

CENTRAL ASIAN JOURNAL OF MEDICAL AND NATURAL SCIENCES
https://cajmns.casjournal.org/index.php/CAJMNS
Volume: 08 Issue: 01 | January 2027 ISSN: 2660-4159

Article

Targeted Molecular Screening of blaCTX-M, blaNDM, and blaKPC and Antimicrobial Resistance Profiling in Clinical Klebsiella pneumoniae Isolates from Baghdad Hospitals

Muhannad Moeen Abdallah[1]*

1. Lecturer, Directorate General of Education Baghdad Rusafa-3. The Ministry of Education. Baghdad, Iraq
* Correspondence: Mohanadalhasany@gmail.com

Abstract: Background: In microbiology procedure, *Klebsiella pneumoniae* develops particularly problematical after urine and blood specimens missing sensitivity to regularly used beta-lactam medical drug. Into hospitals, domestic information is required since the virulence manner may possibly vary in relation to antibiotic treatment, hospital environment and the Drug-resistant factors Spread by mixing isolates. Objective: This investigation measured the phenotypic antibiotic sensitivity of medical K. pneumoniae Collected inside Baghdad hospitals and surveyed the existence of three certain beta-lactam resistance genes blaNDM, blaCTX-M and blaKPC, by means of traditional PCR. Methods: A Prevalence study was done on 120 Patient samples, including 70 urine samples and 50 blood samples, Obtained during April to November 2024. Twenty-two unrefined K. pneumoniae bacteria existed identified through ordinary culture and biochemical processes. Sensitivity testing was accomplished through the Kirby-Bauer disc diffusion technique Based on CLSI guidance, and PCR yields were estimated through agarose gel electrophoresis Results: The maximum resistance rate was Observed for amoxicillin-clavulanic acid (18/22, 81.8%; P = 0.003). Insensitivity was as well highly to ceftriaxone and ceftazidime (16/22 each, 72.7%; P = 0.033), after that cefotaxime (15/22, 68.2%; P = 0.088). Carbapenems indicated minimum resistance rates, by 5/22 (22.7%) resistant to meropenem and 6/22 (27.3%) resistant to imipenem. PCR reveal blaCTX-M in 12/22 isolates (54.5%), blaNDM in 9/22 (40.9%), and blaKPC in 5/22 (22.7%). Conclusions: Enclosed by the limits of this isolate set, the results indicate a distinguished native load of ESBL-associated resistance and the existence of carbapenemase-related genes. The Investigation supports by repetitive sensitivity testing collected with select molecular showing that K. pneumoniae isolates are collected, in particular within serious infections or hospital sections wherever resistant strains possibly will spread.

Keywords: Resistance; CTX-M; NDM; Baghdad; *Klebsiella*; *ESBL*.

Citation: Abdallah, M. M. Targeted Molecular Screening of blaCTX-M, blaNDM, and blaKPC and Antimicrobial Resistance Profiling in Clinical Klebsiella pneumoniae Isolates from Baghdad Hospitals . Central Asian Journal of Medical and Natural Science 2027, 8(1), 111-121.

Received: 24th Aug 2026
Revised: 27th Sep 2026
Accepted: 20th Oct 2026
Published: 19th Nov 2026

Copyright: © 2027 by the authors. Submitted for open access publication under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/)

1. Introduction

Klebsiella pneumoniae is a main associate of Enterobacterales in clinical microbiology. It is collected from urinary tract patient, bloodstream, pneumonia, wound and device-related infections. Its significance is not restricted to matching at the bench; the bacterium is also known for its capability to obtain resistance factors that create routine treating further problematic (1, 2).

A public attention in *K. pneumoniae* due resistance to beta-lactam antibiotics. Extended-spectrum beta-lactamases (ESBLs), principally CTX-M-category enzymes, decrease the action of third-generation cephalosporins for example cefotaxime,

ceftriaxone, and ceftazidime. Such has been described in diverse clinical and environmental locations and residues pertinent for local hospital proceed (3-5).

Carbapenems are frequently kept for critical infections Resulting from ESBL-Providing Enterobacterales, but then the rate reduces while carbapenemase genes are existing. NDM and KPC enzymes are amongst the mechanisms that possibly will boost carbapenem resistance, moreover alone or composed with porin loss, efflux action, or additional beta-lactamases (6-9).

Intended for the analytic laboratory, phenotypic antimicrobial sensitivity testing remains the base for therapeutic management for it indications the last in vitro reaction of the isolate to the antibiotic. Molecular workout does not exchange this result, but it can explain whether significant convertible genes are existing. This is advantageous for surveillance, infection mechanism, and for explains uncommon or extreme resistance patterns.

Therefore, the recent study observed clinical K. pneumoniae isolates recovered from Baghdad hospitals from both phenotypic sensitivity to certain antibiotics and PCR recognition of blaCTX-M, blaNDM, and blaKPC. The aim was to existing a Cautiou: local report of the resistance form lacking claims further than the existing isolate-level data.

2. Materials and Methods

2.1 Study Design and Sample Collection

This Investigation was intended as a Observational laboratory investigation. Clinical samples were collected from patients Hospitalized to five main hospitals in Baghdad, Iraq, through the dated from April to November 2024. The obtained material involved 120 specimens: 70 urine samples and 50 blood samples. Each specimen was handled aseptically and processed within approximately two hours. After culture and identification, 22 non-duplicate K. pneumoniae isolates were included in the analysis.

2.2 Bacterial Isolation and Identification

Specimens were inoculated onto routine bacteriological media, including MacConkey agar, blood agar, and cystine-lactose-electrolyte-deficient agar for urine specimens. Suspected K. pneumoniae colonies were selected according to colony appearance, Gram-staining reaction, and conventional biochemical tests, including citrate utilization, urease, indole, triple sugar iron, methyl red, and Voges-Proskauer tests. Only one isolate from each patient/specimen episode was retained to avoid duplicate counting (10).

