

# Molecular Diagnosis of *Pseudomonas Aeruginosa* Isolated from Urinary Tract Infections and Evaluation of the Effect of *Solanum Nigrum* Extract on its Growth

Inas Ahmed Zaynal, Randa Salim Bayat

Biology Dept., College of Pure Sciences, University of Kirkuk. Iraq

Shanay A. Mohammed

Technical Medical Institute, Kirkuk, Northern Technical University, Iraq

**Received:** 2024, 15, Oct

**Accepted:** 2025, 21, Nov

**Published:** 2025, 05, Dec

Copyright © 2025 by author(s) and BioScience Academic Publishing. This work is licensed under the Creative Commons Attribution International License (CC BY 4.0).



Open Access

<http://creativecommons.org/licenses/by/4.0/>

**Annotation: Background & aim:** Antimicrobial resistance, biofilm formation, and a number of other virulence features make *Pseudomonas aeruginosa* a well-known gram-negative pathogenic bacterium. So, this study was aimed to molecular diagnosis of *P. aeruginosa* isolated from urinary tract infections and evaluation of the effect of *Solanum nigrum* extract on its growth.

**Materials & Methods:** During November 2024 to February 2025, 140 clinical samples of who had been admitted to Kirkuk Hospital in Kirkuk City after consulting with a specialist physician and being sent to the laboratory were gathered. The samples were then brought directly to the laboratory for culture on culture media.

**Results:** The findings demonstrated that, when grown in the optimal culture medium, 34 (24.3%) of the total samples had favorable results for bacterial growth. Out of all the samples, 106 (75.7%) had negative bacterial growth results. *P. aeruginosa* was highly responsive to gentamicin (82.3%), imipenem (91.2%), amikacin (97.1%), and ampicillin (88.3%). However, *P. aeruginosa* was 100% responsive to tobramycin. The findings showed that the ability of *S. nigrum* for bacteria inhibition, where the 50ul concentration showed the least efficiency against *P. aeruginosa*, as the diameter of the inhibition zone reached

6.13±1.07mm, while the 75ul concentration showed the highest inhibition, reaching 16.1±1.8mm, and the highest inhibition zone was recorded at the 100ul concentration, reaching 29.12±3.7mm. In the current study from 34 isolate, 34(100.0%) *Pseudomonas aeruginosa* isolates possessed *16S RNA* gene.

**Conclusion:** *P. aeruginosa* isolates are resistant to most antibiotics, with amikacin and topromycin being the most effective. *S. nigrum* extract exhibits antibacterial activity, and the 16S rRNA gene is a reliable marker for isolate identification.

**Keywords:** *P. aeruginosa*, 16S RNA, *S. nigrum*, Antimicrobial resistance.

---

## Introduction

Natural products have been crucial to health care and disease prevention for thousands of years [1]. The plant has a variety of antibacterial, bacteriostatic, and chemotherapeutic properties [2]. In general, plants generate a large number of secondary metabolites, which are a significant source of insecticides, microbicides, and numerous pharmacological medications. Numerous polyphenols, including flavonoids, hydrolyzable tannins, and phenolic acid, exhibit antibacterial properties [3, 4]. *Solanum nigrum* is a member of the Solanaceae family and has been shown to have anti-inflammatory, antibacterial, and anti-cancer properties [5]. Long used to treat a variety of ailments, the whole plant and its roots are employed, but the black fruits of *S. nigrum* are hazardous (mostly due to their high solanine content) and should not be consumed [6,7]. Gram-negative, aerobic, motile, and somewhat curved, *P. aeruginosa* is a bacterium that can be found in a variety of environments, including soil, water, air, and plant and animal tissues [8]. *P. aeruginosa* is a well-known opportunistic human pathogen that can cause a variety of deadly acute and chronic infections, such as meningitis, and infections of the urinary tract, especially in individuals with cystic fibrosis. Every year, it kills over 90,000 people and infects over 2 million people, making it one of the top three causes of opportunistic infections in humans [8,9]. High rates of morbidity and mortality are linked to *P. aeruginosa* UTIs in older adults. Compared to *E. coli* isolates, *P. aeruginosa* isolates from UTIs usually exhibit higher levels of antibiotic resistance [10,11]. One of the most significant bacteria producing complex clinical issues is *P. aeruginosa* [12]. One major issue facing world health is antimicrobial resistance. Antimicrobial resistance has developed as a result of the increased use of antibiotics in recent years, making infection treatment challenging [13]. So, this study was aimed to molecular diagnosis of *Pseudomonas aeruginosa* isolated from urinary tract infections and evaluation of the effect of *Solanum nigrum* extract on its growth.

