Al-Qadisiyah Journal of Pure Science
ISSN(Printed): 1997-2490 ISSN(Online): 2411-3514
DOI: 10.29350/jops
Al-Qadisiyah Journal of Pure Science

Molecular Detection of Metallo-β-Lactamase Genes in Carbapenem-Resistant *Klebsiella pneumoniae* from Urinary Tract Infections

Rehab Dawas Jaber Al-Humaidi[1], Mithal Kareem A bass Al-Hassani[2]

[1, 2]Department of Biology, College of Education, University of Al-Qadisiyah, Iraq.
[*]Corresponding author email: sci.bio.mas.20.13@qu.edu.iq

Received: 24/01/2026; Revised: 07/03/2026; Accepted: 09/03/2026.

Abstract

Klebsiella pneumoniae is a notoriously known opportunistic pathogen that causes a broad range of healthcare-associated infections, especially the urinary tract infections. The immediate increase in the antimicrobial resistance, particularly the resistance to the β-lactam antibiotics, has become a significant clinical and social health issue on the global stage. The study was intended to phenotypically and molecularly characterize β-lactam-resistant K. pneumoniae isolates that were collected on patients diagnosed with urinary tract infections. Two hundred and fifty urine samples were cultured, and a total of 35 Klebsiella pneumoniae isolates were detected, representing 16.06% of the positive cultures. The isolates showed high resistance rates as all the isolates were fully resistant to amoxicillin-clavulanate, ticarcillin-clavulanate, ceftazidime, cefotaxime, ceftazidime-avibactam, and fosfomycin. Carbapenems resistance rates were also high with 83 percent of the isolates resistant to imipenem and meropenem. PCR analysis revealed that all carbapenem-resistant isolates ($n = 29$) carried the metallo-β-lactamase genes *blaNDM* and blaFIM, and the presence of the genes was strongly related to carbapenem resistance ($p < 0.01$). The great popularity of metallo-β-lactamase-producing K. pneumoniae with multiple β-lactam resistance highlights the necessity to improve the means of infection control and to develop effective alternative therapeutic strategies to reduce the number and effects of such multidrug-resistant pathogens.

Keywords: Klebsiella pneumoniae, UTI, Carbapenem resistance, Metallo-β-lactamase, *blaNDM*

1. Introduction

Klebsiella pneumoniae is a Gram-negative bacillus, non-sporing bacterium that has one of its distinguishing features a pronounced polysaccharide capsule and belongs to the family Enterobacteriaceae [1]. It is an opportunistic pathogen that is often involved in diverse healthcare-associated infections, such as pneumonia, septicemia, postoperative wound infection, and urinary tract infection [UTI] [2]. The growing level of antimicrobial resistance in K. pneumoniae, especially resistance to β-lactam antibiotics that are typically used as a first-line treatment is a serious risk to the health of the population [3]. More so, the occurrence and spread of multidrug-resistant and widely drug-resistant organisms have significantly caused increased

morbidity and mortality rates, as well as the increased healthcare expenditure, because of the reduced therapeutic choice [4].

Klebsiella pneumoniae urinary infections in women are a major clinical issue because it is one of the most common healthcare-associated infections with up to 35 percent of all nosocomial infections [5]. Klebsiella species are the second most common causative agents of UTI in women after the Escherichia coli, and in this case the species has been cited as the causative organisms of about 8-15% of all UTI cases [6]. The clinical picture of such infections differs significantly and can be characterized by such complications as asymptomatic bacteriuria, ischemic and life-threatening urosepsis, and the severity is more pronounced in women with predisposing risk factors, including diabetes mellitus, structural abnormalities of the urinary tract, or weakened immune response [7].

Treatment of UTIs in K. pneumoniae has grown more complex due to the growing speed of antimicrobial resistance, especially to β-lactam antibiotics, such as penicillins, cephalosporins, and carbapenems, which previously was the cornerstone of treatment [8]. Rapid spread of resistance mechanisms, in particular, the expression of extended-spectrum β-lactamases, carbapenemases, and others, have significantly decreased the effectiveness of these agents [9]. Extended-spectrum β-lactamases confer the resistance to a large range of β-lactam-based antibiotics, the third-generation cephalosporins, whereas carbapenemases, including metallo-β-lactamases, undermine the action of carbapenems which are generally considered to be the last resort of treatment of severe cases of Klebsiella infection [10].

The dissemination of ESBL producing and carbapenem resistance K. pneumoniae has been extensively reported, and currently is considered to be one of the most significant public health problems, with numerous outbreaks spread around the world [11]. To counter this emerging danger, the Centers of Disease Control and Prevention in the United States declared carbapenem-resistant Enterobacteriaceae, such as K. pneumoniae, as an emergency to the general health [12].

