Journal of Medical Genetics and Clinical Biology
Homepage : https://journal.antispublisher.id/index.php/JMGCB
Email : admin@antispublisher.com

e-ISSN : 3032-1085
JMGCB, Vol. 3, No. 5, May 2026
Page 66-77

Detection of CTX-M and SHV Genes in Extended Spectrum Beta-Lactamase Producing *Pseudomonas aeruginosa* Isolated from Wounds and Burns at Al-Diwaniyah Hospitals

Nada Ahmed Fairouz
Qadesiya Al-Furat Al-Awsat Technical University, Iraq

DOI : https://doi.org/10.61796/jmgcb.v3i5.1738

Sections Info
Article history:
Submitted: January 07, 2026
Final Revised: February 26, 2026
Accepted: March 18, 2026
Published: April 10, 2026
Keywords:
P.aeruginosa
blaSHV gene
bla CTX-M gene

ABSTRACT

Objective: *To investigate the impact of graded doses of ginger extract on male sexual maturation, focusing on hormonal profiles, reproductive organ weights, and sperm characteristics in prepubertal mice.* ***Method:*** *Male mice (21–28 days old) were randomly assigned to four groups receiving 0 (control), 100, 200, or 400 mg/kg ginger extract orally for 28 days. Serum testosterone, luteinizing hormone (LH), and prolactin (PRL) were measured, and reproductive organ weights and sperm parameters were evaluated.* ***Results:*** *Ginger supplementation significantly increased testosterone, LH, and PRL in a dose dependent manner. Reproductive organ weights (testes, epididymis, prostate) and sperm quality indices (count, motility, viability) also improved significantly in treated groups compared with controls.* ***Novelty:*** *Ginger extract significantly enhances male reproductive development and function in mice, likely through endocrine stimulation and improved sperm physiology, supporting its potential use as a natural reproductive enhancer*

INTRODUCTION

Burn Infection can be described as skin injury that protects the epithelial membrane, with or without the muscle, bone or nerve connective tissue injury, It can be caused by fire, heat blast, chemical agent, hot liquid, high-temperature, cold, electrical currents, or by exposure to radiation [1]. Burn injuries cause an estimated 180,000 deaths per year, according to the World Health Organization, making them a major public health problem [2]. Breaks in skin epithelial integrity lead to wound infections and may result in additional distraction of skin anatomy, physiology, and its functions. Wounds can be divided into two types, severe and chronic [3]. The severity of P. aeruginosa. infection in burn patients is very high and is constantly increasing due to several factors such as the patient's age, the number of bacteria present in the burn, the type and quantity of toxins produced, the nature and depth of the wound, the site of colonization, and the degree of tissue invasion by the bacteria [4]. One of the key causes of nosocomial contagions were because of their acquisition resistance to a various antibiotics, which make it a main world threat [5]. Of greater significance is the emergence of other types of infections, such as wound infections, hospital-acquired pneumonia, bacteremia, and urinary tract infections. This gram-negative bacterium is recognized as a major opportunistic pathogen in healthcare settings due to its ability to form biofilms, produce multiple virulence factors, and display both intrinsic and acquired resistance mechanisms. P. aeruginosa is considered one of the most challenging bacteria to manage, as it can quickly

develop resistance to multiple drugs. Antimicrobial resistance (AMR) represents one of the most significant challenges confronting modern medicine. AMR, as expected, will be responsible of 10 million deaths in 2050 if there is no action taken, largely because of Gram-negative bacteria (GNB). The GNB infections can be rated according to resistance degree, either to the pan-drug resistant (PDR) or the extensively drug resistant (XDR) the multi-drug resistant (MDR). The first one resists all kinds of antibiotics [6]. The consequence is the emergence of a different set of cellular structures and extracellular molecules, which contribute significantly to increase pathogenicity [7].

