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High Prevalence of *bla*$_{NDM}$ and *bla*$_{OXA}$ Carbapenemases in Multiple Antibiotic Resistant *Acinetobacter baumannii* from Iraqi Hospital

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ABSTRACT

Background: *Acinetobacter baumannii is a critical nosocomial pathogen with escalating antimicrobial resistance, particularly to carbapenems. Its ability to survive in hospital environments and acquire resistance genes poses a significant challenge in clinical settings. Carbapenem-resistant A. baumannii (CRAB) has been prioritized by the WHO for urgent research because of its association with high morbidity and mortality.* ***Objective***: *This study aimed to evaluate antibiotic susceptibility profiles and characterize carbapenem resistance genes (bla*$_{OXA-23}$*, bla*$_{OXA-48}$*, bla*$_{OXA-51}$*, bla*$_{NDM}$*, bla*$_{VIM}$*) in A. baumannii isolates from Iraqi hospitals.* ***Materials and Methods:*** *A cross-sectional study was conducted in Babylon and Al-Najaf hospitals (August and November 2024). Of the 125 clinical specimens, 50 A. baumannii isolates were identified using Vitek-2 and biochemical tests. Antibiotic susceptibility was assessed using the Kirby-Bauer disc diffusion method (CLSI 2024 guidelines). PCR was performed to detect carbapenemase genes.* ***Results:*** *High rates of resistance were observed: 100% for ampicillin, 90% for imipenem, 84% for meropenem, and 93% for bla*$_{NDM}$*. The following resistance genes were prevalent: bla*$_{OXA-51}$ *(86%), bla*$_{NDM}$ *(93%), bla*$_{OXA-48}$ *(81.3%), and bla*$_{OXA-23}$ *(76.7%). All the isolates tested negative for bla*$_{VIM}$*. Multidrug resistance (MDR) and extensive drug resistance (XDR) were detected in 38% and 62% of the isolates, respectively.* ***Conclusion:*** *The high prevalence of carbapenem resistance genes, particularly bla*$_{NDM}$ *and bla*$_{OXA-48}$*, highlights the genetic complexity that drives CRAB in Iraqi healthcare settings. These findings highlight the urgent need for robust infection control measures and antibiotic stewardship to curb the spread of XDR A. baumannii.*

Keywords: ***Acinetobacter baumannii,*** **Antimicrobial resistance, Carbapenemase genes, PCR, XDR.**

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INTRODUCTION

Acinetobacter baumannii, recognized as an opportunistic pathogen, is responsible for diverse infections, such as pneumonia, bacteremia, urinary tract infections, wound infections, and meningitis (1). Its significant capacity to persist within healthcare environments and withstand multiple antibiotics substantially contributes to its role in causing prevalent nosocomial infections (2). In recent decades, *A. baumannii* has become a major global concern as a problematic hospital-acquired pathogen (3) that poses a particular challenge in intensive care units (ICUs), frequently leading to healthcare-associated infections (HAIs) and persistent outbreaks. These include ventilator-associated pneumonia (VAP), bloodstream infections (BSI), urinary tract infections, wound infections, and meningitis (4,5). Although primarily hospital-associated, community-acquired *A. baumannii* infections have also been documented, often affecting individuals with pre-existing health conditions (6).

A defining feature of *A. baumannii* is its intrinsic resistance to various antibiotics. Compounding this issue is the tendency to acquire additional resistance genes, driving increasingly complex antimicrobial resistance (AMR) profiles (7). This evolution generates highly resistant pathogens and presents significant difficulties for healthcare providers (8). The World Health Organization (WHO) identifies antibiotic resistance as a critical worldwide health threat (9), with projections indicating that resistant infections could cause up to 300 million premature deaths by 2050 (10). Reflecting this urgency, carbapenem-resistant *A. baumannii* (CRAB) was designated by the WHO Health Organization in 2018 as the highest-priority pathogen requiring new antibiotics. Carbapenem resistance serves as a key indicator because of its frequent association with broad resistance to multiple classes of antibiotics (11).

This study aimed to assess the antibiotic susceptibility profile of *A. baumannii* isolates and molecularly characterize the specific carbapenem resistance determinants. Initial susceptibility testing evaluated resistance patterns against a panel of antibiotics, including commonly used agents and critically important carbapenems. These results provide essential data regarding the effectiveness of various antibiotics against this pathogen. Subsequently, PCR analysis was employed to detect and characterize the presence of specific carbapenemase genes (bla_OXA-23, bla_OXA-51, bla_OXA-48, bla_NDM, and bla_VIM), which are known to mediate carbapenem resistance in *A. baumannii*.

