Assessment of the Antimicrobial Resistance Spectrum and Identification of Extended-Spectrum ß-Lactamase (ESBL) in *Acinetobacter Baumannii* from Clinical Samples in Erbil City

Sayran Sabr Qadr[1*], Pishtiwan Ahmed Hamad[2], Sozan Hamashrif Aziz[3], Rebwar Muhammad Hamasalih[2],Mohsin Ali Ahmed[4]

1 Department of Medical Microbiology, College of Science, International University of Erbil, Erbil, 44001, Iraq.

2 Department of Biology, College of Education, Salahaddin University-Erbil, Erbil, Iraq.

3 Department of Medical Laboratory Technology, Erbil Technical College, Erbil Polytechnic University, Erbil, Iraq.

4 Department of Animal Resources, College of Agricultural Engineering Sciences, Salahaddin University-Erbil, Erbil, Iraq.

ABSTRACT

Acinetobacter baumannii (*A. baumannii*) is a dangerous opportunistic pathogen causing various infections, particularly in healthcare settings, affecting immunocompromised individuals. It is a significant source of nosocomial infections due to its ability to produce extended-spectrum β-lactamases (ESBLs) and carbapenemase enzymes, which are a major concern for antibiotic resistance.

To investigate the significant occurrence of ESBL-producing *A. baumannii* in hospitalized individuals, a total of 250 clinical specimens were obtained. Samples were collected aseptically from patients and cultured on blood agar and MacConkey agar media. Identification of isolates was conducted using both conventional microbiological techniques and the automated VITEK 2 system. Duplicate isolates and specimens from colonization-prone sites, including throat and perianal areas, were excluded. Antimicrobial susceptibility and ESBL production were evaluated according to CLSI standards.

Out of 250 clinical specimens, 60 out of 250 (24%) had a culture-positive *A. baumannii* infection. Thirty out of sixty isolates (50%) had an *A. baumannii* infection that produced ESBL. 86.67% of the isolated bacteria had multidrug resistance overall (52/60). Amikacin had

preprint

the greatest resistance rate among the 60 isolates (100%), whereas Tigecycline had the lowest resistance rate among just 10 isolates (16.67%). At the same time, the resistance rate was 0.00%, and the antibiotic that worked best against *A. baumannii* was Colistin. It was discovered that ESBL genes were correlated with antibiotic resistance, particularly with cephalosporin medicines.

In conclusion, the present study highlights the prevalence of ESBL-producing *A. baumannii* strains, emphasizing the need for cautious antibiotic use and systematic monitoring of resistance mechanisms. The emergence of new ESBL strains necessitates continuous surveillance and further research on other ESBL-associated genes.

Keywords: *Acinetobacter baumannii*, Antibiotic resistance, Extended-spectrum β-lactamase genes.

1. Introduction

The Gram-negative (G^-) bacteria Acinetobacter baumannii (*A. baumannii*) is usually small, almost spherical, and rod-shaped (*coccobacillus*). It cause blood, urinary tract, and lung infections (pneumonia), as well as sores in other areas of the body. In patients with open wounds or respiratory secretions (sputum), it may also "colonize" or remain there without producing illnesses or symptoms (1).

This organism, recognized as an opportunistic pathogen predominantly impacts individuals with compromised immune responses. and is increasingly acknowledged as a significant nosocomial pathogen (2). Unlike bacteria equipped with flagella, Acinetobacter species exhibit alternative motility mechanisms, such as twitching and swarming, which are likely facilitated by type IV pili—elongated structures capable of extension and retraction (3).