RESEARCH METHOD

Isolation and Identification of *P. aeruginosa*

Swabs taken from burn, water, oil, flame and Electric. while from wound taken from D.f wound, Sharp tools, Surgical Wound and Car accident for microbiological study. Then clinical samples were cultured on MacConkey agar, blood agar and cetrimide agar using sterile loop spread on the surface of agar media and incubated at 37 C° for 24 hr. Then some morphological and biochemical tests were used to diagnose it [8]. Bacteria shape, size, texture, and colony arrangement were observed after their growth. One colony was selected, Gram stained, to be inspected by light microscope (100x) using oil emersion [8]. The bio matrix Vatic 2 system by (bioMérieux origin France) and PCR were used for confirmation of suspected isolates of *P. aeruginosa* .

Antibiotic Susceptibility Testing for *P. aeruginosa*

For this study, antibiotic disks of cefepime (30 µg), cefixime (5 µg) ceftriaxone (30 µg), cefotaxime (30 µg), meropenem (10 µg), nalidixic acid, ciprofloxacin (5 µg). Amikacin (30 µg) Gentamicin (10 µg) The susceptibility of bacterial isolates to the nine antibiotics listed was determined in accordance with the guidelines of the Clinical and Laboratory Standards Institute. Isolates were activated by culturing them in brain heart infusion broth for 18 hours at 37°C, and the bacterial growth was then adjusted to the 0.5 McFarland standard. Subsequently, the suspension was spread onto Mueller-Hinton agar (MHA) using a sterile cotton swab. Antibiotic disks were placed on the MHA plates inoculated with the bacteria and incubated for 24 hours at 37°C. After incubation, the diameters of the inhibition zones were measured and interpreted as indicating sensitivity or resistance (CLSI 22).

Polymerase chain reaction (PCR)

The detection of 16SrRNA and beta-lactamase genes (blaCTX-M and blaSHV,) in *Pseudomonas aeruginosa* isolates, the PCR (polymerase chain reaction) technique is employed to examine the primers used and their correct homology on bacterial DNA template, NCBI database and BLAST were employed for synonymous oligonucleotide analysis.

Table 1. Sequence of gene primers

Primer	Sequence	Product Size
16SrRNA	**F-5′- TGCCTGGTAGTGGGGGATAA-3′**	
	F-5′-GGATGCAGTTCCCAGGTTGA-3′	**400 bp**
blaSHV	**F-5′- ATGCGTTATATTCGCCTGTG-3′**	
	R-5′ TGCTTTGTTATTCGGGCCAA -3′	**490 bp**
blaCTX-M	**F-5′ CGCTTTGCGATGTGCAG -3′**	**300 bp**
	R-5′ ACCGCGATATCGTTGGT -3′	

Reaction mixture for propagation:

Table 2. Reaction mixture for propagation

PCR reaction composition	Concentration (Lμ)
Master Mix	12.5
Primer F	0.5
Primer R	0.5
Nuclease Free water	8.5
DNA	3
the final Volume	25

Table 3. PCR thermocycling Programs used for the detection of ESBL genes

Gene name	Temperature (°C)/Time Cycling condition					Cycle number
	Initial denaturation	Denaturation	Annealing	Extension	Final extension	
16SrNA	95/5 sec	95/30sec	58/30sec	72/30sec	72/5min	32
$bla_{\text{CTX-M}}$	94/30 sec	94/30 sec	60/1 min	72/1 min	72/10 min	35
bla_{SHV}	94/30 sec	94/30 sec	60/1 min	72/1 min	72/10 min	35

RESULT AND DISCUSSION

Isolation of *P. aeruginosa* from the burn and wound patient:

A total Eighty burn and wound swabs in all were gathered. From October 1, 2024, to April 1, 2025, these were gathered in Al-Diwaniyah City (Al-Diwaniyah Teaching Hospital and B|urn Specialist Hospital) using sterile cotton swabs (transport media swabs).These isolates were obtained from hospital patients of various ages and genders.46 (57.5%) of the isolates were found in burn samples, whereas 34 (42.5%) of the isolates were found in wound samples. A significant rate of *P. aeruginosa* bacterial isolation from burns and wounds has been established by numerous research; Saleh's, study found that 51.75% of burn infections contained this bacterium [9].