MATERIALS AND METHODS

Specimen Collection and identification of bacteria isolates:

A cross-sectional study investigation was conducted at hospitals in Babylon and Al Najaf between August and November 2024. This study involved 125 clinical specimens obtained from patients with symptoms suggestive of infection, as determined by their physicians. The specimens were promptly transported to the microbiology laboratory for analysis.

Identification of Isolates:

Gram-negative bacterial isolates were identified using standard morphological assessment, microscopic examination, and biochemical testing procedures following the methodologies established by MacFaddin and Hart. *Acinetobacter baumannii* isolates were confirmed using the Vitek 2 compact system. For specimens presenting diagnostic challenges, CHROM Agar™ Acinetobacter was used, and subsequent characterization was performed using ID-GN cards.

Antibiotic Susceptibility Tests

The antibiotic susceptibility profile of the *A. baumannii* isolates was determined using the Kirby-Bauer disc diffusion method. Antibiotic disks were selected based on the recommendations of the CLSI, 2024. The interpretation of susceptibility results adhered to the standard breakpoints provided by CLSI (2024). Quality control for antibiotic testing was performed using the reference strain, Escherichia coli ATCC 25922. Isolates were categorized as MDR or XDR according to the definitions and guidelines jointly issued by the CDC and the ECDC. producers (17), and were subjected to further molecular evaluation.

Following the instructions provided by the manufacturer, genomic DNA was extracted from bacterial cells utilizing the Favorgen (Taiwan) extraction kit. By monitoring absorbance ratios at 260 and 280 nm, a Biophotometer Plus (Eppendorf) was used to assess the content and purity of the extracted DNA. To identify carbapenemase genes, *bla*$_{NDM}$, *bla*$_{VIM}$, *bla*$_{OXA\text{-}23}$, and *bla*$_{OXA\text{-}48}$ were amplified using specific PCR.The reactions used the primer pairs PCR condition were published elsewhere (12,13), Each PCR mixture (25 µL total volume) contained 10 µL Promega Master Mix, 2.5 µl (10 µM) forward primer, 2.5 µl (10 µM) reverse primer, 5 µL template DNA, and 5 µL sterile deionized distilled water. Amplification was performed on a T3000 thermocycler (Biometra). The resulting amplicons were separated by electrophoresis on 1.5% (w/v) agarose gel stained with ethidium bromide. Positive results were identified by the presence of DNA bands that matched the expected product size.

RESULTS

A total of 125 specimens were collected from Babel Hospitals and Al-Sadder Medical City in Babel and Najaf, between August 2024 and November 2024. From hospital specimens, positive culture findings revealed 25 specimens (20%) of *Pesudomonas species* and 20 (16%) *Klebsiella pneumoniae*; 50(40%) were identified as *A. baumannii*, and 30 (24%) of the remaining specimens showed no growth. The characteristics of the *A. baumannii* phenotype were determined using a Vitek-2 compact system (BioMérieux,France) and morphological testing.

The specimens comprised 22 sputum specimens, 14 wound swabs, 3 HVS, and 1 Bronchial secretion, and four fluids and six urine samples representing 44%, 28%, 6%, and 2%, and 8% and 12% of the total, respectively. Age was categorized into five groups: 1-20, 21-40, 41-60, 61-80, > 80 years. The analysis revealed that the highest percentage of specimens was observed in age group 21-40 years represented (n=22; 44%), whereas the lowest percentage was observed in age group over 80 years represented (n=1; 2%).The source and type of the specimens are shown in table (2). A study of 50 Acinetobacter baumannii isolates evaluated their susceptibility to 20 antibiotics across eight antimicrobial classes. Universal resistance (100%) was observed for ampicillin. Resistance to beta-lactam/beta-lactamase inhibitor combinations was widespread, including piperacillin (92%), ampicillin-sulbactam (60%), piperacillin-tazobactam (88%), and ticarcillin-clavulanic acid (98%). High resistance rates were also observed for cephalosporins (ceftazidime, 96%; cefotaxime, 96%; ceftriaxone, 90%; cefepime, 92%) and carbapenems (imipenem, 90%; meropenem, 84%).