In this respect, this study was intended to establish the antimicrobial susceptibility profile of the K. pneumoniae isolates identified by identification of the association of the isolates with women with UTI, to identify the genes linked with the expression of the metallo-β-lactamase-mediated resistance at the molecular level, and to determine the genetic relatedness of the resistant K. pneumoniae isolates using the multilocus sequence typing. The acquisition and transfer of resistance determinants by Klebsiella species via mobile genetic units, particularly plasmids is major in the development and persistence of antimicrobial resistance. Such factors as the use of antibiotics in excess and improper use, improperly controlled infection control practices, and pressures related to hospitals contribute to the further promotion of the process [13–15]. One of the most important factors related to the emergence of the multidrug-resistant K. pneumoniae is the expression of β-lactamases [and, in particular, extended-spectrum β-lactamases and carbapenemases] [13,16,17].

Of particular concern is that ESBN producing and carbapenem-resistant K. pneumoniae has resulted in a decreased treatment option and poor clinical outcomes in women, increased morbidity, mortality, and medical expenses [18]. The use of last-resort antibiotics such as colistin, tigecycline, and new combinations of antibiotics can be less efficient, more toxic, and expensive to use by women with ESBL-producing or carbapenem-resistant strains of Klebsiella [13,16,19].

Measures to reduce the spread of antibiotic-resistant K. pneumoniae in patients with UTI are highly significant to improve the patient outcomes and burden the health care system. The solutions may be improved antimicrobial stewardship programs, improved infection management, development of new drugs or other interventions, and the emergence of fast diagnostics to apply the right antibiotics [13–15].

Despite the increasing global prevalence of carbapenem-resistant *Klebsiella pneumoniae*, limited molecular data are available regarding metallo-β-lactamase-producing isolates among urinary tract infection patients in Iraq, particularly in Babylon province. Therefore, this study aimed to determine the antimicrobial

susceptibility profile of *Klebsiella pneumoniae* isolated from urinary tract infections and to detect metallo-β-lactamase genes using PCR.

2. Materials and Methods

Isolation and Culture Conditions of Bacteria.

This study was designed as a cross-sectional laboratory-based study to investigate antimicrobial resistance and the presence of metallo-β-lactamase genes in Klebsiella pneumoniae isolates obtained from urinary tract Between November 2025 and December 2025, a total of 250 clinical urine samples were collected infections. from patients with suspected urinary tract infections and subjected to bacterial isolation of *Klebsiella* The samples were collected from patients *pneumoniae* using selective and non-selective culture media. attending hospitals in Babylon Governorate, Iraq. Urine specimens were obtained from patients with clinically suspected urinary tract infections and processed in the microbiology laboratory according to standard microbiological procedures.

The preliminary growth was done on the MacConkey agar (HiMedia, India) and Pseudomonas Chromogenic agar (Paronadisa, Spain). After isolation, the purification of the bacteria colonies was done on Brain Heart Infusion agar (HiMedia, India). The confirmed isolates were preserved in Brain Heart Infusion broth (HiMedia, India) and stored at −80 °C for further analysis

Ethical Approval

The Ethics Committee of the Department of Biology, College of Education, University of Al-Qadisiyah, Iraq had accepted the study (Ethical Approval No. 598, 13 November 2025). All the procedures were performed as per institutional ethics and declaration of Helsinki. The informed consent was provided in the cases where it was necessary and all data were handled confidentially.

Bacterial Identification

Initial suspicion of the isolates of K. pneumoniae was done using the conventional biochemical tests, such as catalase test, oxidase test, and motility test. The positive identification was made with the help of the automated Vitek 2 system (bioMerieux, France) that has Gram-negative identification cards.

Antimicrobial Susceptibility

Antimicrobial Susceptibility Testing (AMST) is a laboratory procedure which is applied to comply with the responsiveness of bacterial isolates to antimicrobial agents and identify antimicrobial resistance patterns.
The susceptibility of the isolates to antimicrobials was determined by disk diffusion test on Mueller-Hinton agar (HiMedia, India) as per the recommendations of Clinical and Laboratory Standard Institute (CLSI, 2023). Escherichia coli ATCC 25922 was used as a quality control strain. The antibiotics that were evaluated were amoxicillin-clavulanate, ticarcillin-clavulanate, ceftazidime, cefotaxime, ceftazidime-avibactam, fosfomycin, imipenem, and meropenem. The selected antibiotics represent commonly used antimicrobial agents for the treatment of urinary tract infections and include different classes of β-lactam and non-β-lactam antibiotics commonly used in clinical practice.

Molecular Diagnosis of Metallo β-Lactamase Genes.

Genomic DNA Extraction

In vivo bacterial cultures were grown overnight after which genomic DNA was extracted by using the Presto™ Mini gDNA Bacteria Kit (Geneaid, Taiwan) under the protocol of the manufacturer. NanoDrop Lite UV-Vis spectrophotometer (Thermo Scientific, USA) was used in the determination of quality and concentration of the extracted DNA.

The MBL Genes were amplified using PCR.

Assays of polymerase chain reactions were conducted with the help of the specific sets of primers to the *blaNDM* and blaFIM genes of metallo- β-lactamase. Table 2 summarizes the sequences of the primers used in this study.