## Materials & methods

### Specimen Collection

140 clinical samples were taken from Kirkuk Hospital in Kirkuk City between November 2024 and February 2025 from women who had been admitted after consulting with a specialist physician and being sent to the laboratory. The following procedures were part of the sample collection process: Women with UTIs between the ages of 20 and 68 had their urine samples collected. The samples were then sent straight to the laboratory for culture on culture media.

## **Bacterial Identification**

Bacteria were diagnosed based on the following aspects:

### **Morphological diagnosis**

Based on their cultural properties, the *P. aeruginosa* colonies growing on ceftrimide and blood agar were identified, and they were subsequently incubated for 24 hours at 37.0C.

### **Direct examination**

Bacterial colonies were studied using a microscope to examine the morphological characteristics of the bacterial cells, focusing on their reaction with Gram stain, which allows differentiation of the type of reaction as well as the shape and arrangement of the cells.

### **Biochemical reaction and motility test**

Multiple biochemical tests were performed to diagnose the bacteria, including H<sub>2</sub>S, methyl red, citrate, urease, Voges-Proskauer, catalase, oxidase, and indole.

### **Identification by VITEK2**

The VITEK 2 device, which represents advanced colorimetric technology and is one of the latest devices for microbial diagnosis, was used. All steps were carried out in accordance with the manufacturer's instructions, Biomerieux.

### **Antibiotic susceptibility test (AST)**

Antibiotic susceptibility testing was performed on each isolate using the Kirby-Bauer method on Mueller-Hinton agar, in accordance with CLSI guidelines (2020).

### ***Solanum nigrum* leave extraction**

In January 2025, the leaves were gathered from Kirkuk's local marketplaces. 150 mL of water was used to macerate the dried and powdered leaves (5 g) for 24 hours at room temperature. After three iterations of the extraction process, the solvent extracts were mixed and separated from the residue using a Buchner funnel and vacuum-assisted filtration using Whatman N. 1 filter paper. The extract of water was freeze-dried. [14,15].

### **The test of antimicrobial activity for extracts**

The diffusion approach was used to assess the antibacterial activity on agar [16]. A bacterial strain culture was made with  $1 \times 10^6$  cells per milliliter using the McFarland opacity standard. Using a technique known as the spreading method, 0.1 ml of each bacterial isolate ( $1 \times 10^6$  cells per ml) was added to the Mueller Hinton agar plates. Ten milliliters of extract were applied to each well as a control. Thirty minutes before the petri plates were put in the incubator, they were held. For a whole day, each petri dish was incubated at 37°C. Inhibitory zone measurements were performed.

## **Genetic Study**

### **DNA extraction**

The Wizard® Genomic DNA Purification Kit was used to isolate and separate DNA from Gram-negative bacteria. This kit enables the extraction of purified DNA from bacterial cells, facilitating its use in molecular analyses such as polymerase chain reaction (PCR) and gene sequencing, while maintaining the quality and density of the DNA to meet the requirements of rigorous laboratory experiments.

### **PCR procedure**

Using 12.5 µl of the PCR Mastermix, 2 µl primers, 3 DNA templates, and 7.5 free nuclease water, the traditional PCR method was used to detect the 16S RNA sequences. Ten pmol/µl was the concentration utilized for all primers. Table 1 contains a list of the primers used in the research that was presented.

Table (1): 16S RNA gene PCR assay primer

Primer	Primer sequence	Length (bp)	Ref.
27F	`AGAGTTTGATCCTGGCTCAG-3`	1500	17
1492R	5`TACGGTTACCTTGTACGACTT-3		

### Agarose Gel Electrophoresis of DNA

Electrophoresis has been utilized to determine the outcome of the PCR interaction in the presence of standard DNA or to detect DNA fragments following the extraction process in order to differentiate the bundle size of the PCR interaction on the agarose gel.

### Ethical approval

These investigations were accepted, according to the native ethics group, and all participating patients provided informed consent and knowledge about the purpose of the study.

### Results and discussion

#### Samples distribution

The current investigation includes 140 urine samples from UTI patients (table 1). The data indicated that when cultivated in the optimal culture medium, 34 (24.3%) of the total samples exhibited favorable results for bacterial growth. Out of all the samples, 106 (75.7%) had negative results for bacterial growth.