Aminoglycoside resistance was prevalent (amikacin, 76%; gentamicin, 68%; tobramycin, 60%; netilmicin, 84%), whereas tetracycline resistance was lower (doxycycline, 24%; minocycline, 10%). Resistance to fluoroquinolones (ciprofloxacin, 84%; levofloxacin, 72%) and trimethoprim/sulfamethoxazole (74%) was also significant. Classifying the resistance phenotypes showed that 62% (31 isolates) were XDR and 38% (19 isolates) were MDR; no PDR isolates were detected.

The initial genus confirmation via PCR for bla $_{\text{OXA-51}}$-like identified 43 positive isolates (86%), which proceeded to further molecular testing. Among these, carbapenemase genes were highly prevalent: bla_{NDM}dominated (93%, 40/43), followed by bla $_{\text{OXA-48}}$ (81.4%, 35/43), and $bla_{\text{OXA-23}}$ (76.7%, 33/43). bla_{VIM} is not detected. The diverse distribution of carbapenemase genes highlights their importance in mediating carbapenem resistance in these isolates.

Table (1): The Primers used in the study. All of them are provided from Macrogen/ Canda

Primer Name		**Primer sequence**	**Product(bp)**	**References**
$bla_{OXA\text{-}48}$	F	5’-TTGGTGGCATCGATTATCGG-3’	744	(12)
	R	5’-GAGCACTTCTTTTGTGATGGC-3’		
$bla_{OXA\text{-}23}$	F	GATCGGATTGGAGAACCAGA	501	(12)
	R	ATTTCTGACCGCATTTCCAT		
$bla_{OXA\text{-}51\text{-}}$	F	TAATGCTTTGATCGGCCTTG	353	(12)
	R	TGGATTGCACTTCATCTTGG		
bla_{VIM}	F	5'-AGTGGTGAGTATCCGACAG-3'	212	(13)
	R	5’-TCAATCTCCGCGAGAAG-3’		
bla_{NDM}	F	5’-TGGCAGCACACTTCCTATC-3’	488	(13)
	R	5’-AGATTGCCGAGCGACTTG-3’		

Table (2): Comparison of Clinical Sample Distribution Across Hospitals.

Hospital	Specimens						Total %
	Sputum No. (%)	Wound swab No. (%)	HVS No. (%)	Bronchial section No. (%)	Fluid	Urine	
Babyl hospitals	13(26%)	6(12%)	3(6%)	1(2%)	1(2%)	4(8%)	28 (56%)
Al Sadder Medical City	9 (18%)	8(16%)	0	0	3(6%)	2(4%)	22 (44%)
Total (%)	22 (44%)	14 (28%)	3 (6%)	1(2%)	4(8%)	6(12%)	50(100%)

Table (3) Prevalence Rates of MDR, XDR, and antibiotic relared genes.

Genes	Antibiotic susceptibility		Total
	XDR	MDR	
bla_{NDM}	25(62.5%)	15(37.5%)	40(93%)
bla_{OXA48}	23(65.7%)	12(34.3%)	35(81.4%)
bla_{OXA51}	26(60.5%)	17(39.5%)	43(100%)
bla_{OXA23}	21(63%)	12(36%)	33(76%)
bla_{VIM}	0	0	0