According to research by Al-Kazrage and Naji *et al*, the isolation rate for burn injuries was 57.6% and 55%, respectively, whereas it was 44% and 45% for wound injuries

[10], [11]. According to Hasoon [12], burn samples had the highest occurrence in his isolations (56.4%), followed by wounds (18.75%). It was isolated from burns at a rate of 46.8% in Younis and Faisal's study [13]. It was isolated from burns at a rate of 9.6% by Araya *et al*. [14].

The reason for the high isolation rate in the burn samples observed in the current study is due to damage to the skin cells when exposed to the burn. The large area resulting from the injury provides these germs with a suitable environment for invasion and colonization of tissues and the formation of vital membranes over the entire affected area. These results in an increase during the infection period, making treatment with antibiotics difficult [15]. In addition to the ability of these bacteria to resist antibiotics, their low nutritional requirements and their growth under various physical conditions contribute to the rapid spread of these germs and their active role as an opportunistic organism [16]. and high affinity for infecting burnt skin cells due to the breakdown of blood vessels in the skin and the difficulty of accessing to immune factors such as T-lymphocytes to the site of infection [17]. **(Table 1).**

Table 1. Types, numbers and percentage of clinical isolates collected from the patient.

Clinical isolates	Total No.	Percentage %
BURN	46	57.5%
WOUND	34	42.5%
Total	80	100

Distribution of Isolates According to Age and Gender

The results indicated that the maximum rate of Pseudomonas spp. infection in this study is in the (1-20) age group, followed by the (21- 40) age group. The reason for this high rate in these age groups is attributed to their greater activity levels, which makes them more susceptible to infection, and perhaps also to their greater physical activity compared to others. The lack of adherence to health guidelines by this age group exacerbates their health condition, as confirmed by Al- Abood. In his study, the infection rate among those under 40 years of age reached 62.1%.

Table 2. Distribution of Isolates According to Age

Age group/year	No. of isolations	Percentage%
1-20	33	41.25
21-40	25	31.25%
41-60	21	26.25%
61-71	1	1.25%

The percentage of infected patient isolates is,49 isolates (61.25%) in female and 31 (38.75%) in male, the percentage of infection in female. was higher than male This is agreed with the findings of Kirkuk university recorded for female (52.97%) and for male

(49.01%) and agreed with Sulaimaniyah [18], Iraq score for females (57%) and males (43%) [19]. while not agree with study in Baghdad university [20], where male appear high to positive isolates 32 (65.3%) Than The female recorded isolates 17(34.7%).

Table 3. Patient Percentage of clinical isolates collected according to gender identification of *Pseudomonas aeruginosa*.

No	Gender	NO. of *P.aeruginosa*	Precentage %
1	Female	49	61.25%
2	Male	31	38.75%
Total	80		100%

Microscopic Characteristics

The samples give positive growth (bacterial growth) after cultured on MacConkey agar, blood agar and and cetrimid agar and stained by gram stain and inspected under light microscope, concerning identification gram-negative bacteria. Figure (1) shows the finding of gram stain

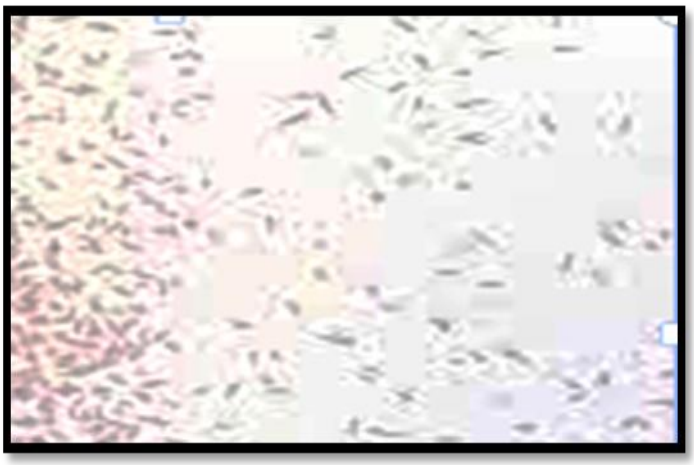

Figure 1. Gram stain for bacterial cells for gram-negative bacteria

Additionally, pyocyanin was formed by the growth on cetrimide agar at 44°C overnight to a blue-greenish color. This particular selective medium was created to separate *P. aeruginosa* from other Pseudomonas species, as seen in Figure (2). In addition to their function as virulence factors in *P. aeruginosa* pathogenicity, these pigments have a pigmentation characteristic that continues to be important among the Pseudomonas genus' diagnostic characteristics [21].