Table 2. Primer sequences, PCR amplification of metallo- β-lactamase gene.

Primer	Sequence (5'-3')		Product Size	Genbank
bla-IMP	F	TGGGGCGTTGTTCCTAAACA	371bp	LC103182.1
	R	CTTTCAGGCAGCCAAACCAC		
bla-VIM-1	F	TCCACGCACTTTCATGACGA	503bp	NG_050336.1
	R	AAGTCCCGCTCCAACGATTT		
bla-AIM-1	F	CCACAGATCCTGGCCAACAT	409bp	NG_048689.1
	R	GGAAGACGTCGTCCGAGATC		
bla-NDM	F	CAGTCGCTTCCAACGGTTTG	529bp	MF379690.1
	R	ATCACGATCATGCTGGCCTT		
bla-SPM	F	GTTTTCGTCGTCACAGACCG	439bp	KC710242.1
	R	GAGCCGGTCCTGGAAATGAA		
bla-GIM	F	ATGAAGATCGCACTGCTGGT	379bp	NG_049143.1
	R	CTTCCAACTTTGCCATGCCC		
bla-FIM	F	TGGAGGATTCTTATGCGCCC	519bp	NG_049960.1
	R	AATGACCAGCGGATGCAGAA		

Polymerase chain reaction PCR was done in a T100 Thermal Cycler (Bio-Rad, USA) GoTaq Green PCR Master Mix (Promega, USA). The individual amplification reactions were composed of 5 µL of genomic DNA template (50ng/5mmol), 1 µL of forward and reverse primer at a concentration of 10pmol/uL, 12.5 µL of GoTaq -Green Master Mix and 5.5 µL of nuclease free water. The PCR amplification regime was a preliminary denaturation period of 95°C in 5 min, 35 cycles of denaturation of 95°C in 30 s, primer annealing of 58°C in 30 s, and extension of 72°C in 1 min. An extension step was finally done at 72°C with 5 minutes after which the reactions were maintained at 4 °C. Positive and negative controls were included in each PCR run to ensure the reliability of amplification results. Sterile nuclease-free water was used as a negative control, while previously confirmed positive isolates were used as positive controls.

Agarose gel electrophoresis

Agarose gel electrophoresis was used to resolve the amplified PCR products using 2% gel of agarose that was stained in 0.5X TrisborateEDTA buffer and ethidium bromide (BioBasic, Canada). Separations were performed in 100 V with a 60-minute power supply on a PowerPac HC power supply (Bio-Rad, USA). The DNA bands were visualised and documented under ultraviolet light using a UV transilluminator (Wised, Korea).

Statistical analysis

The statistical analysis was conducted to determine the relationship between the existence of the metallo-β-lactamase genes and the resistance against carbapenems. Where appropriate, a chi-square test was conducted and the level of statistical significance was considered to be p-value less than 0.05.

3. Results

Bacterial Isolation and Prevalence

Out of 250 urine samples, bacterial growth was detected in 218 samples (87.2%), while no bacterial growth was observed in 32 samples (12.8%). *Klebsiella pneumoniae* was the most prevalent isolate in the 35 cases, which is 16.06 out of the total positive cultures. Other dominant species were Escherichia coli (44.49 percent), Proteus spp. (14.22 percent), Enterobacter spp. (13.76 percent) and Pseudomonas spp. (11.47 percent) (Table 1).

Table 1: Bacterial culture distribution in a urine culture (n= 218).

Cultivation on MacConkey agar	Isolate	Frequency	%
Growth	*Klebsiella pneumoniae*	35	16.06
	Escherichia coli	97	44.49
	Proteus spp.	31	14.22
	Enterobacter spp.	30	13.76
	Pseudomonas spp.	25	11.47
Total		218	100

Klebsiella pneumoniae antimicrobial Susceptibility Profile.

The 35 isolates of *Klebsiella pneumoniae* were shown to have an extraordinarily high level of resistance to β-lactam antibiotics and β-lactam / -lactamase inhibitor combinations. A hundred percent resistance was seen against amoxicillin -clavulanate (AMC), ticarcillin -clavulanate (TIM), ceftazidime (CAZ), cefotaxime (CTX), ceftaroline -avibactam (CPA), piperacillin -tazobactam (TZP), and fosfomycin (FOS). The resistance to carbapenem was not consistent: imipenem (IPM) had a resistance of 83 percent, and meropenem (MEM) had a susceptibility of 83 percent. Aztreonam (ATM) and amikacin (AN) were considered to be highly active (91% and 97% susceptibility, respectively). Ciprofloxacin (CIP) and levofloxacin (LVX) showed high resistance and effectiveness, respectively, in 94 and 94 percent of isolates respectively in the group of fluoroquinolones. The activity of ceftolozane-tazobactam (CT), tigecycline (TGC), and chloramphenicol (C) was excellent (Table 2).

Table 2. Patterns of antimicrobial resistance against *Klebsiella pneumoniae* (n = 35).