Infections caused by Acinetobacter baumannii are more frequently encountered in individuals who have prolonged hospital stays, compromised immune systems, advanced age, underlying medical conditions, severe trauma or burns, prior antibiotic usage, or those requiring invasive procedures. Patients with indwelling medical devices such as catheters or mechanical ventilators are particularly at risk for such infections (4). Finding an exact death rate for critically ill patients with A. baumannii infections is hard because their prognosis is already not good (5). However, rough death rates have ranged from 23% to 68%. Currently, The cause of variations in clinical presentation between community-acquired and hospital-acquired infections, whether attributable to host or bacterial variables, remains unclear (6).

preprint

Hospitalized patients, especially those with prolonged hospital stays or those who have received broad-spectrum antibiotics or anticancer medications, are increasingly experiencing *A. baumannii* colonization. Spreading genes that are not sensitive to antibiotics has become a big problem in treating *A. baumannii* infections, leading to multiple drug resistance (MDR). Previous investigations have consistently demonstrated that A. baumannii displays resistance to a broad spectrum of antibiotics, encompassing fluoroquinolones, cephalosporins, carbapenems, tetracyclines, and aminoglycosides. The mechanisms of resistance entail both intrinsic and acquired approaches, including enzymatic inactivation, genetic mutations at the target sites, modifications in outer membrane permeability, and the excessive expression of efflux pumps. Notably, efflux pump systems contribute to multidrug resistance (MDR) by enabling bacteria to expel antibiotics effectively (7).

This hospital-acquired disease is mostly resistant to antibiotics because of β-lactamases, changes to membrane porin channels, and mutations that change how cells work. The main way that bacteria become resistant is by making hydrolytic enzymes that attack antibiotics, especially extended-spectrum β-lactamases (ESBLs) (8). The predominant mechanism underpinning the resistance of A. baumannii to β-lactam antibiotics and various other antimicrobial agents in recent years has been elucidated as the production of Extended-Spectrum Beta-Lactamases (ESBLs); These enzymes are responsible for conferring resistance to a broad range of antibiotics, including monobactams, cephalosporins, and penicillins. Hospitals worldwide are increasingly seeing MDR patterns brought on by pathogenic bacteria's development of extended-spectrum beta-lactamases. Because it results in treatment failures, longer hospital stays, and increased mortality rates, this is a public health issue (9).

In excess of 300 unique extended-spectrum β-lactamase (ESBL) variants have been delineated within Gram-negative bacterial populations, with blaTEM and blaSHV emerging as the predominant genetic determinants on a global scale. In recent years, there has been a notable augmentation in the prevalence of the blaCTX-M gene family among clinical isolates. This gene family encompasses more than 130 β-lactamase variants, which are systematically classified into five distinct categories: blaCTX-M-1, blaCTX-M-2, blaCTX-M-8, blaCTX-M-9, and blaCTX-M-25 (10).

Recent trends in adjacent locations indicate a comparable rise in antibiotic resistance, especially for ESBL-producing bacteria. Researchers in Saudi Arabia have found that *blaCTX-M*, *blaSHV*, and *blaTEM* genes are commonly found in clinical isolates. This shows a pattern of resistance in the region that is a public health concern for everyone (11).

preprint

Furthermore, a research conducted in Iran demonstrates a heightened incidence of ESBL-encoding genes in *A. baumannii* isolates (12). In order to develop evidence-based strategies to address antibiotic resistance in clinical settings, it is essential to characterize the resistance genes encoding ESBL-producing *A. baumannii* (2, 11).

Objectives

This study aims to investigate the antimicrobial resistance patterns of clinical strains and evaluate the prevalence of blaSHV, blaTEM, and blaCTX genes in A. baumannii isolates collected from various hospitals in Erbil city. The study underscores the critical role of ESBLs in antibiotic resistance and their implications for treatment failures.

2. Materials and methods

2.1. Collection and identification of isolates

Patients were selected based on clinical indications of infection, including symptoms such as fever, inflammation, and purulent discharge, as well as laboratory findings suggestive of bacterial infection. Samples were collected from patients across different departments, including intensive care units, surgical wards, and outpatient clinics, to capture a broad spectrum of A. baumannii infections.