2.3 Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed by the Kirby-Bauer disc diffusion method on Mueller-Hinton agar. Zone diameters were interpreted according to CLSI criteria for Enterobacterales (6). The antibiotic panel included amoxicillin-clavulanic acid, ceftriaxone, cefotaxime, ceftazidime, meropenem, imipenem, gentamicin, ciprofloxacin, and nitrofurantoin. For the present analysis, the working dataset was summarized as sensitive or resistant.

2.4 DNA Extraction and PCR Amplification

Bacterial DNA was extracted by the boiling-lysis method. Conventional PCR was performed in 25 μL reaction mixtures containing approximately 1× PCR buffer, 1.5-2.0 mM $MgCl_2$, 200 μM dNTPs, 0.4 μM of each primer, 1 U Taq DNA polymerase, and approximately 2 μL of DNA template. The amplification program included initial denaturation at 95°C for 5 minutes; 30-35 cycles of denaturation at 95°C for 30 seconds, annealing at 55-60°C for 30 seconds, and extension at 72°C for 45 seconds; followed by final extension at 72°C for 5-7 minutes.

Table 1. Primer sequences, expected amplicon sizes, and reference records used for PCR detection of resistance genes (11-17).

Target gene	Primer / direction	Sequence (5'-3')	Amplicon size (bp)
blaCTX-M	CTX-M-U1 / Forward	ATGTGCAGYACCAGTAARGTKATGGC	~593
blaCTX-M	CTX-M-U2 / Reverse	TGGGTRAARTARGTSACCAGAAYCAGCG	~593
blaNDM	NDM-F / Forward	GGTTTGGCGATCTGGTTTTC	~621
blaNDM	NDM-R / Reverse	CGGAATGGCTCATCACGATC	~621
blaKPC	KPC-F / Forward	CGTCTAGTTCTGCTGTCTTG	~798
blaKPC	KPC-R / Reverse	CTTGTCATCCTTGTTAGGCG	~798

2.5 Gel Electrophoresis

PCR amplicons were separated on 1.5% agarose gel stained with ethidium bromide and visualized under ultraviolet illumination. A 100-bp DNA ladder was used as a molecular size marker. Bands at the expected approximate product size were recorded as positive reactions for the corresponding target gene.

2.6 Data Analysis

Data analysis was kept descriptive because the available dataset was aggregate rather than isolate-by-isolate. Frequencies and percentages were used to summarize susceptibility and PCR findings. Chi-square goodness-of-fit analysis was used to compare categorical counts where appropriate, and Fisher's exact test was considered when expected cell counts were small. A P value below 0.05 was treated as statistically significant. Correlation analysis, odds ratios, and phenotype-genotype association testing were not calculated because paired isolate-level data were not available.

3. Results and Discussion

3.1 Isolation of K. pneumoniae

Among the 120 clinical specimens processed during the study period, 22 non-duplicate K. pneumoniae isolates were recovered. This represented an overall recovery rate of 18.33%. These 22 isolates were used for the antibiotic susceptibility profile and PCR screening presented in the following sections.

3.2 Antimicrobial Susceptibility Profile

Resistance was mainly concentrated among beta-lactam agents commonly used in clinical settings (Table 2). Amoxicillin-clavulanic acid showed the highest resistance frequency (18/22, 81.8%; P = 0.003). Ceftriaxone and ceftazidime each showed resistance in 16/22 isolates (72.7%; P = 0.033), while cefotaxime resistance was observed in 15/22 isolates (68.2%; P = 0.088). Carbapenem resistance was lower, with 5/22 isolates (22.7%) resistant to meropenem and 6/22 (27.3%) resistant to imipenem. Gentamicin, ciprofloxacin, and nitrofurantoin showed variable resistance frequencies.

Table 2. Antimicrobial susceptibility profile of K. pneumoniae isolates with simple chi-square and P-value analysis.

Antibiotic	Sensitive n (%)	Resistant n (%)	χ^2	P value	Significance
Amoxicillin-clavulanic acid	4/22 (18.2)	18/22 (81.8)	8.91	0.003	**
Ceftriaxone	6/22 (27.3)	16/22 (72.7)	4.55	0.033	*
Cefotaxime	7/22 (31.8)	15/22 (68.2)	2.91	0.088	NS
Ceftazidime	6/22 (27.3)	16/22 (72.7)	4.55	0.033	*
Meropenem	17/22 (77.3)	5/22 (22.7)	6.55	0.011	*
Imipenem	16/22 (72.7)	6/22 (27.3)	4.55	0.033	*
Gentamicin	11/22 (50.0)	11/22 (50.0)	0.00	1.000	NS

Antibiotic	Sensitive n (%)	Resistant n (%)	χ^2	P value	Significance
Ciprofloxacin	9/22 (40.9)	13/22 (59.1)	0.73	0.394	NS
Nitrofurantoin	8/22 (36.4)	14/22 (63.6)	1.64	0.201	NS

Note. Chi-square values were calculated as simple goodness-of-fit comparisons between sensitive and resistant counts. *P < 0.05; **P < 0.01; ***P < 0.001; NS = not significant.