Table (1): Distributed of study samples according to UTI

	No. (%) +ve culture	No. (%) -ve culture	Total No.(%)	P value
UTI Patients	34(24.3%)	106(75.7%)	140(100.0%)	0.001

Some studies revealed rates that were significantly lower than the current study; in Italy, the rate was 3.5% [18], whereas in Egypt and Saudi Arabia, the rates were 10% and 6.7%, respectively [19]. Concerning earlier research from Iraq and other nations, they documented varying patient *P. aeruginosa* infection rates. Baghdad, 36% [20], Kirkuk, 21.6% and Nasiriyah, 19.5% [21], 15.5% [22] Babylon, 25% [23], and Basra, 50.63% [24]. rates of 32.8% and 30% in Saudi Arabia and Egypt, respectively [25]. Variations in *P. aeruginosa* prevalence between studies may be due to different sanitary methods, geographical regions, examined populations, hospital types, and clinical specimen types.

### Antibiotic susceptibility test

*P. aeruginosa* showed high resistant toward Ampicillin (88.3%), and a high sensitive toward Gentamicin (82.3%), Imipenem (91.2%) and Amikacin (97.1%). On the other hand, *P. aeruginosa* was completely sensitive (100%) toward Tobromycin respectively (table 2).

Table (2): Antibiotic susceptibility test of *P. aeruginosa*

Antibiotics	Sensitive %	Intermediate %	Resistant %	P value
Ampicillin	8.8	2.9	88.3	0.001
Clindamycin	47.1	2.9	50.0	
Trimethoprim	58.8	0.0	41.2	
Cefotaxime	70.6	5.9	33.5	
Gentamicin	82.3	0.0	17.7	
Imipenem	91.2	2.9	5.9	
Ciprofloxacin	61.8	11.8	26.4	
Levofloxacin	52.9	14.7	32.4	
Azithromycin	73.5	2.9	23.6	

Amikacin	97.1	0.0	2.9
Tobramycin	100.0	0.0	0.0

The most common and significant mechanism of resistance in Gram-negative bacteria is the production of  $\beta$ -lactamase enzymes by *P. aeruginosa*. The outer membrane of Gram-negative bacteria has porin channels that  $\beta$ -lactamase either diffuses through or directly passes through. *P. aeruginosa* lowered permeability and either enhanced efflux or decreased the synthesis of porins [26]. The results of the study by [27] showed that the percentage of isolates that were resistant to meropenem (77.5%), tobramycin (75%), ceftriaxone (75%), ciprofloxacin (67.5%), gentamicin (65%), and ceftazidime (65%) decreased gradually as the percentage of isolates that were resistant to cefepime (62.5%), norfloxacin (60%), and imipenem (with percentages as 55%). 20 isolates, or 42.6%, however, demonstrated ciprofloxacin resistance. This study's 42.6% resistance result was higher than the 31% from several clinical sources [29] and the 9% from a prior local investigation in Baghdad [28]. Our findings, however, were more in line with those of non-local research. As compared to 64% of 100 isolates from various clinical specimens in Iran [31] and 100% (81 isolates) in Tunisia [32], 38 clinical isolates of *P. aeruginosa* obtained from various clinical sources in north Lebanon shown 57.89% resistance to ciprofloxacin [30]. Isolation from various departments, patient groups, and undoubtedly variations in the dosage of this antibiotic administered by various institutions could all be reasons for variations in resistance rates. However, because of the abuse by the community and hospitals, the resistance rate is rising annually [33].

Table (4) showed the ability of *S. nigrum* for bacteria inhibition according to concentration. 50, 75, 100ul of *S. nigrum* was caused in inhibitory effect on *P. aeruginosa* isolates. The 50ul concentration showed the least efficiency against *P. aeruginosa*, as the diameter of the inhibition zone reached  $6.13 \pm 1.07$ mm, while the 75ul concentration showed the highest inhibition, reaching  $16.1 \pm 1.8$ mm, and the highest inhibition zone was recorded at the 100ul concentration, reaching  $29.12 \pm 3.7$ mm.