From March 20, 2024, to June 19, 2024, a total of 250 infected samples were obtained from various clinical specimens: sputum (n=87), wound swab (n=64), stool (n=51), and burn (n=48). The samples were moved right away to the lab in an ice-pack-equipped cooler. Clinical samples were cultured on Blood and MacConkey agar (Merck, Germany) and incubated aerobically at 37°C for 24 hours. To isolate pure colonies, non-lactose fermenting colonies on MacConkey agar, as well as non-hemolytic, creamy, and opaque colonies on blood agar, underwent further sub-culturing on MacConkey agar with an additional incubation period of 24 hours under the same conditions. Identification of A. baumannii isolates was performed through morphological examination of colonies and Gram staining results. Verification of A. baumannii was achieved using the VITEK 2 system and standard biochemical tests, including oxidase, catalase, citrate utilization, urease activity, and indole production.

Further molecular confirmation was carried out using polymerase chain reaction (PCR) targeting the 16S rRNA gene. Amplification utilized the Alpha PCRmax system (UK) with specific primers (Forward: CACCTTCCGATACGGCTACC; Reverse: GTTGACTGCCGGTGACAAAC). The PCR mixture consisted of 12.5 µL of master mix

preprint

(AMPLIQON, Denmark), 1.0 µL of each primer, 1.5 µL of genomic DNA, and PCR-grade water to achieve a final volume of 25 µL. Amplification conditions included 40 cycles of denaturation at 95°C for 30 seconds, annealing at 59°C for 45 seconds, and extension at 72°C for 60 seconds, with a final elongation at 72°C for 10 minutes. The resulting amplicons were analyzed on a 1.2% agarose gel, revealing an expected size of 372 base pairs for the amplified 16S rRNA gene (13).

2.2. Antimicrobial susceptibility screening

In accordance with the guidelines established by the CLSI (14), the assessment of antimicrobial susceptibility was conducted employing the disk diffusion methodology. The antibiotic susceptibility tests involved a panel of antibiotics, including Amikacin (AK, 30 µg), Cefepime (CFP, 30 µg), Ceftazidime (CAZ, 30 µg), Ciprofloxacin (CIP, 5 µg), Colistin (CST, 5 µg), Gentamicin (G, 10 µg), Imipenem (IMP, 30 µg), Levofloxacin (LEV, 5 µg), Meropenem (MEM, 10 µg), Netilmicin (NET, 30 µg), Piperacillin (PIP, 30 µg), Tigecycline (TGC, 30 µg), and Tobramycin (TOB, 10 µg), procured from Bioanalyse, Turkey. Using a sterile brush, 100 µL of inoculum (1.5*10^8 CFU/mL) was evenly distributed across the whole surface of a Mueller Hinton Agar (Himedia, India) plate in line with the 0.5 McFarland standard to create a lawn of A. baumannii. Within fifteen minutes of inoculation, the disks were firmly positioned on the surface of the agar plate (15).

2.3. Extraction of genomic DNA

Genomic DNA extraction was performed using the BETA BAYRN Genomic DNA Extraction Kit (BETA BAYRN, Germany) in accordance with the manufacturer's guidelines. DNA was eluted with 50 µL of elution buffer and stored at -20°C for subsequent PCR analysis. DNA concentration and purity were assessed using a NanoDrop 1000 spectrophotometer (ThermoFisher Scientific, USA).

2.4. Identification of ESBL-related genes through PCR analysis

Conventional multiplex PCR was employed to examine the molecular profile of genes associated with extended-spectrum β-lactamases (blaSHV, blaTEM, and blaCTX) in A. baumannii strains that produce ESBLs. Information regarding the primer sequences and their respective functions can be found in Figure 1 (15).

preprint

Target genes	Primer	Sequence (5′-3′)	Amplicon size
bla$_{TEM}$	Forward	TCG CCG CAT ACA CTA TTC TCA GAA TGA	445-bp
	Reverse	ACG CTC ACC GGC TCC AGA TTT AT	
bla$_{SHV}$	Forward	ATG CGT TATATT CGC CTG TG	747-bp
	Reverse	TGC TTT GTT ATT CGG GCC AA	
bla$_{CTX}$	Forward	ATG TGC AGY ACC AGT AAR GTK ATG GC	593-bp
	Reverse	TGG GTR AAR TAR GTS ACC AGA AYC AGC GG	

Figure 1. List of primers used for Multiplex PCR amplification.