Antimicrobial Agent	Resistant (R)	Intermediate (I)	Susceptible (S)
Amoxicillin-clavulanate (AMC)	35 (100%)	0 (0%)	0 (0%)
Ticarcillin-clavulanate (TIM)	35 (100%)	0 (0%)	0 (0%)
Ceftriaxone (CRO)	34 (97%)	1 (3%)	0 (0%)
Ceftazidime (CAZ)	35 (100%)	0 (0%)	0 (0%)
Cefotaxime (CTX)	35 (100%)	0 (0%)	0 (0%)
Ceftazidime-avibactam (CPA)	35 (100%)	0 (0%)	0 (0%)
Aztreonam (ATM)	3 (9%)	0 (0%)	32 (91%)
Imipenem (IPM)	29 (83%)	0 (0%)	6 (17%)
Meropenem (MEM)	5 (14%)	1 (3%)	29 (83%)
Amikacin (AN)	1 (3%)	0 (0%)	34 (97%)
Ciprofloxacin (CIP)	33 (94%)	0 (0%)	2 (6%)
Levofloxacin (LVX)	2 (6%)	0 (0%)	33 (94%)

Chloramphenicol (C)	0 (0%)	0 (0%)	35 (100%)
Ceftolozane-tazobactam (CT)	0 (0%)	3 (9%)	32 (91%)
Tigecycline (TGC)	2 (6%)	0 (0%)	33 (94%)
Fosfomycin (FOS)	35 (100%)	0 (0%)	0 (0%)
Piperacillin-tazobactam (TZP)	35 (100%)	0 (0%)	0 (0%)

Classification of Isolates by Resistance Level

The 35 *Klebsiella pneumoniae* isolates were classified into multidrug-resistant and extensively drug-resistant phenotype on the basis of antimicrobial resistance profiles. None of the isolates was classified as either non-multidrug or pandrug-resistant. Six isolates (17.14%), fulfilled the definition of the multidrug resistance, as they were indicated to be resistant to three or more antimicrobial classes, and the highest percentage of the isolates was 29 (82.86%), as indicated in Table 3.

Table 3: Resistance pattern classification of *K. pneumoniae* isolates (n = 35).

Resistance Pattern	Definition	Number of Isolates	Key Antibiotics Resistant
Non-MDR	Susceptible to all or resistant to 1–2 classes	0 (0%)	None
MDR	Resistant to ≥3 antibiotic classes	6 (17.14%)	β-lactams, CIP; susceptible to MEM, AN, LVX, ATM
XDR	Resistant to all but 1–2 classes	29 (82.86%)	β-lactams (including carbapenems), CIP, FOS; susceptible only to AN, LVX, ATM, CT, TGC
PDR	Resistant to all tested classes	0 (0%)	None

Molecular Detection of Metallo-β-Lactamase (MBL) Genes

PCR analysis was performed on 29 *K. pneumoniae* isolates to detect seven MBL genes. The *blaNDM* and *bla*FIM genes were present in all 29 isolates (100%). In contrast, *bla*SPM, *bla*GIM, *blaVIM*, *blaIMP*, and *bla*AIM were not detected in any isolate (0%) (Table 4). Agarose gel electrophoresis confirmed the amplification of *blaNDM* (529 bp) and *bla*FIM (519 bp), while no bands were observed for the other MBL genes (Figures 1–8 in supplementary data).

Table 4: PCR results for MBL gene detection in *K. pneumoniae* isolates (n = 29).

Gene	Positive (n)	Positive (%)	Negative (n)	Negative (%)
blaNDM	29	100%	0	0%
*bla*FIM	29	100%	0	0%
*bla*SPM	0	0%	29	100%
*bla*GIM	0	0%	29	100%
blaVIM	0	0%	29	100%
blaIMP	0	0%	29	100%
*bla*AIM	0	0%	29	100%

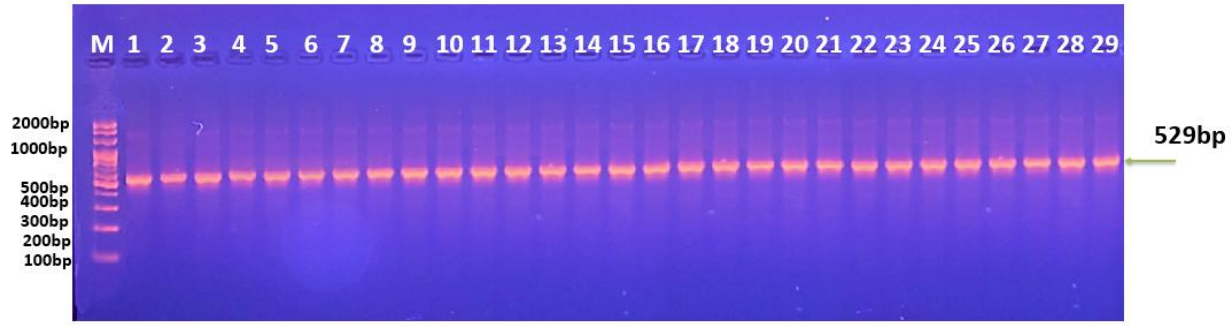

Figure 1. Agarose gel electrophoresis which demonstrates PCR amplification of the metallo- β-lactamase encoding gene *blaNDM* in carbapenem-resistant isolates of Klebsiella pneumoniae. Lane M is the size marker of the molecules (100-2000 bp), and lanes 1-29 are isolates that are positive *blaNDM* gene combines and they produced an amplicon of 529 bp.

