THE PREVALENCE OF BACTERIAL SPECIES ISOLATED FROM IRAQI SOIL

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ABSTRACT

The important role of different bacterial species in the environment especially in soil was held to be the aim of this study to discover the variation of soil bacteria. Samples of soil were collected from different areas that included Abu Ghraib and the Department of plant protection from various crops such as (cucumbers, tomatoes, eggplant, wheat and corn) in addition to the nurseries and gardens houses from Al-Adhamiya district and Hay Al-banuk region and from Al-Kut, samples collection lasted for 3 months. Bacteria were isolated from all these samples primarily depending on morphological and physiological characterization after cultured on macconkey agar and then identification were carried by using the Vitek2 compact device. Enterobacterspp. reached the largest isolated species from Iraq soils in different areas which comprised (34%) followed by Pseudomonasspp. was the second species in about (17.55%), followed by Ralstoniaspp. was the third species in about (12.76%), followed by Proteusspp. was the fourth species in about (10.10%), also recorded others species in lowest ratio such as Aeromonasspp. was the fifth species in about (3.19%), followed by Burkholderiaspp. was the sixth species in about (2.65%), followed by Pantoeasspp. was the seventh species in about (2.12%), then followed by Raoultellaspp. in about (1.59%), then followed by Achromobacterspp, Escherichia coli and Leclerciaspp. in same percentage in about (1.06%),

Keywords: Gram negative bacteria, prevalence, Iraqi soil.

How to cite this article: Al-Sudani SFK, Alash SA (2020): The prevalence of bacterial species isolated from Iraqi soil, Ann Trop Med & Public Health; 23(S10): SP231031. DOI: http://doi.org/10.36295/ASRO.2020.231031

INTRODUCTION

Microbiota found in the soils is greatly important for planetinourlife, including its role in the cycling of nitrogen, carbon and other nutrients. Fertile soils provided a good environment for a wide range of microorganisms but the bacterial population in the soil exceeds that of all other aggregates of microorganisms in number and type.

Bacteria and other soil microorganisms are the agents of biotransformation of soil organic matter and nutrients and of most key soil processes. Their activities are influenced by both soil physicochemical processes and ecological interactions.

Soils bacteria are very important in biogeochemical cycles and it have been used for crop production for decades. Plant–bacterial interactions in the rhizosphere are the determinants of plant health and soil fertility. Free-living soil bacteria is beneficial to plant growth, which referred to as plant growth promoting rhizobacteria (PGPR), which are capable of promoting plants growth by colonizing the plants root. PGPR are...
also called plant health promoting rhizobacteria (PHPR) or nodule promoting rhizobacteria (NPR). These are associated with the rhizosphere, which are an important soils ecological environment for plant–microbe interactions

The strain of bacteria that founded in the soil possess an enormous variety of resistant genes. Most of research has found the previously pathogenic pathogens can acquire resistance genes quickly from bacteria that found in the environment. Genetic bases of antibiotic resistance in bacteria and how resistance can spread between the environment and medical clinics are topics of current interest this time.

Without human intervention, the resistance selection is already occurring naturally in soil microbial organisms and other habitats, but the uses of antibiotics with the big quantities that reach to the hundreds-thousands of tons/year and subsequent emission of antibiotics residues into the environment that leads to the sharp changes in the value of selection pressures that leading to the increase in antibiotic-resistant bacteria.

Once consumed, the antibiotic drugs are excreted without metabolism addition to the resistant bacteria, which can then pass either through drainage systems or directly to the soil mix with the bacteria that found in the environment in the presence of other pollutants that may added more pressure to help chooses the antibiotic resistance, directly or indirectly picture. The extent to which the environment contributes to this problem is under intense scrutiny, but the answers will be depend on the part or the level of environmental pollution and the length of time that the antimicrobial remains in active state. Human exposure to environmental bacteria and antibiotic resistance genes can occur but another issue is the extent to which the resistant bacteria are spread through direct or indirect contact with the environment. For example, research has shown that even with high investment levels in wastewater treatment, there is an estimated with 6 million exposure events to one type of E-coli that resistance to the antibiotic each year in the UK's coastal recreational waters. There are several cases that well document emphasizes the development of antibiotic-resistant bacteria within the soil and their subsequent spread or transport to humans.