Table (5): show the effect of aqueous extract of *S. nigrum* at different concentrations

Treatment Bacteria type	<i>S. nigrum</i>		
	50ul	75ul	100ul
<i>P. aeruginosa</i>	$6.13 \pm 1.07$	$16.1 \pm 1.8$	$29.12 \pm 3.7$

The antibacterial properties of this plant are probably why it has been used traditionally to treat bacterial illnesses. Many steroidal alkaloids from *Solanum* may exhibit unique pharmacological properties in their biological activity, as suggested by Stebbins and Poddock [34]. Phytochemical screening has identified flavonoids, phenols, alkaloids, and tannis, all of which have been shown to possess antibacterial properties [35]. The search for solasodine glycosides in various plants has been the focus of multiple articles due to the importance of solasodine to the pharmaceutical industry [36]. Therefore, these compounds—solasodine in particular—may be responsible for the antibacterial effect. One possible mode of action for this component is to impede the production of proteins, membrane phospholipids, and nucleic acids [37]. The results of the current study contradict the assessment by Patil et al. [38] of the antibacterial properties of a complete methanol extract of *Solanum surattense* using the disk diffusion method on agar. The previous study demonstrated antibacterial activity against Gram-positive bacteria with limited effect against Gram-negative bacteria. In contrast, the results of the current study showed that the *Solanum surattense* extract possesses strong activity against Gram-negative bacteria. Depending on the phytoconstituent, the plant may exhibit antimicrobial activity through a number of mechanisms, including disruption of the cell membrane, inhibition of cell wall formation, deactivation of microbial adhesins, inhibition of enzymes, or inhibition of nucleic acid synthesis [39]. Because they shield the plants from infection, the physiologically recognized substances

are effective. Potentially helpful structures for the creation of novel chemotherapeutic drugs can be found in the significant sources of medicinal plants. The antioxidative, antidiabetic, anticarcinogenic, antibacterial, antiallergic, antimutagenic, and anti-inflammatory properties of phytochemical phenolic substances are well-established [40]. It is well known that tannins have broad antibacterial and antioxidant properties [41], this explains the results of the current study, where *Solanum nigrum* extract was able to inhibit the growth of *Pseudomonas aeruginosa*.

### Genetic study

In the current study from 34 isolate, 34(100.0%) *Pseudomonas aeruginosa* isolates possessed *16S RNA* gene as shown in figure (1).

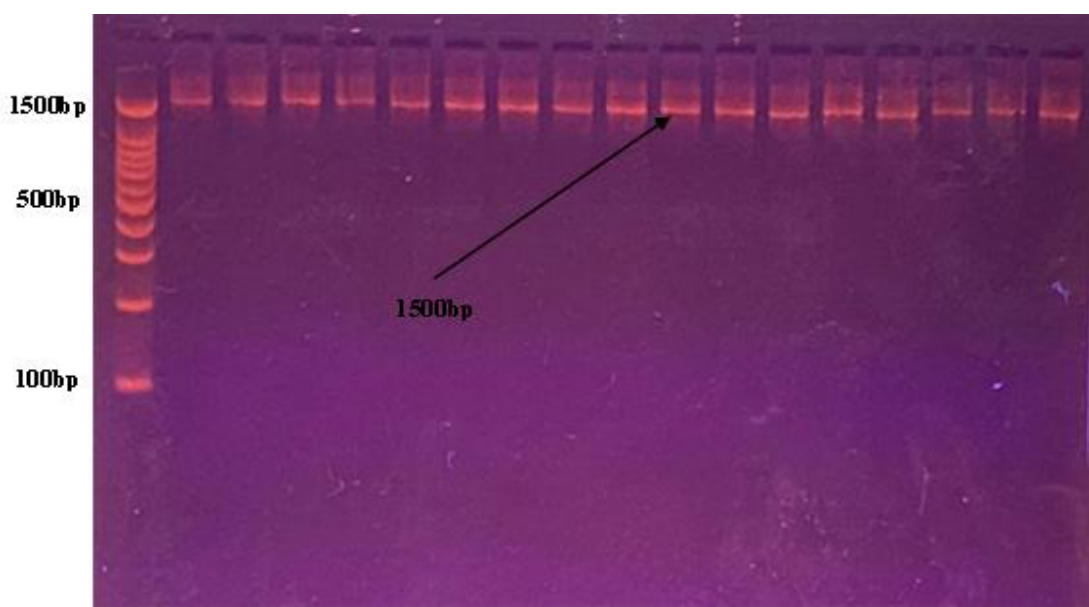


Figure (1): PCR amplification of 1500bp *16S RNA* gene by 1.4% agarose gel electrophoresis.