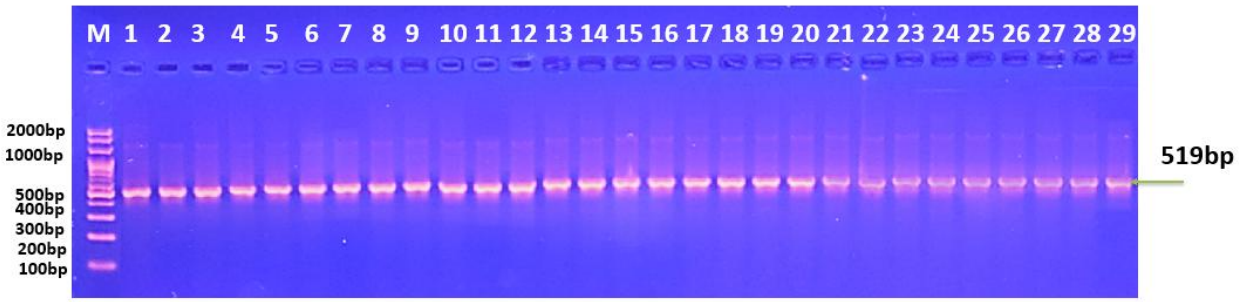

Figure 2. The electrophoresis shown in agarose gel confirms the amplification of the metallo-blaFIM gene of blaFIM gene in carbapenem-resistant isolates of Klebsiella pneumoniae. Lane M shows the molecular weight marker (100 -2000 bp) and lanes 1-29 are the isolates that were positive in the blaFIM gene, and a certain amplicon of 519 bp was obtained.

Figure 3. An agarose gel electrophoresis with the PCR analysis of the metallo-β-lactamase-coding blaSPM gene across the carbapenem-resistant *Klebsiella pneumoniae* isolates. The size marker (M) was used to mark the size of the molecules in lane M and lanes 1-29 do not exhibit amplification of the blaSPM gene as the particular size of the PCR product of 409 bp is not observed.

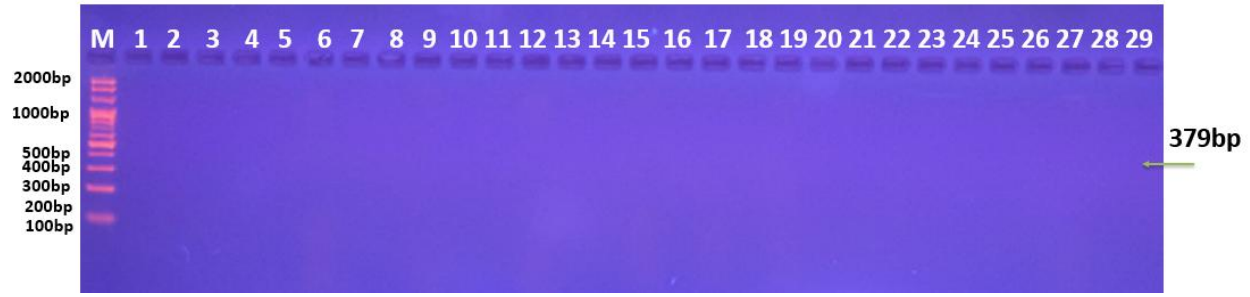

Figure 4. Agarose gel electrophoresis demonstrating screening of the PCR-encoded metallo- β-lactamase-binding blaGIM gene in the carbapenem-resistant isolates of Klebsiella pneumoniae. Lane M is the marker of molecular weight (100-2000 bp), and the rest of the lanes 1-29 are not amplified with the blaGIM gene, this is determined by the lack of the expected 409 bp PCR product.

Figure 5. Agarose gel electrophoresis representing PCR analysis of the gene encoding metallo-β-lactamase-*blaVIM*-1 in carbapenem resistant isolate of Klebsiella pneumoniae. Lane M is the marker corresponding to the molecular sizes (100 2000 bp), whereas lanes 129 indicate a lack of amplification of the *blaVIM*-1 gene, which is indicated by the lack of the predicted 503 bp PCR product.

Figure 6. Agarose gel electrophoresis showing PCR screening *blaIMP* gene encoding metallo- β-lactamase in carbapenem-resistant isolates of Klebsiella pneumoniae. Lane M represents the molecular weight maker (1002000 bp), and lane 129 does not amplify the bla IMP gene, as compared by the lack of the 371 bp PCR band.