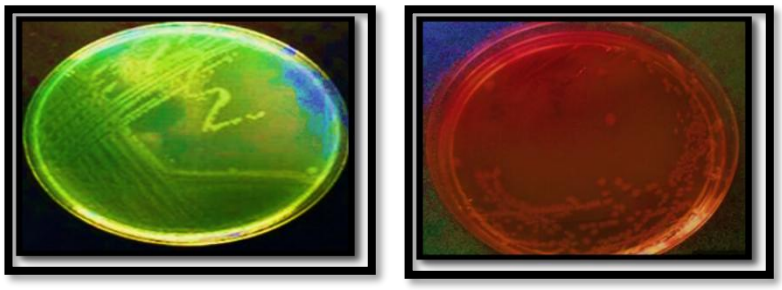

Figure 2. A-P. aeruginosa on cetrimide agar .B - P. aeruginosa colonies on McConkey agar

Detection of 16S rRNA for identifying *P. aeruginosa*

Fifty isolates of the *P. aeruginosa* were selected. Their identification was definitively confirmed molecularly using two primers for the 956-base-pair SrRNA16 gene, and by polymerase chain reaction (PCR) and thermal cycler. The results showed that all the bacterial isolates belonged to the *P. aeruginosa*, as illustrated in Figure (3). These isolates were used in the molecular study. Genotype-based identification techniques overcome the issue of variable phenotypic expression, offering more precise species identification. Nevertheless, the taxonomic complexity, unclear evolutionary relationships, and the limited availability of genomic sequence data for the numerous species within the extensive genus Pseudomonas pose a challenge to the development of genotypic identification assays. The region of DNA most frequently employed for bacterial taxonomic classification is the 16S rRNA gene [22]. Also the regions of this gene are highly stable and do not change over time [23]. Because of the rotten results of tests like biochemical tests, which sometimes unable to identify the isolate name, this study accreditation used a universal primer pair, showing a PCR product of 400 bp. The results of the amplification coincided with the online amplification of the same primer pair with *P. aeruginosa*.

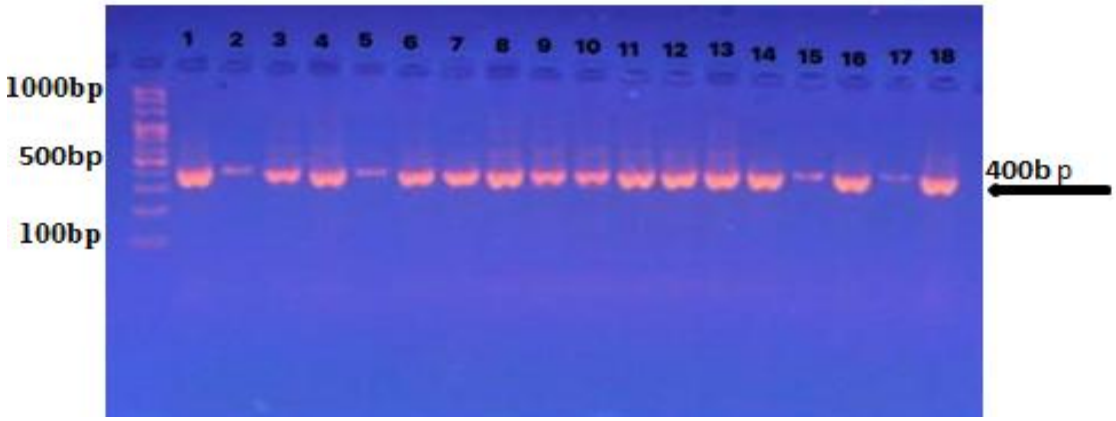

Figure 3. 16SrNA gene in *pseudomonas aeruginosa* isolates by PCR amplification using agarose gel electrophoresis, showing separation of DNA fragments on a 1.5% agarose gel stained with ethidium bromide. All lanes show a positive amplification product at 400 bp. Lane M: DNA molecular weight index 100–1000 bp.

