, *Bacillus foraminis*, *Pseudomonas stutzeri*.

### تسجيل جديد في بنك الجينات لبكتيريا مكسرة للنفط معزولة من تربة ملوثة

فاصل نعمة الكنعان، ستار عزيز غميس، رعد شبر جعفر، عمر عبدالامير البدران

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**المستخلص** - يهدف هذا العمل إلى عزل وتشخيص البكتيريا السائدة الموجودة في التربة الملوثة بالنفط، وكذلك تسجيل العزلات الجديدة في بنك الجينات. تم قياس بعض المتغيرات الكيميائية للتربة الملوثة، وتم تحديد وتشخيص 10 عزلات اعتماداً على الاختبارات البيوكيميائية، وكذلك الخصائص الوراثية باستخدام rRNA 16S. بعد مقارنتها بالعزلات المسجلة في بنك الجينات، ومن خلال الكشف عن الاختلافات في تنابعات القواعد النتروجينية، تم تسجيل هذه العزلات المحلية الجديدة في بنك الجينات تحت أرقام انضمام جديدة؛ (OK576381.1، OK662612، OK662613، OK662614، OK662615، OK662616، OK662617، OK662618، OK662619، OK662620). تم اعتماد مرق وسط أملاح معدنية (MSM) المدعم بالنفط الخام كمصدر وحيد للكربون لعزل البكتيريا. تم دعم الاوساط الزرعية بنفس المعلمات الكيميائية كما موجود في عينات التربة من أجل محاكاة المعايير الفيزيوكيميائية للبيئة. الأجناس التي تم تشخيصها وتسجيلها بنجاح والعائدة لارقام الانضمام المذكورة أعلاه كانت؛

*Pseudomonas aeruginosa*, *Acinetobacter radioresistens*, *Pseudomonas oryzihabitans*, *Aeromonas hydrophila*, *Pseudomonas putida*, *Micrococcus luteus*, *Pseudomonas guariconensis*, *Achromobacter xylosoxidans*, *Bacillus foraminis*, *Pseudomonas stutzeri*.

**الكلمات المفتاحية:** البكتيريا المكسرة للنفط، التربة الملوثة، تسجيل جديد، عزلات محلية.

## Introduction

Basrah city is the center of major oil companies operations in Iraq. (Republic of Iraq, 2016). Crude oil has properties that make it a substantial and effective pollutant of the ecosystem, causing severe harm to humanity. Chemical, physical, and biological treatments have all been employed to treat oil spills, but bioremediation is the most important of them (Yavari *et al.*, 2015). In oil-

contaminated soils, bacteria play an important role in environmental and biodegradable function processes (Peng *et al.*, 2015). Petroleum components are released into the environment on a regular basis as a result of petroleum exploration, accidents, transportation, and leakage from waste disposal or storage sites, as well as from industrial sites (Ghoreishi *et al.*, 2017). Petroleum can harm plants, animals, and humans since it includes hazardous compounds like benzene, toluene, ethyl benzene, xylene, and naphthalene (Sarkar *et al.*, 2005). Petroleum (crude) oil is made up of a complex mixture of thousands of compounds. Petroleum hydrocarbons make up 50–98% of crude oil, making them a significant component depending on the source of the oil. Petroleum hydrocarbons could be biodegraded using a variety of microbes. Bacteria, on the other hand, are key biodegradable microorganisms that play an important role in hydrocarbon decomposition (Udgire *et al.*, 2015). By far the most commonly housekeeping genetic marker has been the use of 16S rRNA gene sequences to investigate bacterial phylogeny and taxonomy. Universal PCR primers were employed to amplify the 16s rRNA gene, which is useful to diagnose bacterial species. The development of tools for analyzing the 16S rRNA gene sequence in a natural sample has gradually improved our ability to discover and identify bacteria (Azizan *et al.*, 2018). The microbial population in the oil-contaminated environment of Basrah is predicted to change day by day as a result of extensive human activities related to the oil industry. The identification of bacterial strains reported in petroleum-contaminated locations will aid in understanding the dynamics of bacterial communities in oil-contaminated soils and provide helpful and necessary information for future petroleum-contaminated soil bioremediation efforts (Zhang *et al.*, 2010). However, there are many more unknown petroleum-degrading bacteria in the environment than recognized isolates (Nie *et al.*, 2014). Isolation of various bacteria from petroleum-contaminated soils has been accomplished utilizing culture-independent methods based on 16S rRNA genes (Jiao *et al.*, 2016). The current study aimed to isolate oil-degrading bacteria from long-term polluted soils near oil companies in Basrah city, identifying and documenting of the new isolates in a GeneBank, and finally evaluate the distribution of new adapted bacteria due to prolonged oil waste exposure.