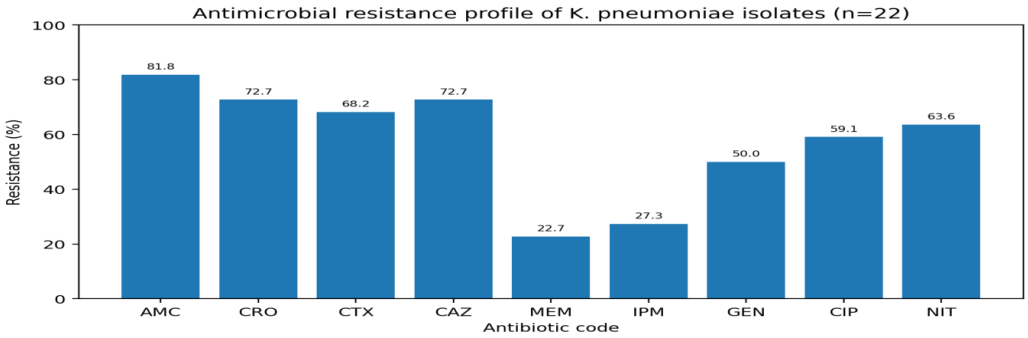


Figure 1. Aggregate resistance percentages among clinical K. pneumoniae isolates (n = 22). AMC = amoxicillin-clavulanic acid; CRO = ceftriaxone; CTX = cefotaxime; CAZ = ceftazidime; MEM = meropenem; IPM = imipenem; GEN = gentamicin; CIP = ciprofloxacin; NIT = nitrofurantoin.

3.3 Molecular Detection of Resistance Genes

PCR screening showed that blaCTX-M was the most frequent target, being detected in 12/22 isolates (54.5%; P = 0.670). The blaNDM gene was detected in 9/22 isolates (40.9%; P = 0.394), while blaKPC was detected in 5/22 isolates (22.7%; P = 0.011). The gel electrophoresis images showed bands at the expected approximate sizes for the tested genes.

Table 3. Molecular detection of resistance genes by PCR with simple chi-square and P-value analysis.

Resistance gene	Positive n (%)	Negative n (%)	χ^2	P value	Significance
blaCTX-M	12/22 (54.5)	10/22 (45.5)	0.18	0.670	NS
blaNDM	9/22 (40.9)	13/22 (59.1)	0.73	0.394	NS
blaKPC	5/22 (22.7)	17/22 (77.3)	6.55	0.011	*

Note. Chi-square values were calculated as simple goodness-of-fit comparisons between PCR-positive and PCR-negative counts. *P < 0.05; **P < 0.01; NS = not significant.

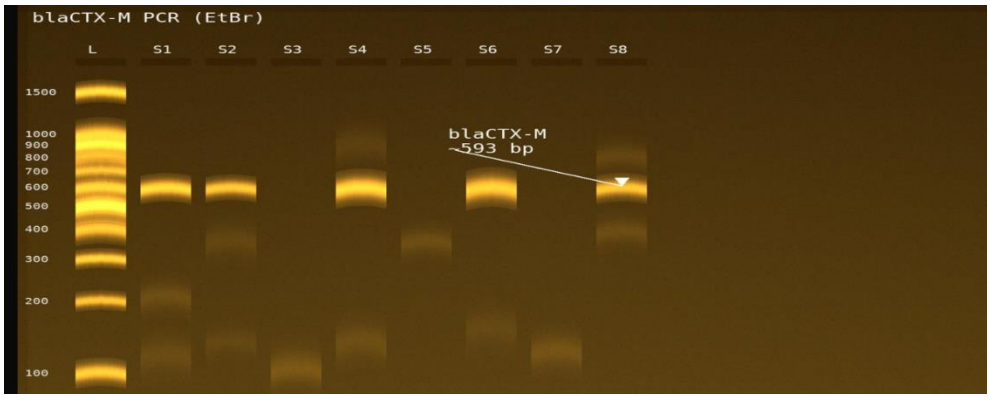


Figure 2. Agarose gel electrophoresis of PCR-amplified blaCTX-M (~593 bp) using EtBr staining. Lane L: 100-bp DNA ladder; lanes S1-S8: representative *K. pneumoniae* isolates. Bands at the expected size indicate blaCTX-M-positive reactions.

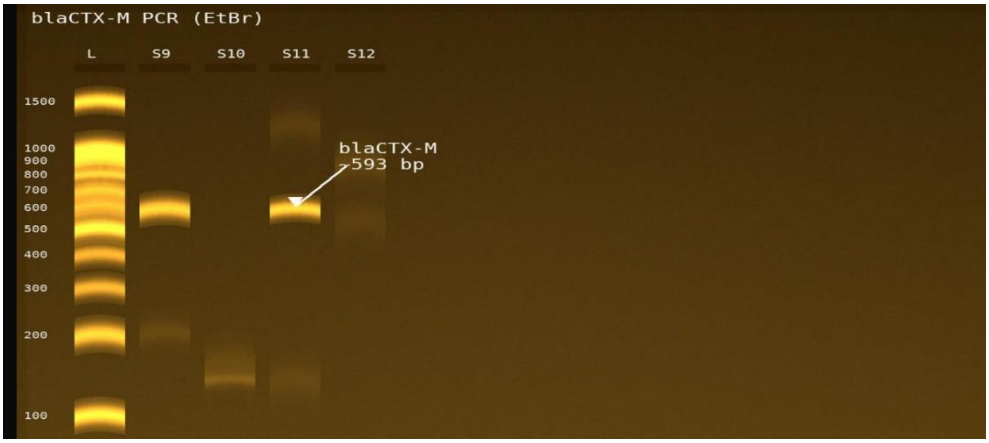


Figure 3. Agarose gel electrophoresis of PCR-amplified blaCTX-M (~593 bp) using EtBr staining. Lane L: 100-bp DNA ladder; lanes S9-S12: representative *K. pneumoniae* isolates. Bands at the expected size indicate blaCTX-M-positive reactions.