For detecting ESBL genes, PCR reactions were set up in a 25 µL reaction volume containing 7 µL of PCR-grade water, 10 µL of master mix, 1 µL of primer mix, and 2 µL of genomic DNA. The cycling parameters included an initial denaturation at 95°C for 10 minutes, followed by 40 cycles of denaturation (95°C for 30 seconds), annealing (60°C for 90 seconds), and extension (72°C for 120 seconds), with a final extension step at 72°C for 10 minutes. PCR amplicons were separated by electrophoresis on a 1.2% agarose gel containing Red Safe dye and visualized under UV light.

2.5. Data analysis

GraphPad Prism (V. 9.3) software was employed for statistical analysis. Qualitative data were evaluated using the chi-square test. A p-value below 0.05 was considered statistically significant for all analyses.

2.6. Ethical Considerations

The research received ethical clearance from the Ethics Committee of Salahaddin University-Erbil, with the permission number IR.BMSU.REC.1399.296. The study adhered to the ethical guidelines outlined by the committee, ensuring that all patient data were anonymized and handled confidentially. Informed permission was acquired from all participants or their legal guardians prior to sample collection. The current study was executed in compliance with the Declaration of Helsinki and other local rules, emphasizing the reduction of possible hazards to participants while enhancing the scientific merit of the research.

preprint

3. Results and Discussion

3.1. Detection of A. baumannii isolates

The study analyzed 250 clinical samples comprising sputum (n=87), wound swabs (n=64), stool samples (n=51), and burn samples (n=48). Out of these, 67 isolates (26.8%) were identified as A. baumannii using biochemical tests and the VITEK 2 system with GN cards. The isolates, collected at the Biotechnology Laboratory, Salahaddin University-Erbil, Iraq, were characterized as Gram-negative coccobacilli. They exhibited oxidase-negative, catalase-positive, urease-negative, citrate-negative, and indole-negative profiles. Verification of the 67 isolates through PCR confirmed the presence of the 16S rRNA gene (Figure 2). Among the isolates, 25 (37.31%) were from females, and 42 (62.69%) were from males, with a mean age of 51.43 ± 0.8 years.

Figure 2. 16S rRNA gene amplification via agarose gel electrophoresis. Lanes 1–12 show a positive amplicon for the 16S rRNA gene at 372 bps, lane M is a 50 bps DNA ladder, and lane NC is a negative control.

3.2. Detection of ESBL genes

Among the 67 A. baumannii isolates examined, 53 (83.58%) contained the blaSHV gene, while 34 (50.74%) harbored the blaCTX gene. The blaTEM gene was found to be the most common, present in all analyzed isolates, as illustrated in Figure (3).