**MATERIALS AND METHODS**

**Samples collection**

Twenty eight soil samples were collected from different areas of Iraq between April 2019 to July 2019. The samples gathered about a depth of (5-10) cm. from the soil surface near the roots area using sterile tools and transferred to the laboratory by sterile cans.

**Isolation of bacterial colonies**

One gram of each soil samples was taken and suspended with 9 ml. distal water, then a series of decimal was done till the tenth dilution. MacConkey agar was planted with each dilution. All plated were incubated at different temperatures ranging from 25-37°C for 3 days followed by the formed bacterial colonies were purified by sub-culturing on nutrient agar medium and set to be diagnosed.

**Identification of bacterial**

VITEK 2 compact system device (Biomerienx USA) located in AL-Askandronalaboratories used to identify the pure bacterial isolates. This device composed of (47) biochemical tests.
identification, Gram-negative bacteria card was used; it is a complete system for routine identification of most significant fermenting and non-fermenting Gram-negative bacilli or cocci bacteria.

**RESULTS**

The identification results which was done by VITEK 2 compact system for bacterial isolats(Figure 1, 2) showed that *Enterobacter* spp. was the largest isolated species from Iraq soils in different areas which comprised (34%). This percentage distributed between *Enterobacter cloacae complex* in about (31.9%), *E. aerogenes* (0.53%), *E. asburiae* (1.06) and *E. kobei* (0.53%).*Pseudomonas* spp. was the second species in about (17.55%), also this percentage distributed between *P. putidain* about(6.91%), *P. aeruginosa* (4.78%), *P. fluorescenc* (3.19%), *P. luteola* (2.12%), *P. mendocina* (0.53%).*Ralstonia* spp. was the third species in about (12.76%), also this percentage distributed to *R. mannitolilytica* (12.76%).*Proteus* spp. was the fourth species in about (10.10%), also this percentage distributed to *Proteus mirabilis* (10.10%).*Aeromonas* spp. was the fifth species in about (3.19%), also this percentage distributed between *A. hydrophilia* in about (1.59%) and *A. salmonica* (1.59%).*Burkholderia* spp. was the sixth species in about (2.65%), also this percentage distributed to *Burkholideriaceapacia group* (2.65%).*Pantoena* spp. was the seventh species in about (2.12%), then followed by *Raoulteella* spp. in about (1.59%), also this percentage distributed to *Raoultella ornithinolytica* in about (1.59%) then followed by *Achromobacter* spp. in about (1.06%), also this percentage distributed between *A. denitrificans* in about (0.53%) and *A. xylosoxidans* (0.53%) followed by *Escherichia coli* in about (1.06%) and *Leclercia* spp. in about (1.06%), also this percentage distributed to *Ladecarboxylata* (1.06%) then followed by *Rhizobium* spp. in about (0.53%), that distributed to *Rhizobium radiobacter* (0.53%) followed by *Sphingomonas* spp. in about (0.53%), this percentage distributed to *Sphingomonaspaucomobilis* (0.53%). While the *Acinetobacter* spp. was the last species in about (0.53%), the percentage distributed to *Acinetobacter lwoffii* in about (0.53%).

![](image)

*Figure 1: Distribution of bacterial genera in Iraq soil*
DISCUSSION

Many bacterial species are present in the soil normally and can adapting to the soil conditions. Sometimes different types of bacteria are isolated from soils contaminated with petroleum products and their derivatives that help in the degradation, removing and cleaning the soil from its\textsuperscript{12-14}.