## Materials and Methods

### Soil sample collection

As shown in Table (1) and Figure (1), 250 gm of soil samples (15cm depth) were collected from six various oil-contaminated locations, all these sites were located in the west of Al- Qurna town, Basrah city, South of Iraq. The samples were collected in sterile plastic bags and brought to the laboratory, where they were maintained at laboratory temperature while the pH and salinity of the soil samples were evaluated.

Table 1: Coordination of the sampling stations

No.	Latitude	Longitude
1	30°45'01.29"N	47°19'35.93"E
2	30°48'49.43"N	47°19'30.73"E
3	30°48'46.99"N	47°22'14.13"E
4	30°49'17.04"N	47°19'31.78"E
5	30°52'16.97"N	47°20'06.56"E
6	30°52'40.86"N	47°19'38.22"E



Figure 1: Sampling stations (west of Al- Qurna town, Basrah city, South of Iraq)

#### Isolation of Bacteria

One gram of polluted soil was diluted to  $10^{-4}$  with sterile D.W, grown in a 250 ml conical flask with 100 ml of mineral salts medium (MSM) consisting of (g/l): KCl (0.3),  $K_2HPO_4$ (1.03),  $KH_2PO_4$ (0.53),  $FeSO_4 \cdot 7H_2O$  (0.013), NaCl(1.5),  $MnSO_4 \cdot 7H_2O$ (0.53) and  $CaCl_2$ (0.23).

One hundred microliters of sterilized crude oil served as a sole carbon source (provided by Majnoon oil field) and trace elements stock solution of  $FeCl_3 \cdot 6H_2O$  (0.08 g/L),  $ZnSO_4 \cdot H_2O$  (0.75 g/L),  $COCl_2 \cdot 6H_2O$  (0.08 g/L),  $CuSO_4 \cdot 5H_2O$  (0.075 g/L),  $MgSO_4 \cdot H_2O$  (0.75 g/L),  $H_3BO_3$  (0.15 g/L) and 2ml of  $Na_2MoO_4 \cdot 2H_2O$  (0.05 g/L) were added. In a shaker incubator, they incubated for 7 days at  $30^\circ C$  with shaking at 150 rpm(Fujisawa and Murakami, 1980). The pH of the medium was set at the beginning while the salinity was set at 1.4mg/l. After the incubation period, one ml of the growth culture was diluted with normal saline to a concentration of  $10^{-3}$ , and grown on a nutrient agar medium for 24 hours at  $30^\circ C$ . Then single colonies were selected from the agar to get pure colonies for the following steps.

#### Identification, biochemical characterisation, and molecular criteria

Pure bacterial colonies were cultured for 24 hours, morphological and biochemical criteria were carried out to identify the studied bacteria these include; Gram's staining, cell shape, catalase test, and oxidase test. The DNA was extracted and purified according to the instructions provided by the company (Qiagen/USA). Polymerase chain reaction (PCR) was used to amplify 1450 bp segment of the bacterial 16S rRNA gene using a universal 16S rRNA primers 27F-5'AGAGTTTGATCCTGGCTCAG3', 1492R-5'GGTTACCTTGTTACGACTT3' (Miyoshi *et al.*, 2005), 2µl of pure DNA (50 ng/l), 3µl from each forward and reverse primers (62.5 mol/l), 25 µl Bioneer master mix (Bioneer, Korea) and deionized H<sub>2</sub>O were added to bring the total volume to 50 µl.

Thermocycler (3Prime, UK ) with the following thermal profile; a gene amplification was used to incubate reaction through an initial denaturation at  $96^\circ C$  for 3 min. , followed by 27 cycles of amplification, denaturation at  $96^\circ C$  for 30 s, primer annealing at  $56^\circ C$  for 25 sec., primer extension was at  $72^\circ C$  for 15 sec. and finally at  $72^\circ C$  for 10 min. (Miyoshi *et al.*, 2005). The PCR amplification result was evaluated using a 1.0 % agarose gel and a 100 bp DNA ladder using 1X

TBE buffer for 40 minutes at 120mA and 65V, gel was stained with ethidium bromide solution (0.5 µg/ml) for 20 minutes (Au - Lee *et al.*, 2012). A computerized UV transilluminator was used to observe the amplified nucleic acid (SYNGENE-GBOX F3, UK).