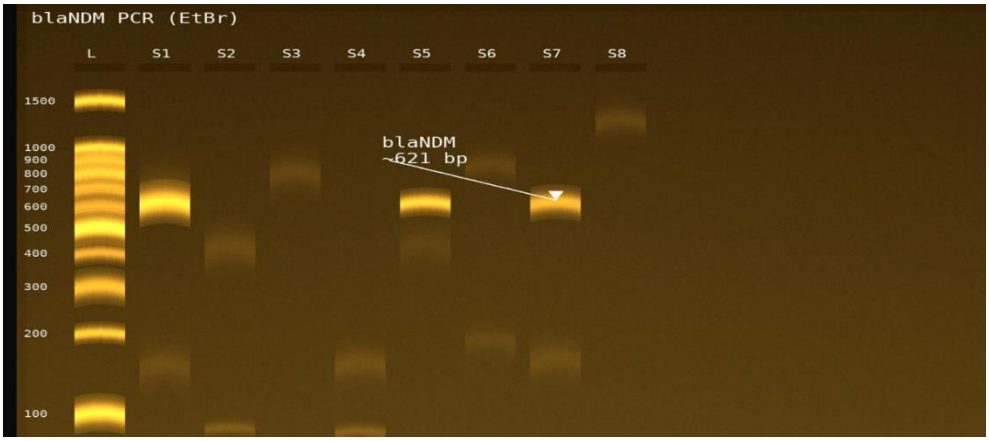


Figure 4. Agarose gel electrophoresis of PCR-amplified blaNDM (~621 bp) using EtBr staining. Lane L: 100-bp DNA ladder; lanes S1-S8: representative *K. pneumoniae* isolates. Bands at the expected size indicate blaNDM-positive reactions.

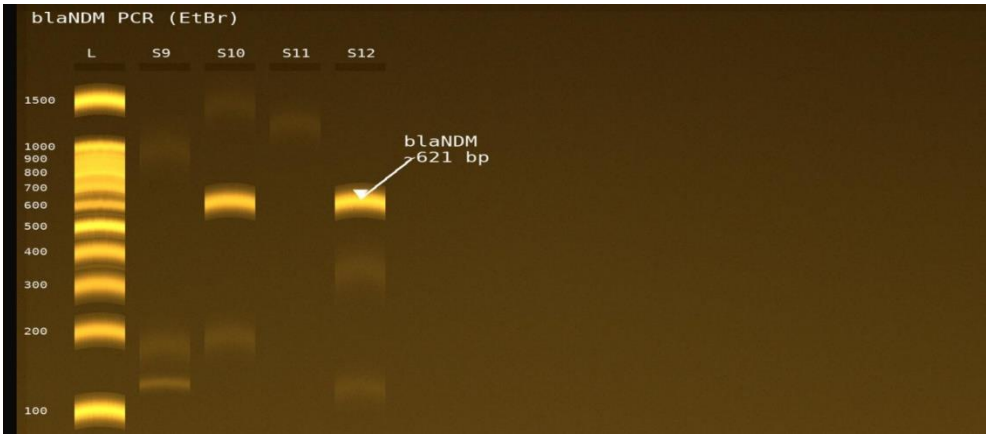


Figure 5. Agarose gel electrophoresis of PCR-amplified blaNDM (~621 bp) using EtBr staining. Lane L: 100-bp DNA ladder; lanes S9-S12: representative *K. pneumoniae* isolates. Bands at the expected size indicate blaNDM-positive reactions.

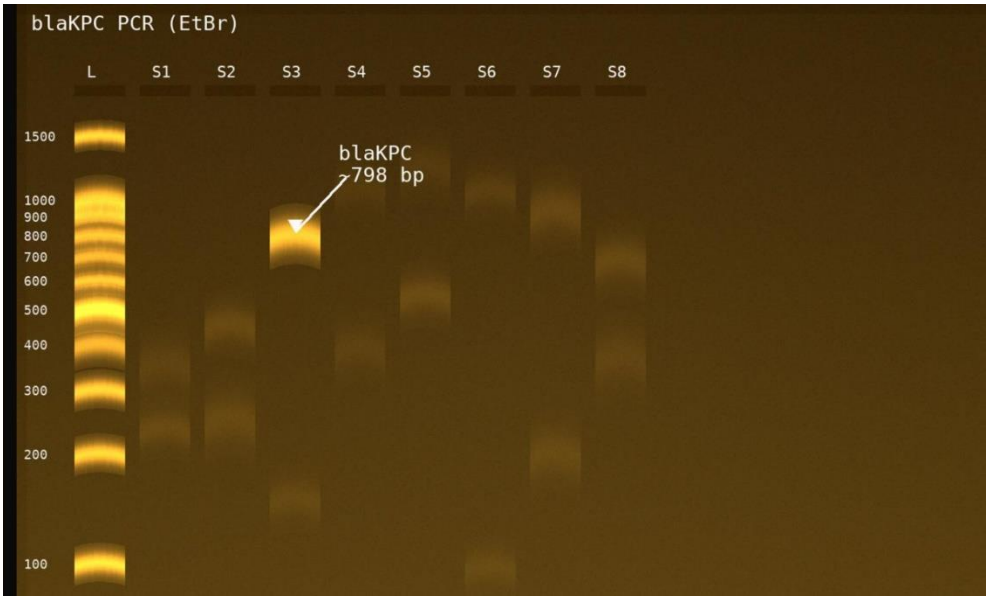


Figure 6. Agarose gel electrophoresis of PCR-amplified blaKPC (~798 bp) using EtBr staining. Lane L: 100-bp DNA ladder; lanes S1-S8: representative *K. pneumoniae* isolates. Bands at the expected size indicate blaKPC-positive reactions.