Antibiotic sensitivity

The study's maximal resistance level for cefotaxime and ceftriaxone was 95%, respectively. These results agree with a study in Wasit [24], [25] which is found extremely resistant to ceftriaxone and cefotaxime (100%), respectively , followed by (cefepime, (82%)meropenem(60%), nalidixic acid, ciprofloxacin and cefixime) (63%),(62%),(60%), respectively. This study was comparable to previous research by Ali *et al*., and Okobi *et al*, which discovered resistance to meropenem (62%) and ciprofloxacin (66.9%) [24], [26].

The resistance of *Pseudomonas aeruginosa*, carbapenem is mainly due to chromosomal mutations that change porins, transform efflux pump activity, and depress intrinsic β-lactamases. Carbapenemase genes that are normally existed on movable genetic elements, have the ability to disseminate rapidly [27]. The maximum resistant of *pseudomonas aeruginosa* has been to amikacin, and gentamicin (45%), (60%) respectively. According to a local investigation by Al-Hashimy *et al*. [28], 36% and 60% of *P. aeruginosa* isolates were resistant to the antibiotics amikacin and gentamicin, respectively. Additionally, according to researcher Khan, [29], the resistance rate to the medications Gentamicin and Amikacin were 50% and 64%, respectively [30], [31], [32], [33].

What contribute to intrinsic antibiotic resistance in pseudomonas aeruginosa is reduced outer membrane permeability, MDR, XDR development, and PDR efflux pumps, and the production of antimicrobial inactivating enzymes all [34]. Figure (3) illustrates the percentages of MDR (60%), XDR (25%), and PDR (15%) in our study. Because the outer membrane's permeability barrier, which is composed of an asymmetric bilayer of phospholipids (the inner layer) and lipopolysaccharide LPS (the outermost layer), keeps antibiotics out of the bacterial cells, it increases the percentage of results of the resistance of multiple drug of isolates to antimicrobials [35].

Table 3. Percentage of MDR, XDR and PDR

	MDR	**XDR**	**PDR**
P. aeruginosa	48(60%)	20(25%)	12(15%)

Detection of the *Pseudomonas aeruginosa* virulence gene:

This study was carried out in order to detect ESBL genes in 50 *P. aeruginosa* isolatesThe detection of the most common ESBL kinds, SHV and CTX-M, was carried out using the molecular method for this purpose. Results revealed that gene blaCTX-M was the most, recovered from the15(30%) of the *P. aeruginosa* isolates (Figure 4), followed by the blaSHV gene 13(26%) as shown in (Figure 5),

Komijani *et al*., (2018) reported frequencies of 30% for blaCTX-M and 22.24% for blaSHV genes in *P. aeruginosa* isolates, Peymani *et al* [36] of 17.3% for blaCTX-M-15 and 10% for two different types of blaSHV in ESBL (extended-spectrum β-lactamase) phenotypes. These variations in gene prevalence can be attributed to differences in the statistical population, geographical location, sample types, and study periods in each community [37], [38], [39]. The increasing resistance and prevalence of resistance genes in Iraqi society highlight the importance of periodically and systematically examining resistance patterns in bacteria. Reporting the results of such studies to healthcare professionals can assist in determining the frequency of bacterial resistance and sensitivity to different antibiotics, thereby enhancing the chances of successful treatment of infections. It is crucial to maintain a medical surveillance system that regularly monitors resistance patterns and provides up-to-date information to healthcare providers. This enables them to make informed decisions regarding antibiotic prescription, optimize treatment strategies, and combat the growing problem of antimicrobial resistance.

Our findings did not agree with those of another study conducted in Jimma, Ethiopia Kumar *et al*; Majid Issa *et al*.,[5] which reported a prevalence of 3% and 8.2%, respectively, of the blaCTX-M2 gene [40], [41], [42].