Ladder: M, Lane (1-17): PCR product of 17 *P. aeruginosa* isolates from urine samples

In the current study, all 34 (100%) *Pseudomonas aeruginosa* isolates were found to contain the 16S rRNA gene. This finding provides strong evidence that the 16S rRNA gene is a reliable marker for identifying this bacterium at the genome level, as it is a gene with a conservative sequence and can be used to identify microorganisms with high accuracy [42]. It also demonstrates that all analyzed isolates are indeed *Pseudomonas aeruginosa*, further enhancing the effectiveness of genetic identification techniques in verifying bacterial identity. It is noteworthy that the presence of the 16S rRNA gene in all isolates reflects the stability and widespread distribution of this gene among *Pseudomonas aeruginosa* species, making it a valuable tool for classifying this bacterium even in cases of variation in its morphological or biochemical characteristics [43]. Although this gene is widely used in identifying the genetic identity of bacteria, the presence of the 16S rRNA gene in 100% of the isolates may also indicate that these isolates have not undergone genetic processes that could cause mutation or loss of this gene [44]. The 16S rRNA gene can be considered an effective criterion for the diagnosis of *P. aeruginosa* in microbiological studies, but it remains important to explore other techniques such as microscopic examination or biochemical reactions to ensure the accuracy of the diagnosis in clinical settings [45].

### Conclusions

Based on the results of the current study, *P. aeruginosa* isolates exhibit high resistance to many current antibiotics, and the best antibiotics are Amikacin and Tobromycin. *S. nigrum* extract also demonstrated high antibacterial activity against *P. aeruginosa*. The 16S RNA gene can also be considered a good indicator for identifying 16S RNA gene isolates.

## References

1. Upadhyay P., Shabina A., Prakash P. Antibacterial and Antioxidant Activity of Solanum nigrum Stem and Leaves. *Chemical Science Transactions*. 2015; 4(4): 1013-1017.
2. Venkatesan D, Karrunakaran C M and Selva S K, *Ethnobotanical Leaflets*, 2009; 13(1): 1485-1503.
3. Ibrahim MA, Hayawi JA, Sultan FI. Effect of extracts of some medicinal plants and duration of soaking on the growth of seedlings of three cultivars of barley. *AIP Conference Proceedings*. 2023;2862(1):020053.
4. Bolat E., Sümeyye S., Hatice D., Furkan E., Emir A., Sercan K., Anna Maria W. Polyphenols: Secondary Metabolites with a Biological Impression. *Nutrients*. 2024; 16(15): 2550.
5. Sonkamble P. S., Nagoba S. N., Sarukh V., Shinge K. R. Systematic review on Solanum nigrum. *WJPLS*, 2019; 5(2): 109-112.
6. Jain, R., A. Sharma, S. Gupta, I.P. Sarethy, and R. Gabrani. 2011. Solanum nigrum: current perspectives on therapeutic properties. *Altern. Med. Rev.* 16(1):78-85.
7. Chauhan, R., K.M. Ruby, A. Shori, and J. Dwivedi. 2012. Solanum nigrum with dynamic therapeutic role: A review. *Inter. J. Pharm. Sci. Rev. Res.* 15(1): 65-71.
8. Li X, Gu N, Huang TY, Zhong F and Peng G (2023) *Pseudomonas aeruginosa*: A typical biofilm forming pathogen and an emerging but underestimated pathogen in food processing. *Front. Microbiol.* 13:1114199.
9. Wood S. J., Timothy M. K., Sasha H. S. *Pseudomonas aeruginosa*: Infections, Animal Modeling, and Therapeutics. *Cells*. 2023; 12(1), 199.
10. Khorsheed M. B., Salah S. Z. The frequency of *Pseudomonas aeruginosa* bacteria with some pathogenic bacteria in burns injuries and study their resistance to antibiotics. *Kirkuk University Journal /Scientific Studies*, 2017, 12(1): 123-140.
11. Thamer, R. A., Hammo, A. H., Fadhil, S. J., Alhafidh, N. M., Al-Rawi, A. M., Saadi, A. M., & Al-Bajari, S. A. Phenotypic and molecular detection of multidrug-resistant *Pseudomonas aeruginosa* isolated from urinary tract infection cases in Mosul, Iraq. *International Journal of Design & Nature and Ecodynamics*, 2025; 20(9): 2167–2176.
12. Estaji M, Tabasi M, Sadeghpour Heravi F, Kheirvari Khezerloo J, Radmanesh A, Raheb J, et al. Genotypic identification of *Pseudomonas aeruginosa* strains isolated from patients with urinary tract infection. *Comp Immunol Microbiol Infect Dis* 2019;65:23-8.
13. Bayyigit A., Mustafa G. E., Özge Ü., Mehmet D. Urinary Tract Infections Caused by *Pseudomonas aeruginosa*: An 11-Year Retrospective Analysis on Antimicrobial Resistance. *Eur Arch Med Res*. 2023; 39(3):189-195.
14. Abbood, H.A.R., Saleh, A.H. The potential role of alkaloid extract against phospholipase extracted from *Aspergillus flavus* in Male rats. *Journal of Global Pharma Technology*, 2019, 11(7), pp. 548–551.
15. Abdul, M.R., Rahim, S.M., Saleh, A.H. Cardioprotective Activity of Costus Root Ethanol Extract in Experimentally-Induced Hypothyroidism in Female Albino Rats. *HAYATI Journal of Biosciences*, 2023, 30(6), pp. 1054–1060.
16. Liaw, S. J.; AI, H.C.; HO, S.W.; Luh, K.T.; Wang, W.B. Inhibition of virulence factor expression and swarming differentiation in *Proteus mirabilis* by p-nitrophenyl glycerol. *J. Med. Microbiol.* 2000; 49(8): 725-731.