Figure 7. Agarose gel electrophoresis that illustrates PCR analysis of a metallo- β-lactamase -encoding blaAIM -1 gene in carbapenem resistant isolates of Klebsiella pneumoniae. Lane M indicates the size of the molecular size marker (1002000 bp), and lanes 1-29 depict no amplification of the blaAIM-1 gene, and this is confirmed by the lack of 409 bp of the anticipated PCR product.

Statistical Association Between MBL Genes and Carbapenem Resistance

A strong statistical association was observed between the presence of *blaNDM* and *bla*FIM genes and resistance to imipenem ($p < 0.01$). All 29 isolates harboring these genes were resistant to imipenem, confirming the role of MBL production in carbapenem resistance.

4. Discussion:

The current article examined the phenotypic and molecular phenotypes of the β-lactam-resistant *Klebsiella pneumoniae* isolates obtained in women with urinary tract infections [UTIs] in Hospitals in Babylon Governorate. The results show a worrying pattern of high prevalence of antibiotic resistance, especially to those that are widely used such as β-lactams, dominance of genes that encode metallo- β-lactamase [MBL] that imparts resistance to carbapenems.

The proportion of the K. pneumoniae isolates [16.06] in the urine samples is similar to the earlier findings that indicate Klebsiella spp. as the second pathogen that causes UTIs in women, second to Escherichia coli [20]. This underscores the clinical significance of K. pneumoniae as an additional important opportunistic organism in this category of patients.

The high resistance rates observed in this study may be attributed to the widespread use and misuse of β-lactam antibiotics in clinical practice. The continuous exposure of bacterial pathogens to these antibiotics facilitates the selection of resistant strains and promotes the dissemination of resistance genes among *Klebsiella pneumoniae* populations [21]. It is possible to explain the resistance by the expression of extended-spectrum β-lactamases [ESBLs] and carbapenemases that are the most well-known resistance mechanisms in K. pneumoniae [22].

The observed difference in susceptibility between imipenem and meropenem may be attributed to variations in resistance mechanisms, including differential expression of carbapenemase enzymes, porin loss, or efflux pump activity. Similar variations in carbapenem susceptibility patterns have been reported in previous studies of *Klebsiella pneumoniae* isolates [23].

Of particular concern is the fact that the rate of resistance to carbapenems, which is typically regarded as the last resort in treating infections caused by Klebsiella is quite elevated [24]. It is not the only one to discover it as the global tendency is to increase the resistance to carbapenems in K. pneumoniae which is proclaimed by the Centers of Disease Control and Prevention [CDC, 2021] as an immediate public health emergency [25].

All 29 isolates of K. pneumoniae possessed *blaNDM* and *blaFIM MBL* genes (100%) by molecular identification. This high prevalence of the MBL genes is consistent with the observed carbapenem resistance profile and demonstrates the significance of the same resistance determinants in this case of the K. pneumoniae isolates. These findings are also clinically relevant as shown by the statistical association that exists between the presence of MBL genes and resistance to carbapenems. The high prevalence of *blaNDM* detected in this study is of particular concern, as this gene is one of the most widely distributed carbapenemase genes among Gram-negative bacteria worldwide. The presence of *blaNDM* significantly contributes to carbapenem resistance and facilitates the rapid dissemination of resistant strains through mobile genetic elements such as plasmids. Similar findings have been reported in several regional and international studies, highlighting the growing public health threat posed by NDM-producing *Klebsiella pneumoniae*.

Similar findings have been reported in several studies conducted in different regions worldwide. Previous studies have documented a high prevalence of multidrug-resistant *Klebsiella pneumoniae* and the increasing dissemination of *blaNDM* genes among clinical isolates, highlighting the global spread of carbapenem-resistant strains [26,27].

Particular attention should be paid to an increase and distribution of MBL-producing K. pneumoniae, which limited the existing treatment options greatly. The necessity to use last-resort antibiotics, such as colistin, tigecycline, or new combinations of antibiotics, which are less effective, more toxic, and costly, is typically observed in such infections [13,16,19].

The high prevalence of MBL-producing K. pneumoniae isolates with extensive β-lactam resistance is a major issue of concern to this research population with UTIs. These infections predispose the woman and can result in the asymptomatic bacteriuria up to life-threatening urosepsis, and they are more susceptible to these infections due to other anatomical and physiological factors [27].

ESBL-producing and carbapenem-resistant K. pneumoniae spreading is a global single public health concern, and extensive epidemics of the bacteria have been reported across the world [26]. This study outcome belongs to an ever-increasing body of literature to highlight how these resistant strains occur in women with UTI which further accentuates the fact that a holistic approach should be developed in order to counter this health hazard to the population.

Tough measures to contain the occurrence of antibiotic-resistant K. pneumoniae in the woman with UTIs are necessary to improve patient outcomes and reduce healthcare system associated pressure. These strategies may include improved antimicrobial stewardship interventions, improvement of infection control, development of new antimicrobials or alternative treatments, and provision of rapid diagnostic tests to inform proper antimicrobial use [13–15].