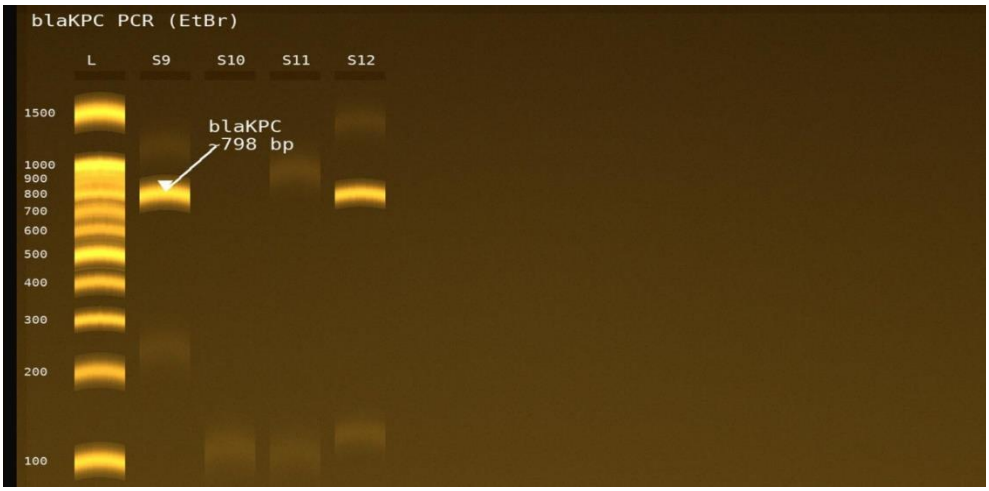


Figure 7. Agarose gel electrophoresis of PCR-amplified blaKPC (~798 bp) using EtBr staining. Lane L: 100-bp DNA ladder; lanes S9-S12: representative *K. pneumoniae* isolates. Bands at the expected size indicate blaKPC-positive reactions.

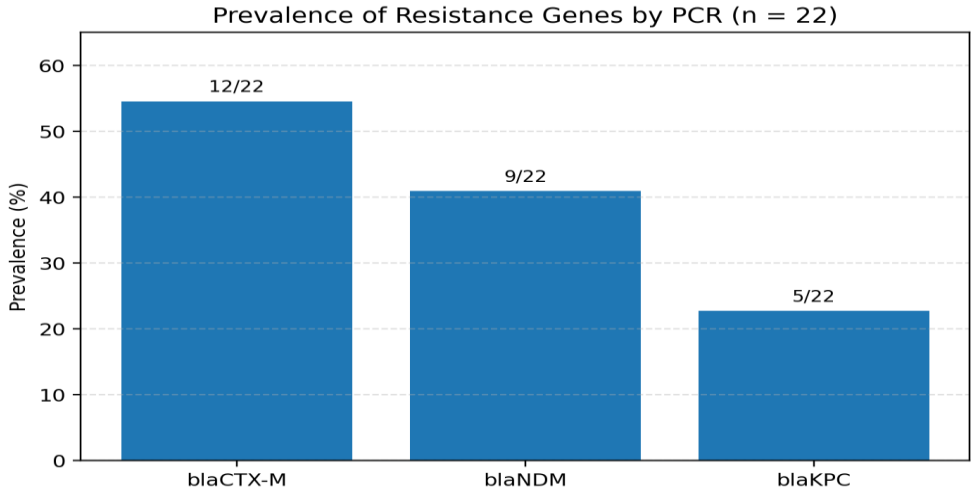


Figure 8. Prevalence of blaCTX-M, blaNDM, and blaKPC among *K. pneumoniae* isolates.

3.4 Distribution of Resistance Genes by Specimen Type

The distribution of gene-positive isolates according to specimen type is presented in Table 4. Of the blaCTX-M-positive isolates, 8/12 were recovered from urine and 4/12 from blood. For blaNDM, 6/9 positive isolates were from urine and 3/9 from blood. For blaKPC, 2/5 positive isolates were from urine and 3/5 from blood. Because the specimen-specific denominator of K. pneumoniae isolates was not available, these data are shown as distribution counts rather than as true specimen-specific prevalence rates.

Table 4. Distribution of resistance gene-positive isolates by specimen type.

Gene	Urine positive n (%)	Blood positive n (%)	Total positive	χ^2	P value	Significance
blaCTX-M	8/12 (66.7)	4/12 (33.3)	12	1.33	0.248	NS
blaNDM	6/9 (66.7)	3/9 (33.3)	9	1.00	0.317	NS
blaKPC	2/5 (40.0)	3/5 (60.0)	5	0.20	0.655	NS

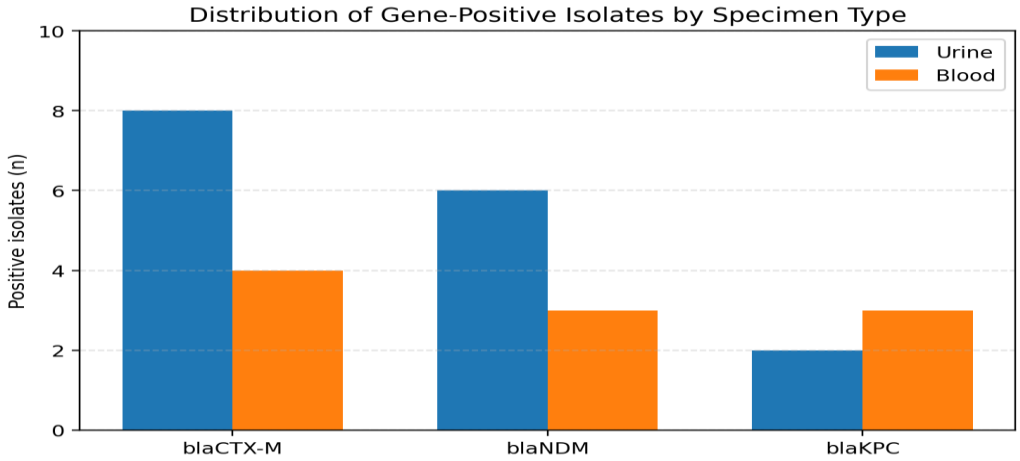


Figure 9. Distribution of resistance gene-positive isolates by urine and blood specimens.