17. Atheer A. R., Hasanain K. S. Isolation and Analysis of Nucleotide Sequences of the 16SrRNA Gene of *Pseudomonas aeruginosa* Isolated from Clinical Samples. *Indian Journal of Forensic Medicine & Toxicology*, 2021; 15(1): 2193-2198.
18. Crivaro V, Di Popolo A, Caprio A, Lambiase A, Di Resta M, Borriello T, Scarcella A, Triassi M, Zarrilli R. *Pseudomonas aeruginosa* in a neonatal intensive care unit: molecular epidemiology and infection control measures. *BMC Infect Dis*. 2009; 9(70): 7.
19. Mansour SA, Eldaly O, Jiman-Fatani A, Mohamed ML, Ibrahim EM. Epidemiological characterization of *P. aeruginosa* isolates of intensive care units in Egypt and Saudi Arabia. *East Mediterr Health J*. 2013; 19(1):71–80.
20. Al-Zaidi JR (2016). Antibiotic susceptibility patterns of *Pseudomonas aeruginosa* isolated from clinical and hospital environmental samples in Nasiriyah, Iraq. *Afr J Microbiol Res*. 10:844–849.
21. Al-Saffar MF, Jarallah EM. Isolation and characterization of *Pseudomonas aeruginosa* from Babylon Province. *Biochem Cell Arch*. 2019; 19(1):203–209.
22. Hasan SA, Najati AM, Abass KS. Isolation and identification of multi-drug resistant “*pseudomonas aeruginosa*” from burn wound infection in Kirkuk City, Iraq. *Eurasia J Biosci*. 2019; 13:1045–1050.
23. AL-Fridawy RAK, Al-Daraghi WAH, Alkhafaji MH. Isolation and Identification of multidrug resistance among clinical and environmental *Pseudomonas aeruginosa* isolates. *IJB*. 2020; 19(2):3–45.
24. Alkhulaifi ZM, Mohammed KA. Prevalence and molecular analysis of antibiotic resistance of *Pseudomonas aeruginosa* isolated from clinical and environmental specimens in Basra, Iraq. *Iran J Microbiol*. 2023; 15(1):45–54.
25. Mansour SA, Eldaly O, Jiman-Fatani A, Mohamed ML, Ibrahim EM. Epidemiological characterization of *P. aeruginosa* isolates of intensive care units in Egypt and Saudi Arabia. *East Mediterr Health J*. 2013; 19(1):71–80.
26. Ammeter D, Idowu T, Zhanel GG, Schweizer F. Development of a nebramine-cyclam conjugate as an antibacterial adjuvant to potentiate  $\beta$ -lactam antibiotics against multidrug-resistant *P.aeruginosa*. *J Antibiot (Tokyo)* 2019;72:816-26.
27. Shatti H. H., Wisam M., Mohammed I. N. Effect Biofilm Formation in *Pseudomonas aeruginosa* Resistance To Antibiotic. *Mustansiriya Medical Journal*, 2022; 21(1): 13-17
28. AL-Taei, A. M. M. and Delool, R. Genetic study of ciprofloxacin resistant *Pseudomonas aeruginosa* (Doctoral dissertation, M. Sc. Thesis, College of Science, Al-Mustansiriyah University), 2012.
29. Al-Marjani, M., Kadhim, K. A. and Kinani, Y. “Ciprofloxacin resistance in *Staphylococcus aureus* and *Pseudomonas aeruginosa* isolated from patients in Baghdad”. *Int J Pharm Sci Res*, 2015; 6(2): 382-385.
30. Salma, R., Dabboussi, F., Kassaa, I., Khudary, R. and Hamze, M. “*gyrA* and *parC* mutations in quinolone-resistant clinical isolates of *Pseudomonas aeruginosa* from Nini Hospital in north Lebanon”. *Journal of Infection and Chemotherapy*, 2013; 19(1): 77-81.
31. Nouri, R., Ahangarzadeh, M., Hasani, A., Aghazadeh, M. and Asgharzadeh, M. “The role of *gyrA* and *parC* mutations in fluoroquinolones-resistant *Pseudomonas aeruginosa* isolates from Iran”. *Brazilian Journal of Microbiology*, 2016; 47(4): 925-930.
32. Nejma, M. B., Sioud, O. and Mastouri, M. “Quinolone-resistant clinical strains of *Pseudomonas aeruginosa* isolated from University Hospital in Tunisia”. *3 Biotech*, 2018; 8(1): 1.