The programs of antimicrobial stewardship will be oriented at maximizing the existing antibiotics, reasonable use of carbapenems, and de-escalation strategies because they would reduce the selection pressure by which the resistance would increase. Realizing the place of spread of resistant Klebsiella strains in healthcare facilities could be contained through the introduction of superior measures in infection control, such as the increased effectiveness of hand hygiene, the environmental cleaning process, and the screening and isolation practice [27].

One of the possible alternatives to treating infections caused by MBL-producing K. pneumoniae can be innovations regarding the development of new antibiotics or other types of treatment, such as the use of a combination of already known antibiotics, the phage therapy, or the adjuvant treatment [19,29]. Moreover, the prompt identification of the presence of the resistance mechanisms, such as MBLs, through the use of the rapid diagnostic tests may inform the selection of the appropriate antibiotic therapy and determine the employment of the infection control measures [14].

The high prevalence of carbapenem-resistant Klebsiella pneumoniae observed in this study has important clinical implications. Infections caused by these resistant strains limit available treatment options and may lead to increased morbidity, prolonged hospitalization, and higher healthcare costs. It is on some limitations that the results of this study can be interpreted. It was conducted within a single healthcare facility and the sample size was representative of the local epidemiology but might not be applicable at larger geographical locations. Further studies of bigger and multi-centre cohorts would introduce a more in-depth view of the tendencies in the regional and national profiles of K. pneumoniae resistance.

In conclusion, the existing study introduces the problem of disastrous rates of MBL-producing, β-lactam-resistant K. pneumoniae in women with UTIs in hospitals in Babylon Governorate, Iraq. The high resistance rates, in particular, the carbapenem resistance, and the high frequency of *blaNDM* and blaFIM MBL genes all underline the relevance of improved infection control measures and improved antimicrobial stewardship, as well as the development of novel treatment methods to deal with this threat to the general health. To

improve patient outcomes and reduce healthcare systems cost, there is a necessity to solve the problems of antibiotic-resistant K. pneumoniae in UTI among women.

Conclusion

According to this paper, urinary tract infections are major infections that are associated with a high prevalence of β-lactam-resistant *Klebsiella pneumoniae* in women. Most β-lactam antibiotics showed very high resistance rates among the isolates, and the rate of resistance to carbapenems was rather high, meditated as the last-resort drugs. Molecular findings indicated the presence of *blaNDM* and blaFIM metallo-β-lactamase in all the carbapenem resistant isolates, a fact that indicated that they significantly contributed to the high levels of drug resistance. The exceptionally high association of the genes with carbapenem resistance illustrates the clinical importance of the genes and absence of treatment interventions to treat form of infection. All these findings underline the need to elevate antimicrobial stewardship, infection control processes, and routine molecular monitoring to reduce the spread of resistant K. pneumoniae and help in the correct selection of antibiotics in the clinical practice.

Acknowledgment

The authors would like to thank the Department of Biology, College of Education, University of Al-Qadisiyah for providing the necessary facilities and support for this study. We also acknowledge the medical and laboratory staff of the hospitals in Babylon Governorate for their assistance in sample collection and laboratory processing, as well as all patients who agreed to participate in this study.

References:

1. Rahana Khan, N., Amjad, D., Khan, M. K., Naseer, T., Shahzadi, Z. K., Shoukat, M. U., et al. (2025). Molecular characterization of *Klebsiella pneumoniae* from poultry. *Frontiers in Medical and Health Research, 3*(9), 51–60.
2. Rana, D. S., Sharma, V., & Sheershwal, A. (2025). Host–pathogen interactions in urinary tract infections. *Urological Science, 36*(2), 61–75.
3. Shah, A. A., Alwashmi, A. S., Abalkhail, A., & Alkahtani, A. M. (2025). Emerging challenges in *Klebsiella pneumoniae*. *Microbial Pathogenesis*, 107399.
4. Gajic, I., Tomic, N., Lukovic, B., Jovicevic, M., Kekic, D., Petrovic, M., et al. (2025). A comprehensive overview of antibacterial agents for combating MDR bacteria. *Antibiotics, 14*(3), 221.
5. Fekadu, S., Weldegebreal, F., Shumie, T., & Mekonnen, G. K. (2025). A comparative study on nosocomial and community-acquired bacterial urinary tract infections. *Frontiers in Epidemiology, 5*, 1517476.
6. Kimunya, F. W. (2025). *Prevalence and antimicrobial susceptibility profiles of urinary tract infections* (Doctoral dissertation). COHES–Jomo Kenyatta University of Agriculture and Technology.
7. Odunmbaku, R. (2025). *Evaluating training interventions* (Doctoral dissertation). University of Portsmouth.
8. Reza, N., Dubey, V., Sharland, M., & Hope, W. (2025). Antimicrobial use and resistance. *BMJ*, 391.
9. Dutta, A., Chowdhury, A., Roy, P., & Bhowmik, P. (2025). Effect of mutations on the evolution of extended-spectrum β-lactamases (ESBL). *Protein Journal*, 1–25.
10. Melinte, V., Radu, M. A., Văcăroiu, M. C., Mîrzan, L., Holban, T. S., Ileanu, B. V., et al. (2025). Carbapenem-resistant *Klebsiella pneumoniae* in Romania. *Antibiotics*.
11. Furlan, J. P. R., Zarrilli, R., Daoud, Z., He, F., & Ruan, Z. (2025). Global dissemination and evolution of epidemic multidrug-resistant Gram-negative bacterial pathogens. *Frontiers in Microbiology, 16*, 1583112.