3.5 Statistical Interpretation of Aggregate Results

The statistical analysis was used only to support the descriptive presentation of the aggregate results. Because the available data were not paired at the isolate level, the most defensible presentation was n (%), chi-square value, P value, and significance category for the main categorical outcomes.

For the antibiotic susceptibility table, the chi-square values indicate whether the sensitive and resistant counts for each drug differed from an equal distribution. This helps identify drugs with a dominant resistance or sensitivity pattern, but it should not be read as a predictor model.

Intended for the PCR table, the P values refer to the Equalize between positive and negative isolates for each aim gene. Directly statistical relationship among genes and antibiotic results was not essayed for the reason that the existing data did not relation to each gene end result to the complete antibiotic sensitivity profile of the similar isolate.

4. Discussion

The recent isolate regular indications a clear beta-lactam resistance problematic in clinical isolates. The manner was not identical across the Susceptibility panel. Resistance was maximum between amoxicillin-clavulanic acid and cephalosporins, although meropenem and imipenem retained Enhance in vitro respond. This particular interpretation Corresponds by means of the molecular results, wherever ESBL- and carbapenemase-linked genes were identified in the same group of isolates.

The collected of 22 K. pneumoniae isolates from 120 specimens provided an isolation percentage of 18.33%. The number is Moderate, so it must not be regarded as a city-wide Frequency Approximation. However, the conclusion is matching with the Ordinary clinical Contribution of K. pneumoniae in urine and blood Lab cultures. These findings of specimen types are advantageous in a Regional study for the reason that urine isolates frequently demonstrate Repetitive antimicrobial Vulnerability, although blood isolates signify a more immediate aggressive infection environment (18).

The furthermost straight phenotypic surveillance was the great resistance to amoxicillin-clavulanic acid in addition to to cephalosporins. In applied terms, these results mean that experiential requirement on ceftriaxone, ceftazidime, as well as cefotaxime would be insecure except sensitivity is definite. The detection of blaCTX-M in more than half of the isolates provides a plausible explanation for a substantial part of this cephalosporin resistance, since CTX-M enzymes are among the most widely reported ESBLs in Enterobacterales (3, 4, 19).

The cephalosporin resistance frequencies were higher than the frequency of blaCTX-M detection. This difference is expected in a PCR panel that targets only one ESBL family. Isolates without blaCTX-M may still carry blaSHV, blaTEM, AmpC enzymes, OXA-type enzymes, or other determinants. In addition, resistance can be strengthened by changes in outer-membrane permeability and efflux activity (7, 9, 20).

The lower resistance to meropenem and imipenem is encouraging, but it does not remove concern. The detection of blaNDM and blaKPC indicates that carbapenemase-related genes are already present in the tested collection. Therefore, the apparent activity of carbapenems in the overall table should be interpreted together with the molecular data, not separately from it.

The blaNDM result is important for hospital practice because NDM-type metallo-beta-lactamases can reduce the usefulness of carbapenems and may be carried on mobile plasmids. The detection of blaKPC adds another resistance mechanism to consider. Similar regional and international work has shown that phenotypic and molecular carbapenemase results need careful interpretation, especially when more than one enzyme type may circulate in hospitals (8, 9, 21, 22).

Resistance was not restricted to beta-lactams. Ciprofloxacin resistance reached 59.1%, gentamicin resistance reached 50.0%, and nitrofurantoin resistance reached 63.6%. These values suggest that the tested isolates may carry resistance beyond the beta-lactam group. However, a formal MDR classification was not calculated because that requires an isolate-by-isolate profile across antimicrobial classes (23).

The specimen-type distribution should be read with caution. More blaCTX-M-positive and blaNDM-positive isolates were counted among urine samples, while blaKPC-positive isolates were slightly more frequent among blood samples. This does not demonstrate a specimen link since the Environment of K. pneumoniae isolates from individually specimen type was not presented. All the same, the existence of carbapenemase genes between blood-derived isolates is clinically significant since resistant K. pneumoniae bloodstream contamination may possibly restrict treatment decisions and raise the essential for immediate infection-control methods.

Related with Iraqi studies, the recent results appropriate inside the broader local Care almost beta-lactam resistance in K. pneumoniae. Earlier studies Sourced from Baghdad and further Iraqi locations have described ESBL and carbapenemase genes in clinical isolates, even though the Specific rate of recurrence vary among studies. To that extent alterations are estimated for the reason that studies show a discrepancy in hospital type, specimen Origin, sampling historical, antibiotic panel, and molecular selected (24-27).

The conclusions are also In agreement by means of varied local and international indication. Assessments from the Arabian Peninsula and global investigation reports

remain to highlight the significance of resistant Gram-negative pathogens, excluding K. pneumoniae, in hospital-related and severe infections (28-32).

For Regular laboratories, the chief message is applied. Disc diffusion remains required because clinicians essential a direct vulnerability analysis for treatment. PCR improves value as soon as the laboratory requests to certificate resistance mechanisms, support local investigation, or study isolates from serious infections, regular infections, severe-care units, or potential hospital bunches.

The research has restrictions that should be set aside noticeable. The isolate number was small, and the accessible data was combined relatively than isolate-level. As a result, the study could not estimate true MDR rate of recurrence, gene-antibiotic relations, odds percentages, or correlation coefficients. The molecular board was also restricted to blaCTX-M, blaNDM, and blaKPC and did not consist of blaOXA-48-like, blaVIM, blaIMP, blaSHV, blaTEM, or AmpC genes. Sequencing and plasmid investigation were not accomplished, therefore the accurate variation, clonal circumstantial, and plasmid context keep on unknown.

Even though these limitations, the study delivers valuable local laboratory data. The approval among in height beta-lactam resistance and recognition of beta-lactamase genes maintenances continuous surveillance in Baghdad hospitals. A more continuation study with isolate-level information would agree to durable statistical analysis and a further correct assessment of multidrug resistance.