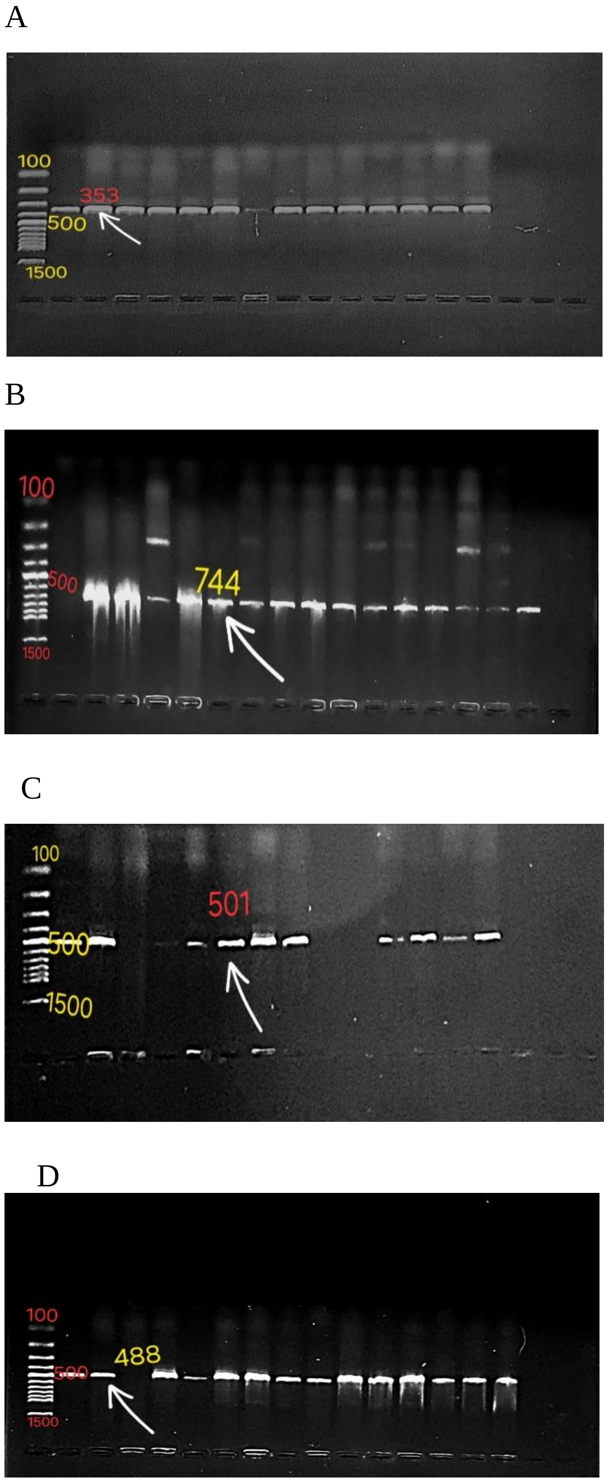

Figure 1. The gel electrophoresis image of PCR product. A. M: DNA ladder 100bp. Amplified fragments of *bla*$_{OXA51}$ gene fragment in clinical *A. baumannii* isolate . B. M: DNA ladder 100bp. PCR amplification of *bla*$_{OXA48}$ gene fragment of *A. baumannii* isolates**,** C. M: DNA ladder 100bp. PCR amplification of *bla*$_{OXA23}$ gene fragment of *A. baumannii* isolates**,** D. M: DNA ladder 100bp. PCR amplification of *bla*$_{NDM}$ gene fragment of *A. baumannii* isolates**.**

Molecular testing of 43 isolates showed that 35 (81.3%) of these isolates were positive for *bla*$_{OXA48}$, 23 (65.7%) isolates were positive for XDR, and 12(34.3%) were MDR isolates. Forty (93%) isolates were positive for *bla*$_{NDM}$, 25(62.5%) for XDR, and 15(37.5%) for MDR. And 33(76.7%) isolates were positive for *bla*$_{OXA23}$, 21(63%) for XDR, and 12(36%) for MDR. All the isolates tested negative for *bla*$_{VIM}$. table (3)

DISCUSSION

The findings of this investigation clarified how *A. baumannii* specimens are distributed in the study population, with a number of important insights. The most frequently collected specimens were sputum specimens, which comprised 47.6% of all specimens. However, one (2%) bronchial secretion according to the distribution of specimen types. This result is in agreement with what was found previously in Najaf and Baghdad hospitals, *A. baumannii* had a greater proportion of sputum (14,15). Respiratory specimens retained the highest percentage of infection predominance among other infection locations. This shows the great concern of how respiratory tract infections primarily aid in the colonization or infection of *A. baumannii* in the study population. Mechanical ventilators are frequently employed in (ICU) to sustain vital functions (16). Without exception, patients undergoing mechanical ventilation are at risk for a wide range of potentially avoidable pulmonary complications such as VAP (17). *A.baumannii* is one of the most common pathogens that cause VAP because of its ability to form biofilms and persist in medical settings (18). This infection affects not only the patient's results but also the overall patient and healthcare system costs. Thus, prevention of VAP is a critical concern in the care of patients admitted to ICUs (19).