Bacteria is among the microorganisms can be promote plant growth and identified as promoting rhizobacteria (PGPR) growth of genera such as (\textit{Acinetobacterspp.}, \textit{Alcaligenesspp.}, \textit{Arthrobacterspp.}, \textit{Azospirilliumspp.}, \textit{Azotobacterspp.}, \textit{Bacillusspp.}, \textit{Beijerinckiassp.}, \textit{Burkholderiasssp.}, \textit{Enterobacterspp.}, \textit{Erwiniaspp.}, \textit{Flavobacteriumspp.}, \textit{Pseudomonasspp.}, \textit{Rhizobioumspp.} and \textit{Serratiaspp.})\textsuperscript{15}. One of very dominant bacteria found in the oil contaminated soil is \textit{Pseudomonas} \textsuperscript{16,17}, while \textit{Bacillus lentus}, \textit{Micrococcus quantity}, \textit{Bacillus alvei}, \textit{Enterobacteraerogene} and \textit{Bacillus pumillus} in the soil with different percentage. Bacterial isolates showed identity to the typical genera of soil bacteria \textsuperscript{19}, including (\textit{Arthrobacterspp},\textit{Bacillusspp.}, \textit{Chryseobacteriumspp.}, \textit{Moraxellusspp.}, \textit{Paenibacillusspp.}, \textit{Pseudomonasspp.},\textit{Rhizobioumspp.}, \textit{Shewanellaspp.}, \textit{Sphingomonasspp.},\textit{Stenotrophomonasspp.} and \textit{Streptomycesssp.})\textsuperscript{20}. Bacteria from taxa division reported to include opportunistic pathogenicity for human or animal such as\textit{Aeromonasspp.}, \textit{Salmonicidasspp.}, \textit{Burkholderiacepacia}, \textit{Chryseobacteriummendingosepticum}, \textit{Moraxella Spp.}, \textit{Photobacteriumdanselsae}, \textit{Pseudomonas fluorescens}, \textit{Sphingomonasmultivorum}, and \textit{Stenotrophomonasmaltophilia} were isolatadd all the spices from soils \textsuperscript{21}. The percentage of \textit{Enterobacterspp.} And\textit{Pseudomonasspp.} agreement with \textsuperscript{22}, while disagreement with \textsuperscript{23} isolate from Ternate Island 10 soil Indonesia samples that obtained the 384 genus were isolated that divided to (81.8%) \textit{Pseudomonas} spp. of which (78%) \textit{P. aureginosa}, (13.4) were \textit{P. fouverence}, (4.2%) were \textit{P. mallei}, (3.1%) were \textit{P. putidea}, (1.3%) were \textit{P. syringe}, while the remain percentage (18.2%) were identified as follows : (6.2%) were \textit{Micrococcus}, (6.0%) were \textit{E.coli}, (3.1%) were \textit{Pasteuella} and (2.9%) were \textit{Staphylococcus}, while\textsuperscript{24} isolated 27 Potassium-solubilizing bacteria (KSB) strains from tobacco and identified through the comparison of the 16S ribosomal DNA which divided to (62.96%) were found to be closely phylogenetically related to \textit{Klebsiellariavicola}, making \textit{Klebsiellaspp}.the most dominant genus,(18.52%) were found to be closely phylogenetically related to \textit{Enterobactercinclud}\textit{E.spp.}
Enterobacterasburiae and Enterobacteraerogenes) making Enterobacter the second most dominant genus, while the (18.52%) remained were found to be closely phylogenetically related to (Pantoeaagglomerans, Agrobacterium tumefaciens, Microbacteriumfoliorum, Myroidesodoratiminus, and Burkholderiacepacian) respectively. In total 151 isolates were recovered from the six soil samples from organic and conventional wheat field, the majority of the isolates in all the soils belonged to the genus Pseudomonas (79) isolate while the other more abundant genera included (Stenotrophomonas (13) isolates, Bacillus (13) isolates, Sphingobacterium (9) isolates and Cryseobacterium (8) isolates$^{25}$.

**CONCLUSION**

This study showed that Enterobacterspp. and Pseudomonanspp. were the highest rate of G-ve bacteria. The differences in prevalence of bacterial species that found in soils among countries depend on nutrition, compounds, the composition of the rhizobiome and the change in the environments that give the variation of bacterial species that found in soil, and thus antagonism of some microorganism against the other is necessary for the continuity of these microorganisms and in some cases could be ecologically beneficial to the environment.

**ETHICAL CLEARANCE**

The Research Ethical Committee at scientific research by ethical approval of both environmental and health and higher education and scientific research ministries in Iraq

**CONFLICT OF INTEREST**

The authors declare that they have no conflict of interest.

**FUNDING**: Self-funding

**REFERENCES**