The NCBI web site was performed to analyse the degree of similarity between the PCR products and the sequences of other genes via data base queries (National Centre for Biotechnology Information, 2020) .

## Results and Discussion

### Physiochemical parameters

The pH and salinity of the collected samples were measured and listed in Table (2). Salinity and pH of the collected soil samples were identified to simulate environmental characteristics that are reliant on culture media formulation. Samples of soil were collected from various polluted sites with diverse crude oil materials to obtain different bacterial types. Because the enzyme systems found in oil degrading bacteria differ with different available substrates, the diversity of soil contaminated sources leads to the diversity of different bacterial species. Mineral salts and trace elements were primarily used to make MSM media. Only oil degrading bacteria can grow in this media since crude oil is the only source of energy, which could be due to a lack of necessary enzymes to utilise this medium and benefit from hydrocarbons.

Table 2: pH and salinity of the soil samples

Sampling sites	pH	Salinity (ppt)
1	8.2	1.2
2	8.4	1.3
3	8.2	1.6
4	8.2	1.4
5	8.1	1.6
6	8.3	1.4

### Morphological and biochemical criteria

Some morphological and biochemical characteristics of bacteria isolated from polluted soils must be determined prior to genetic identification. Table (3) depicts morphological and biochemical tests of studied bacteria to complete the subsequent genetic identification.

Table 3: Morphological and biochemical test results

Codes of purified bacterium	Gram's stain	Cell shape	Catalase test	Oxidase test
1	-ve	Coccobacillus	+	-
2	-ve	Rod	+	-
3	-ve	Rod	+	+
4	-ve	Rod	+	+
5	+ve	Coccus	+	+
6	-ve	Rod	+	+
7	-ve	Rod	+	+
8	-ve	Rod	+	+
9	-ve	Rod	+	-
10	-ve	Rod	+	+

### Analysis and recording of DNA Sequences

Fifteen PCR products of targeted gene were sent to the MACROGEN/Korea “<http://dna.macrogen.com>” to get the gene sequencing. Using the Geneious Prime 2019 software version 1.1 (<https://www.geneious.com>). The raw sequences were visually reviewed and edited. The sequences were analysed by searching the National Center for Biotechnology Information Database (NCBI) for a similar sequence using the basic local alignment search tool (BLAST) (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

The microbial population in these locations were the most diversified than expected, based on these overview data. *Pseudomonas* spp. is clearly the most dominant bacteria among the isolates (50 %), which may be owing to its own unique enzymes and metabolic pathways required to breakdown crude oil components (Das and Chandran, 2011). Furthermore, it is widely recognized that *pseudomonas* is one of the bacteria with a high hydrocarbon remediation potential (Stamenov *et al.*, 2015). The bacteria isolated in this study were suspected hydrocarbon tolerance and can grow in MSM medium containing 1% crude oil. Ten bacterial species were isolated, characterized, and deposited in a GenBank under a new accession numbers (Table 4).

Table (4): The identification results of 10 isolates of oil degrading bacteria by 16S rRNA sequences.

Sample no.	Bacterial type	Accession numbers (Submission from current study)
1	<i>Acinetobacter radioresistens</i> strain FadSat-1	OK662612
2	<i>Pseudomonas oryzihabitans</i> strain FadSat-5	OK662613
3	<i>Aeromonas hydrophila</i> strain FadSat-10	OK662614
4	<i>Pseudomonas putida</i> strain FadSat-12	OK662615
5	<i>Micrococcus luteus</i> strain FadSat-4A	OK662616
6	<i>Pseudomonas aeruginosa</i> strain alkanany	OK576381
7	<i>Pseudomonas guariconensis</i> strain FadSat-14	OK662617
8	<i>Achromobacter xylosoxidans</i> strain FadSat-19	OK662618
9	<i>Mesobacillus foraminis</i> strain FadSat-26	OK662619
10	<i>Pseudomonas stutzeri</i> strain FadSat-32	OK662620

Generally, the discovery of prominent bacterial communities in oil-contaminated soils in Al-Basrah environment supports in work of biological treatments at a low cost using green technology.

### Acknowledgments

We would like to express our gratitude to the scientists at the Marine Bacteriology Laboratory, marine Science centre for their assistance during the work; also we would like to thank those who helped in sampling.