The rate of specimen wound abscesses was 28%, which was lower than that reported in other studies (87.5% and 47%, respectively) (Shareef and Risan 2021:Jasim et al. 2023). However, another study in Al-Najaf (15) found that the rate of wound abscesses among specimens was 12.3%. Numerous cases of *A. baumannii* infection have been reported in military personnel sustaining traumatic injuries from warfare in Iraq and Afghanistan. Most Afghanistan and Iraq stand out as the most prominent geographical areas where *A.baumannii* is captured from wounds or soft tissue post-traumatic injuries. (21) . The relatively smaller proportion of HVS specimens (6%) and the single bronchial section (2%) suggests a lower involvement of systemic or less common sites in the studied population.

This study used the Kirby-Bauer disk diffusion method to assess the antibiotic resistance of *A. baumannii*. The antibiotic susceptibility test revealed a substantial degree of resistance to the majority of medicines, indicating that the bacterium is resistant to multiple treatments and restricts the available treatment choices. Each isolate showed absolute resistance to ampicillin. The results of this study align with previous research on the resistance patterns of ampicillin (22). And show resistance 92% to piperacillin. These results are consistent with those of previous studies (23). *Acinetobacter baumannii* has high levels of resistance (60%) to ampicillin-sulbactam (88%) to pipracillin-tazobactam and (98%) to ticarcillin-clavulanic acid, which are β-lactam combination medicines, which contradicts the results of (Xie et al. 2018) and (Raheem Al-Hasnawy 2020). The prevalence of *A. baumannii's* resistance to cephalosporins is high. For cefotaxime, 96%; ceftriaxone, 90%; cefepime92%; ceftazidime, 96%. This agrees with the research conducted by (25) and (22).

In relation to carbapenem resistance, the findings indicated that *A. baumannii* exhibited high rates of resistance, with imipenem resistance at 90% and meropenem resistance at 84%. This is consistent with the results reported by (26), but differs from (27) and (22), which reported higher resistance rates.

This study revealed different rates of resistance among the aminoglycosides. The resistance rate to amikacin was 76%, which is consistent with the results reported by (24). Gentamicin demonstrated a resistance rate of 68%, which is similar to that reported previously (28). Tobramycin exhibited a resistance rate of 60%, which is similar to that of (29) and differs from those of (22) and (30).

The rate of resistance to doxycycline was 24%. Minocycline exhibited a significantly low resistance rate of 10%, which is in contrast to previous findings (29). Fluoroquinolones showed a reasonably high level of resistance. Ciprofloxacin exhibited a resistance rate of 84%, similar to (31), whereas levofloxacin showed a resistance rate of 72%, with variations compared to (29). Trimethoprm/sulfamthoxazole demonstrated a 74% rate of resistance of this result resemble to (29).

In the current study, isolates were classified as XDR (62%), MDR (38%), and no PDR. MDR refers to a bacterium that is not susceptible to at least one of three different groups of antimicrobial drugs. XDR refers to the lack of susceptibility to at least one agent in nearly all antimicrobial categories. PDR refers to the condition in which an organism is not susceptible to any antimicrobial category, in accordance with the criteria provided by (32) . The findings of this study are comparable to those obtained by Wasit et al.(33), who demonstrated that XDR (100%) was present among *A. baumannii* isolates. and (84.2%) XDR were present.

One of the most significant challenges facing the world today is the spread of carbapenem resistance in Gram-negative bacterial diseases. Carbapenems have been extensively used to treat severe infections caused by ESBL-positive bacteria because of their wide-ranging efficacy and resistance to destruction by ESBLs. However, extended use of this antibiotic has decreased the efficacy of this treatment category (34). Genes responsible for encoding MBL have been discovered worldwide in GNB across the globe. The presence of these genes has been detected in *Pseudomonas spp*, *Acinetobacter spp*, and members of the *Enterobacterales* family, and can effectively spread through plasmids, leading to hospital-acquired illnesses and outbreaks (35).

Carbapenem resistance can be attributed to the presence of inherent or acquired *bla*$_{\text{OXA}}$ carbapenemase genes. The class D carbapenemase gene *bla*$_{\text{OXA-51}}$ in this study was found in 43(86%), The *bla*$_{\text{OXA-51}}$ like gene is considered a natural component of the *A.baumannii* baumannii chromosome (36). In accordance with previous researches *bla*$_{\text{OXA-51}}$ like was associated with resistance to carbapenems.. Many studies have reported that *bla*$_{\text{OXA-51}}$ is found in all isolates 100% of *A. baumannii* (37)(38)(22). Additionally, the current result was in agreement with results reported in Al-Najaf by (14), who found that 95% of A. baumannii isolates have *bla*OXA-51 like gene, and (15) who found that 80% *A.baumannii isolates* have *bla*$_{\text{OXA-51}}$ like gene. Although *bla*$_{\text{OXA-23}}$ can be transmitted from one generation to another, the expression of this gene by *A. baumannii* is sufficient to produce carbapenem resistance (39). *bla*$_{\text{OXA-23}}$ was detected only in 33(76.7%) isolates, which was lower than the result of (37) with percentage 98%),and another study found *bla*$_{\text{OXA-51}}$ 100% *bla*$_{\text{OXA-23}}$53% by (40). All isolates had *bla*$_{\text{OXA-51}}$ gene and 94% had *bla*$_{\text{OXA-23}}$ (41).