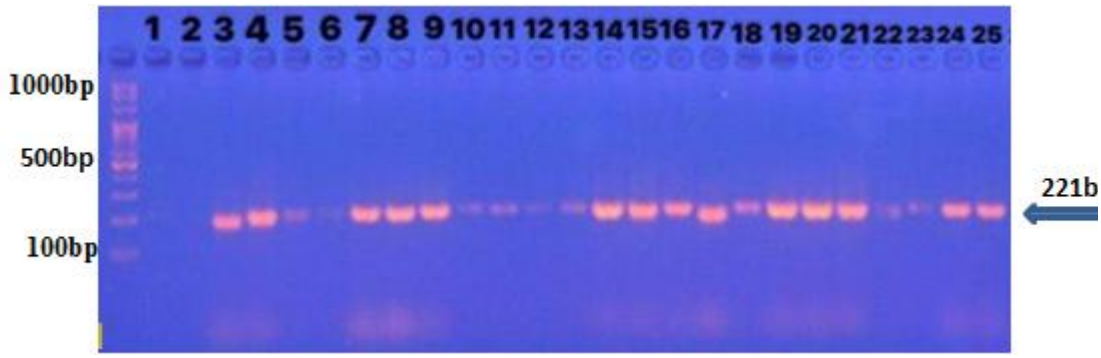

Figure 4. bla CTX-M gene in *Pseudomonas aeruginosa* isolates by PCR amplification using agarose gel electrophoresis, showing separation of DNA fragments on a 1.5% agarose gel stained with ethidium bromide. All lanes show a positive amplification product at 221 bp. Lane M: DNA molecular weight index 100–1000 bp; 15 representative positive samples.

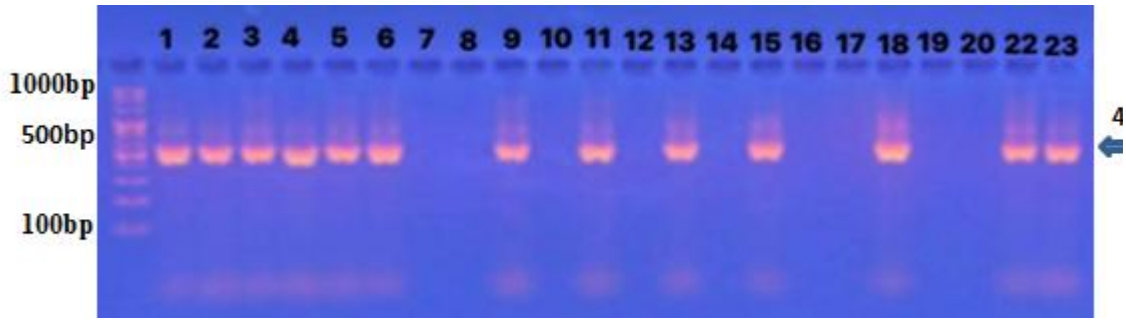

Figure 5. blaSHVgene in *Pseudomonas aeruginosa* isolates by PCR amplification using agarose gel electrophoresis, showing separation of DNA fragments on a 1.5% agarose gel stained with ethidium bromide. All lanes show a positive amplification product at 490 bp. Lane M: DNA molecular weight index 100–1000 bp; 13representative positive samples.

CONCLUSION

Fundamental Finding: The involvement of patients was crucial to the successful completion of this research, and the support of laboratory staff and medical personnel was integral to sample collection and analysis. **Implication:** The study underscores the importance of participant involvement and collaborative efforts from medical and laboratory staff in achieving meaningful results in clinical research. **Limitation:** No financial support or sponsorship was provided for this research, which may have influenced certain aspects of the study's execution. **Future Research:** Future studies could explore opportunities for securing financial support or sponsorship to enhance research capacity and facilitate broader investigations in similar clinical settings.

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*** Nada Ahmed Fairouz (Corresponding Author)**
Qadesiya Al-Furat Al-Awsat Technical University, Iraq
Email: dw.nada@atu.edu.iq