12. Liu, L., Liu, S., Yang, Z., Wang, F., Yuan, H., Xu, H., et al. (2025). Shifts in hospital-associated pathogens. *Journal of Infection in Developing Countries, 19*(7), 1100–1107.
13. Broberg, C. A., Palacios, M., & Miller, V. L. (2016). *Klebsiella*: A long way to go towards understanding this enigmatic jet-setter. *F1000Prime Reports, 6*, 64.
14. Navon-Venezia, S., Kondratyeva, K., & Carattoli, A. (2017). *Klebsiella pneumoniae*: A worldwide source of resistance. *FEMS Microbiology Reviews, 41*(3), 252–275.
15. Rodríguez-Baño, J., Rossolini, G. M., Schultsz, C., Tacconelli, E., & Murthy, S. (2021). A One Health approach to antimicrobial resistance. *Clinical Infectious Diseases, 72*(5), 858–864.
16. Paczosa, M. K., & Mecsas, J. (2016). *Klebsiella pneumoniae*: Going on the offense. *Microbiology and Molecular Biology Reviews, 80*(3), 629–661.
17. Borer, A., Eskira, S., Nativ, R., Riesenberg, K., & Saidel-Odes, L. (2022). Carbapenem-resistant *Klebsiella pneumoniae* infections: Epidemiology, risk factors, and clinical outcomes. *Antibiotics, 11*(4), 506.
18. Gadisa, E., Egyir, B., Adu, B., Ahmed, H., Disasa, G., & Tessema, T. S. (2024). Epidemiology and management of carbapenem-resistant *Klebsiella pneumoniae*. *Annals of Clinical Microbiology and Antimicrobials, 23*(1), 85.
19. Bassetti, M., Righi, E., Vena, A., Gatti, M., Furno, P., & Russo, A. (2023). New antimicrobial agents for the treatment of carbapenem-resistant Gram-negative infections. *Expert Review of Anti-Infective Therapy, 21*(2), 189–204.
20. Bayaba, S., Founou, R. C., Tchouangueu, F. T., Dimani, B. D., Mafo, L. D., Nkengkana, O. A., et al. (2025). High prevalence of multidrug-resistant and extended-spectrum β-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* isolated from urinary tract infections in the West region, Cameroon. *BMC Infectious Diseases, 25*(1), 115.
21. Dean, C. R., De Pascale, G., & Benton, B. (2018). Resistance of Gram-negative bacilli to antimicrobials. In *Antimicrobial resistance in the 21st century* (pp. 71–162). Springer.
22. Abebe, A. A., Birhanu, A. G., & Tessema, T. S. (2025). *Antibiotic resistance and virulence mechanisms in Klebsiella pneumoniae: Understanding for better interventions*. *Bacteria*, *5*(1), 9.
23. Jaramillo Cartagena, A., Taylor, K. L., Lopez, L. C., Su, J., Smith, J. T., Manson, A. L., et al. (2025). Carbapenem inoculum effect. *mBio, 16*(11), e01540-25.
24. Hetta, H. F., Alanazi, F. E., Ali, M. A. S., Alatawi, A. D., Aljohani, H. M., Ahmed, R., et al. (2025). Hypervirulent *Klebsiella pneumoniae*. *Pharmaceuticals, 18*(5), 724.
25. Centers for Disease Control and Prevention. (2021). *Antibiotic resistance threats in the United States, 2021*. U.S. Department of Health and Human Services.
26. Martínez-Álvarez, S. A., Asencio-Egea, M. Á., Huertas-Vaquero, M., Cardona-Cabrera, T., Zarazaga, M., Höfle, U., & Torres, C. (2025). Genomic epidemiology of ESBL- and carbapenemase-producing *Enterobacterales*. *Microorganisms, 13*(8), 1854.
27. Tocco Tussardi, I., Stevanin, G., Montesarchio, L., Palladini, F., Aprili, I., Zandonà, E., et al. (2025). Outbreak of NDM-producing *Klebsiella pneumoniae*. *Healthcare, 13*(12), 1457.
28. Gray, A., Ellis, B., & Loubani, O. (2025). Identification and initial resuscitation of critically unwell older patients. *Emergency Medicine Clinics of North America, 43*(2), 265–279.
29. Rodríguez-Baño, J., Gutiérrez-Gutiérrez, B., Machuca, I., & Pascual, A. (2018). Treatment of ESBL- and carbapenemase-producing *Enterobacteriaceae*. *Clinical Microbiology Reviews, 31*(2), e00079-17.