The present study revealed a distinct prevalence of carbapenemase genes in *A.baumannii* isolates. The complexity of carbapenem resistance pathways is high owing to the variety of carbapenem resistance genes and their combinations. In particular, *bla*$_{\text{OXA48}}$ was present in 35(81.3%) isolates and these rates were alarmingly high. The current results are in contrast with previous studies in Al-Najaf conducted by (14), who found that the rate of *bla*$_{\text{OXA48}}$ was (39%), while another study by (15) found that the rate of *bla*$_{\text{OXA48}}$ was 32%. In addition, the results varied compared with those in (42). A possible conclusion drawn from these findings is that oxacillinases are the most common mediators of carbapenem resistance in isolates.

Class B carbapenemase *bla*$_{\text{VIM}}$ is a distinct type of MBL gene.The VIM-1 version of this gene was first discovered in *Pseudomonas aeruginosa*. This strain was obtained from a patient in Verona, Italy(43)). The *bla*$_{\text{VIM}}$ gene was not found in any of the isolates; this result is identical to that of a previous study (44).

The *bla*$_{\text{NDM}}$ gene was identified in an Indian patient who was living in Sweden and had previously received medical treatment at facilities in New Delhi in 2008 (45). Furthermore, *bla*$_{\text{NDM}}$ was detected in 40(93%) isolates, which differs from the findings of (44), who did not find any indication of *bla*$_{\text{NDM}}$ in any of the isolates. The presence of *bla*$_{\text{NDM}}$ highlights the importance of this gene in conferring resistance to carbapenems as well as the necessity for effective infection control measures to prevent its spread.

Genes encoding class A carbapenemases, which are enzymes that break down penicillins, conventional cephalosporins, monobactam, imipenem, and meropenem, specifically the *bla*KPC gene, were not found in all isolates, which is consistent with the conclusions of previous investigations (46,47), all of which reported that *bla*KPC was absent in all isolates.

The prevalence of carbapenemase-producing isolates is affected by several factors, including geographical location, type of infection, source of the specimen, and selection pressure created by the use of antibiotics. This difference is also connected to the heterogeneity that was noticed across several individuals who were evaluated as well as the variable rates of antibiotic usage in the various healthcare institutions under consideration. The historical and cultural links between countries can affect the variety of carbapenemases, and these relationships can vary from one country to another. It is possible that the presence of wars, medical tourism, and the movement of patients across international boundaries, particularly among workers who arrive in our country, could have a significant influence on the formation and dissemination of different types of genes that encode carbapenemases, and the highest priority to ensure that clear standards and efficient methods for infection control are established to reduce the incidence of diseases such as these among patients (48).

CONCLUSION

This study demonstrated the prevalence of carbapenem-resistant *A.baumannii* in Iraqi hospitals, with high resistance rates to critical antibiotics such as imipenem (90%) and meropenem (84%). Molecular analysis revealed a widespread distribution of carbapenemase genes, notably *bla*NDM (93%) and *bla*OXA-48 (81.3%), emphasizing their role in resistance mechanisms. The dominance of XDR isolates (62%) indicates limited therapeutic options and underscores the need for enhanced surveillance, stringent infection control protocols, and alternative treatment strategies. Future research should focus on genomic epidemiology to track the dissemination of resistance genes and inform public health interventions.

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Ethical approval: The present study entitled. Which is conducted by authors ((**Ali Ahmed Kadum**, Zainab Jaber Hadi) was approved by the Department of Microbiology committee. All the patients were informed about the aim of the present work and the possibility of publication of the results of the outcome of the study. All the patients were willingly agreed to participate and a written consent to indicate their willing to participate have been signed by all of them.

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