5. Conclusion

Clinical K. pneumoniae isolates collected within Baghdad hospitals in this research indicated great resistance to amoxicillin-clavulanic acid and cephalosporins. PCR as well distinguished blaCTX-M, blaNDM, and blaKPC amongst the confirmed isolates. The rate of recurrence of blaCTX-M maintenances an ESBL-associated factor of resistance, even though the existence of blaNDM and blaKPC point to that carbapenemase-related factors are existing in the isolate collection.

In use together, the results support merging phenotypic sensitivity analysis using selected PCR while resistant K. pneumoniae isolates are encountered. The conclusions must keep on restricted to this initial information, but the sample is related for local investigative practice and explains wide-ranging multicenter observation with larger isolate numbers and extended molecular boards.

REFERENCES

[1] Effah, C. Y., Sun, T., Liu, S., & Wu, Y. (2020). *Klebsiella pneumoniae*: An increasing threat to public health. Annals of Clinical Microbiology and Antimicrobials, 19, 1. https://doi.org/10.1186/s12941-019-0343-8

[2] Wyres, K. L., Lam, M. M. C., & Holt, K. E. (2020). Population genomics of *Klebsiella pneumoniae*. Nature Reviews Microbiology, 18(6), 344-359. https://doi.org/10.1038/s41579-019-0315-1

[3] Bush, K., & Bradford, P. A. (2020). Epidemiology of beta-lactamase-producing pathogens. Clinical Microbiology Reviews, 33(2), e00047-19. https://doi.org/10.1128/CMR.00047-19

[4] Ramatla, T., Mafokwane, T., Lekota, K., Monyama, M., Khasapane, G., Serage, N., Nkhebenyane, J., Bezuidenhout, C., & Thekisoe, O. (2023). One Health perspective on prevalence of co-existing extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli and Klebsiella pneumoniae*: A comprehensive systematic review and meta-analysis. Annals of Clinical Microbiology and Antimicrobials, 22, 88. https://doi.org/10.1186/s12941-023-00638-3

[5] Shyaula, M., Khadka, C., Dawadi, P., & Banjara, M. R. (2023). Systematic review and meta-analysis on extended-spectrum beta-lactamases producing *Klebsiella pneumoniae* in Nepal. Microbiology Insights, 16, 11786361221145179. https://doi.org/10.1177/11786361221145179

[6] Clinical and Laboratory Standards Institute. (2024). Performance standards for antimicrobial susceptibility testing (34th ed.; CLSI supplement M100). Clinical and Laboratory Standards Institute.

[7] De Angelis, G., Del Giacomo, P., Posteraro, B., Sanguinetti, M., & Tumbarello, M. (2020). Molecular mechanisms, epidemiology, and clinical importance of beta-lactam resistance in Enterobacteriaceae. International Journal of Molecular Sciences, 21(14), 5090. https://doi.org/10.3390/ijms21145090

[8] Di Pilato, V., Pollini, S., Miriagou, V., Rossolini, G. M., & D'Andrea, M. M. (2024). Carbapenem-resistant *Klebsiella pneumoniae*: The role of plasmids in emergence, dissemination, and evolution of a major clinical challenge. Expert Review of Anti-infective Therapy, 22(1-3), 25-43. https://doi.org/10.1080/14787210.2024.2305854

[9] Tamma, P. D., & Simner, P. J. (2018). Phenotypic detection of carbapenemase-producing organisms from clinical isolates. Journal of Clinical Microbiology, 56(11), e01140-18. https://doi.org/10.1128/JCM.01140-18

[10] Tille, P. M. (2021). Bailey & Scott's diagnostic microbiology (15th ed.). Elsevier.

[11] Ehlers, M. M., Veldsman, C., Makgotlho, P. E., Dove, M. G., Hoosen, A. A., & Kock, M. M. (2009). Detection of blaSHV, blaTEM and blaCTX-M antibiotic resistance genes in randomly selected bacterial pathogens from the Steve Biko Academic Hospital. FEMS Immunology & Medical Microbiology, 56(3), 191-196. https://doi.org/10.1111/j.1574-695X.2009.00564.x

[12] Monstein, H. J., Ostholm-Balkhed, A., Nilsson, M. V., Nilsson, M., Dornbusch, K., & Nilsson, L. E. (2007). Multiplex PCR amplification assay for the detection of blaSHV, blaTEM and blaCTX-M genes in Enterobacteriaceae. APMIS, 115(12), 1400-1408. https://doi.org/10.1111/j.1600-0463.2007.00722.x

[13] Nordmann, P., Poirel, L., Carrer, A., Toleman, M. A., & Walsh, T. R. (2011). How to detect NDM-1 producers. Journal of Clinical Microbiology, 49(2), 718-721. https://doi.org/10.1128/JCM.01773-10

[14] Zhang, P., Li, J., Wang, Y., Yang, F., Qi, J., & Huang, C. (2022). Detection of KPC and VIM genes in carbapenem-resistant *Klebsiella pneumoniae* isolates from blood culture in Southern Anhui, China. Jundishapur Journal of Microbiology, 15(12), e133705. https://doi.org/10.5812/jjm-133705

[15] National Center for Biotechnology Information. (n.d.-a). bla CTX-M-15 [Escherichia coli] (Gene ID: 8319307; RefSeq NC_013122.1). NCBI Gene. Retrieved May 3, 2026, from https://www.ncbi.nlm.nih.gov/gene/8319307

[16] National Center for Biotechnology Information. (n.d.-b). *Klebsiella pneumoniae* plasmid pKpANDM-1 sequence carrying new metallo-beta-lactamase gene blaNDM-1, isolate KP-05-506 (GenBank: FN396876.1). NCBI Nucleotide. Retrieved May 3, 2026, from https://www.ncbi.nlm.nih.gov/nuccore/FN396876

[17] National Center for Biotechnology Information. (n.d.-c). *Klebsiella pneumoniae* blaKPC gene for carbapenem-hydrolyzing class A beta-lactamase KPC-2, complete CDS (NCBI Reference Sequence: NG_049253.1). NCBI Nucleotide. Retrieved May 3, 2026, from https://www.ncbi.nlm.nih.gov/nuccore/NG_049253.1.