### References

Au - Lee, P. Y.; Au - Costumbrado, J.; Au - Hsu, C.-Y. and Au - Kim, Y. H. 2012. Agarose Gel Electrophoresis for the Separation of DNA Fragments. JoVE: e3923. <https://doi.org/10.3791%2F3923>

- Azizan, N. H.;Rami, S. Z. M.;Saedudin, R. R. and Kasim, S. 2018. Phylogenetic Study of Presumptive Oil-degrading Microbes Isolated from The North-western Tip of Pahang. *Int. J. Integr. Eng.* 10: 128-132. <https://doi.org/10.30880/ijie.2018.10.06.017>
- Das, N. and Chandran, P. 2011. Microbial degradation of petroleum hydrocarbon contaminants: an overview. *Biotechnol. Res. Int.* 2011. <https://doi.org/10.4061/2011/941810>.
- Fujisawa and Murakami 1980. Method for screening hydrocarbon-oxidizing bacteria in the sea. *Journal of the Shimonoseki University of Fisheries.* 28.
- Ghoreishi, G.;Alemzadeh, A.;Mojarrad, M. and Djavaheri, M. 2017. Bioremediation capability and characterization of bacteria isolated from petroleum contaminated soils in Iran. *Sustainable Environment Research.* 27: 195-202. <https://doi.org/10.1016/j.serj.2017.05.002>.  
<https://blast.ncbi.nlm.nih.gov/Blast.cgi>. from <https://blast.ncbi.nlm.nih.gov/Blast.cgi>.  
<https://www.geneious.com>.
- Jiao, S.;Liu, Z.;Lin, Y.;Yang, J.;Chen, W. and Wei, G. 2016. Bacterial communities in oil contaminated soils: Biogeography and co-occurrence patterns. *Soil Biology and Biochemistry.* 98: 64-73. <https://doi.org/10.1016/j.soilbio.2016.04.005>.
- Miyoshi, T.;Iwatsuki, T. and Naganuma, T. 2005. Phylogenetic characterization of 16S rRNA gene clones from deep-groundwater microorganisms that pass through 0.2-micrometer-pore-size filters. *Appl. Environ. Microbiol.* 71: 1084-1088. <https://doi.org/10.1128/AEM.71.2.1084-1088.2005>.
- National Centre for Biotechnology Information 2020.[URL](#).
- Nie, Y.;Chi, C.;Fang, H.;Liang, J.;Lu, S.;Lai, G.;Tang, Y. and Wu, X. 2014. Diverse alkane hydroxylase genes in microorganisms and environments. *Sci Rep* 4: 4968. <https://doi.org/10.1038/srep04968>.
- Peng, M.;Zi, X. and Wang, Q. 2015. Bacterial Community Diversity of Oil-Contaminated Soils Assessed by High Throughput Sequencing of 16S rRNA Genes. *International Journal of Environmental Research and Public Health.* 12: 12002-12015. <https://doi.org/10.3390/ijerph121012002>.
- Republic of Iraq, P. o. C. o. M., National Investment Commission 2016. Investment Map of Iraq 71-73.[URL](#).
- Sarkar, D.;Ferguson, M.;Datta, R. and Birnbaum, S. 2005. Bioremediation of petroleum hydrocarbons in contaminated soils: comparison of biosolids addition, carbon supplementation, and monitored natural attenuation. *Environmental pollution.* 136: 187-195. <https://doi.org/10.1016/j.envpol.2004.09.025>.
- Stamenov, D. R.;Đurić, S. S. and Hajnal Jafari, T. I. 2015. Bioremediation potential of five strains of *Pseudomonas* sp. *Matica Srpska J. Nat. Sci.* <http://dx.doi.org/10.2298/ZMSPN1528041S>.  
[URL](#).
- Udgire, M.; Shah, N. and Jadhav, M. 2015. Enrichment, isolation and identification of hydrocarbon degrading bacteria. *J Int of Curr Microbiol Appl Sci.* 4: 708-713.[URL](#).
- Yavari, S.;Malakahmad, A. and Sapari, N. B. 2015. A review on phytoremediation of crude oil spills. *Water, Air, & Soil Pollution.* 226: 1-18. <https://doi.org/10.1007/s11270-015-2550-z>.
- Zhang, Z.;Gai, L.;Hou, Z.;Yang, C.;Ma, C.;Wang, Z.;Sun, B.;He, X.;Tang, H. and Xu, P. 2010. Characterization and biotechnological potential of petroleum-degrading bacteria isolated from oil-contaminated soils. *Bioresour. Technol.* 101: 8452-8456. <https://doi.org/10.1016/j.biortech.2010.05.060>.