33. Naji S. A., Halah A. A. A Study of Urinary Tract Infections Prevalence, Antibiotics Resistance, and Biofilm Formation Capability of the Bacterial Causal Agents. *Tikrit Journal of Pure Science*. 2022; 27(6): 11-18.
34. Stebbins G., Poddock F. The *Solanum nigrum* complex in Pacific North America. *Weed Sci*. 2002; 32, 138-142.
35. AL-Mazini M.A. Isolation and Identification of solasodine compound from leaves of *Solanum nigrum* L. plant and study its, effectiveness as contraceptive and against mycobacterium tuberculosis. *Athesis- college of science- university of Busrah- Iraq*. 2007.
36. Telek, L. Determination of solasodine in fruits of *Solanum* species. *J. Pharm. Sci*. 2003; 66, 699-702.
37. Franklin, J., Snow, G., Barrett-Bee, K. *Biochemistry of antimicrobial action*. Fourth edition. Chapman and Hall London, New York. 1997; pp:71-73.
38. Patil S., Joshi V., Sutar P., Sambrekar S. Screening of whole plant extract of *Solanum surattense* for antibacterial activity. *International Journal of pharmaceutical Sciences*, 2009; 1(1):110-114
39. Cowan, M. M. Plant products as antimicrobial agents. *Clinical microbiology reviews*, 1999; 12(4), 564-582.
40. Abubakar, E. M. M. Antibacterial efficacy of stem bark extracts of *Mangifera indica* against some bacteria associated with respiratory tract infections. *Scientific Research and Essays*, 2009; 4(10), 1031-1037.
41. Mohanta, T. K., Patra, J. K., Rath, S. K., Pal, D. K., & Thatoi, H. N. Evaluation of antimicrobial activity and phytochemical screening of oils and nuts of *Semecarpus nardium* Lf. *Scientific Research and Essays*, 2007; 2(11), 486- 490.
42. Janda JM, Abbott SL. 16S rRNA Gene Sequencing for Bacterial Identification in the 21st Century. *J Clin Microbiol*. 2007;45(9):2761-2769.
43. Muyzer G, De Waal EC, Uitterlinden AG. Profiling of Complex Microbial Populations by Denaturing Gradient Gel Electrophoresis (DGGE) of Polymerase Chain Reaction-Amplified Genes Coding for 16S rRNA. *Appl Environ Microbiol*. 1993;59(3):695-700.
44. Schleifer KH, Ludwig W. Phylogeny of the Genus *Pseudomonas* and Related Bacteria: Evidence from 16S rRNA Sequences. *Int J Syst Bacteriol*. 2000;50(Suppl\_1):35-42.
45. Berg G, Rybakova D, Fischer D, et al. From Lab Strain to Industrial Application: *Pseudomonas* as a Model for the Beneficial Use of Bacteria. *Microbiol Res*. 2015;170:54-61.