[18] Hafiz, T. A., Alghamdi, S. S., Mubaraki, M. A., Alzahrani, S. H., & Alzahrani, A. J. (2023). *Klebsiella pneumoniae* bacteraemia epidemiology: Resistance profiles and clinical outcomes. BMC Infectious Diseases, 23, 550. https://doi.org/10.1186/s12879-023-08563-8

[19] Pishtiwan, A. H., & Khadija, K. M. (2019). Prevalence of blaTEM, blaSHV, and blaCTX-M genes among ESBL-producing *Klebsiella pneumoniae* and Escherichia coli isolated from thalassemia patients in Erbil, Iraq. Mediterranean Journal of Hematology and Infectious Diseases, 11(1), e2019041. https://doi.org/10.4084/MJHID.2019.041

[20] Hussein, R. A., Al-Kubaisy, S. H., & Al-Ouqaili, M. T. S. (2024). The influence of efflux pump, outer membrane permeability and beta-lactamase production on the resistance profile of multi-, extensively- and pan-drug-resistant *Klebsiella pneumoniae*. Journal of Infection and Public Health, 17(11), 102544. https://doi.org/10.1016/j.jiph.2024.102544

[21] Al Rujaibi, A., Al Jabri, Z., Al Jardani, A., Al Rashdi, A., Al Mamari, A., Al Sumri, S., Sami, H., Al Muharrmi, Z., & Rizvi, M. (2025). Assessment of phenotypic tools for detection of OXA-48, KPC, and NDM in *Klebsiella pneumoniae* in Oman. Diagnostics, 15(8), 949. https://doi.org/10.3390/diagnostics15080949

[22] Ma, T., Xie, N., Gao, Y., Fu, J., Tan, C. E., Yang, Q.-E., Wang, S., Shen, Z., Ji, Q., Parkhill, J., Wu, C., Wang, Y., Walsh, T. R., & Shen, J. (2024). VirBR, a transcription regulator, promotes IncX3 plasmid transmission and persistence of blaNDM-5 in zoonotic bacteria. Nature Communications, 15, 5498. https://doi.org/10.1038/s41467-024-49800-1

[23] Magiorakos, A.-P., Srinivasan, A., Carey, R. B., Carmeli, Y., Falagas, M. E., Giske, C. G., Harbarth, S., Hindler, J. F., Kahlmeter, G., Olsson-Liljequist, B., Paterson, D. L., Rice, L. B., Stelling, J., Struelens, M. J., Vatopoulos,

A., Weber, J. T., & Monnet, D. L. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. Clinical Microbiology and Infection, 18(3), 268-281. https://doi.org/10.1111/j.1469-0691.2011.03570.x

[24] Hamad, S. T., & Ghaim, K. K. (2022). Prevalence of carbapenemase genes in *Klebsiella pneumoniae* isolates from patients with urinary tract infections in Baghdad hospitals. Iraqi Journal of Biotechnology, 21(1), 102-114.

[25] Hussein, N., Muhammad, A., & Abozait, H. (2025). Antibiotic resistance in *Klebsiella pneumoniae* in Iraq: A narrative review. Journal of Life and Bio-Sciences Research, 6(2), 64-69. https://doi.org/10.38094/jlbsr602162

[26] Hussein, A. Y., Abdulsattar, B. O., Al-Saryi, N. A., & Edrees, W. H. (2024). Detection of some beta-lactamase genes in *Klebsiella pneumoniae* isolated from some Baghdad hospitals, Iraq. Al-Mustansiriyah Journal of Science, 35(2), 52-60. https://doi.org/10.23851/mjs.v35i2.1472

[27] Hussein, N. H., Kareem, S. M., Al-Kakei, S. N. H., & Taha, B. M. (2022). The predominance of *Klebsiella pneumoniae* carbapenemase (KPC-type) gene among high-level carbapenem-resistant *Klebsiella pneumoniae* isolates in Baghdad, Iraq. Molecular Biology Reports, 49(6), 4653-4658. https://doi.org/10.1007/s11033-022-07314-3

[28] GBD 2021 Antimicrobial Resistance Collaborators. (2024). Global burden of bacterial antimicrobial resistance 1990-2021: A systematic analysis with forecasts to 2050. The Lancet, 404(10459), 1199-1226. https://doi.org/10.1016/S0140-6736(24)01867-1

[29] Idrees, E. K., Aldriwesh, M. G., Alkhulaifi, M. M., & Alghoribi, M. F. (2025). Systematic review of multidrug-resistant *Klebsiella pneumoniae* in the Arabian Peninsula: Molecular epidemiology and resistance patterns. Frontiers in Microbiology, 16, 1489317. https://doi.org/10.3389/fmicb.2025.1489317

[30] Lin, X.-C., Li, C.-L., Zhang, S.-Y., Yang, X.-F., & Jiang, M. (2024). The global and regional prevalence of hospital-acquired carbapenem-resistant *Klebsiella pneumoniae* infection: A systematic review and meta-analysis. Open Forum Infectious Diseases, 11(2), ofad649. https://doi.org/10.1093/ofid/ofad649

[31] World Health Organization. (2024). WHO bacterial priority pathogens list, 2024: Bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance. World Health Organization.

[32] World Health Organization. (2025). Global antibiotic resistance surveillance report 2025: WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS). World Health Organization.