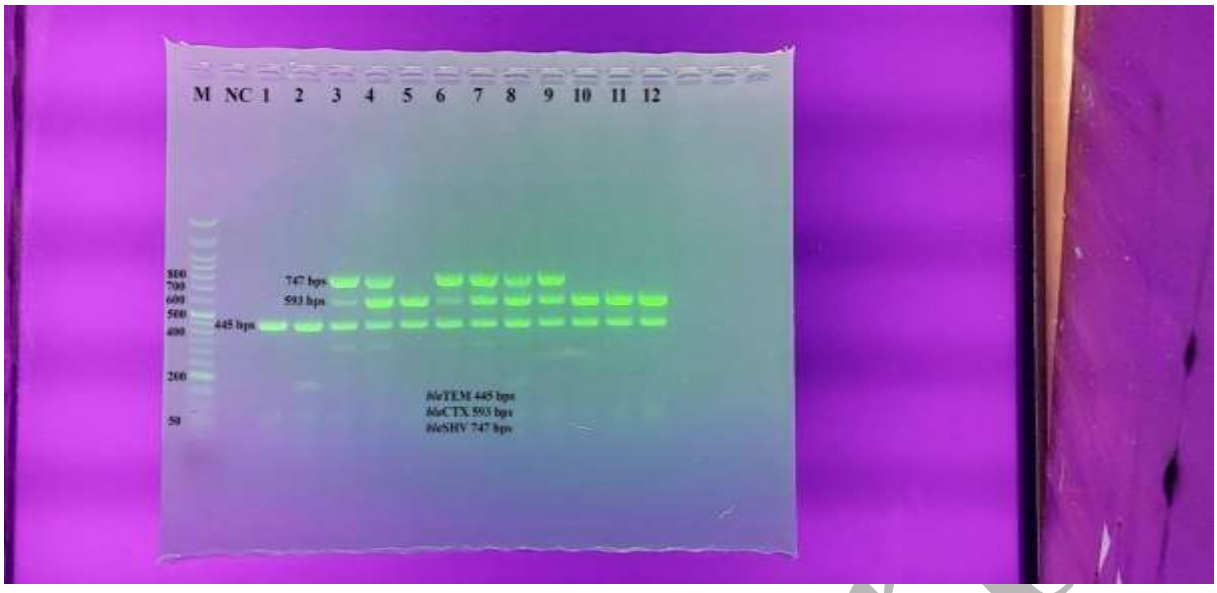

Figure 3. Multiplex PCR of ESBL genes (*blaCTX, blaTEM, and blaSHV*) using agarose gel electrophoresis. Lane M: 100 bps DNA ladder, lane NC: negative control, lanes 1–12 with 445 bps *blaTEM* gene, lanes 3–12 with 593 bps *blaCTX* gene, and lanes 3, 4, 6, 7, 8, and 9 with 747 bps *blaSHV* gene.

The results revealed a significant proportion of A. baumannii isolates producing ESBLs. Studies from Iran have reported alarming levels of drug and multidrug resistance in A. baumannii, including resistance to highly effective antibiotics such as IMP and MEM (16). Ting et al. identified resistance genes—including blaTEM, blaSHV, blaCTX, blaDHA, blaCIT, blaIMP, blaVIM, blaKPC, and blaOXA-23—in seven IMP-resistant A. baumannii strains. The isolates exhibited the presence of *blaTEM* (100%) and *blaOXA-23* (100%) genes. However, the other genes, including *blaSHV*, *blaCTX*, *blaDHA, blaCIT, blaIMP, blaVIM*, and *blaKPC*, were undetectable in seven strains of IMP-resistant A. baumannii. In the current investigation, similar with previous findings, many genes were identified, including *blaSHV* (58%), *blaTEM* (20%), and *blaVIM* (30%). (17). Shahcheraghi et al. conducted a research in Tehran, Iran, demonstrating that the MBL expressing genes identified among 203 *A. baumannii* isolates were *blaVIM*-2, *blaSPM-1*, *blaIMP-2*, *blaGES-1*, *blaOXA-51*, and *blaOXA-23*. Six isolates were discovered to generate MBLs, whereas 94 isolates were found to produce OXA-type carbapenemases. Their research suggests that the prevalence of MBL-producing A. baumannii strains in Tehran is lower than what was observed in the present study from Hamadan City. They detected blaSPM-1, blaGES-1, blaOXA-51, and blaOXA-23 genes in 6, 2, 94, and 84 bacterial isolates, respectively (18). A previous investigation by Rezaee et al. identified genes encoding for 76 Acinetobacter species, including blaIMP,

preprint

blaSPM-1, blaVIM, blaPER-1, blaVEB-1, blaTEM, blaSHV, blaGES-1, and blaCTX-M. Moreover, they noted that 13.15% of their analyzed isolates carried the blaTEM-1 gene, which is similar to the 20% found in the current study, and 37% of isolates harbored at least one of the blaPER-1 or blaTEM-1 genes. Furthermore, none of the A. baumannii isolates they examined contained blaVEB-1, blaSHV, blaCTX-M2, or blaGES-1 (19).

3.3. Antimicrobial resistance

All isolates shown total resistance to AK. CST had the greatest effectiveness against A. baumannii isolates, with all isolates showing sensitivity to CST. Sixty-one isolates (91.04%) exhibited resistance to CFP, CIP, IMP, and LEV, marking the greatest resistance rate after that of the AK antibiotic (Figure 4).

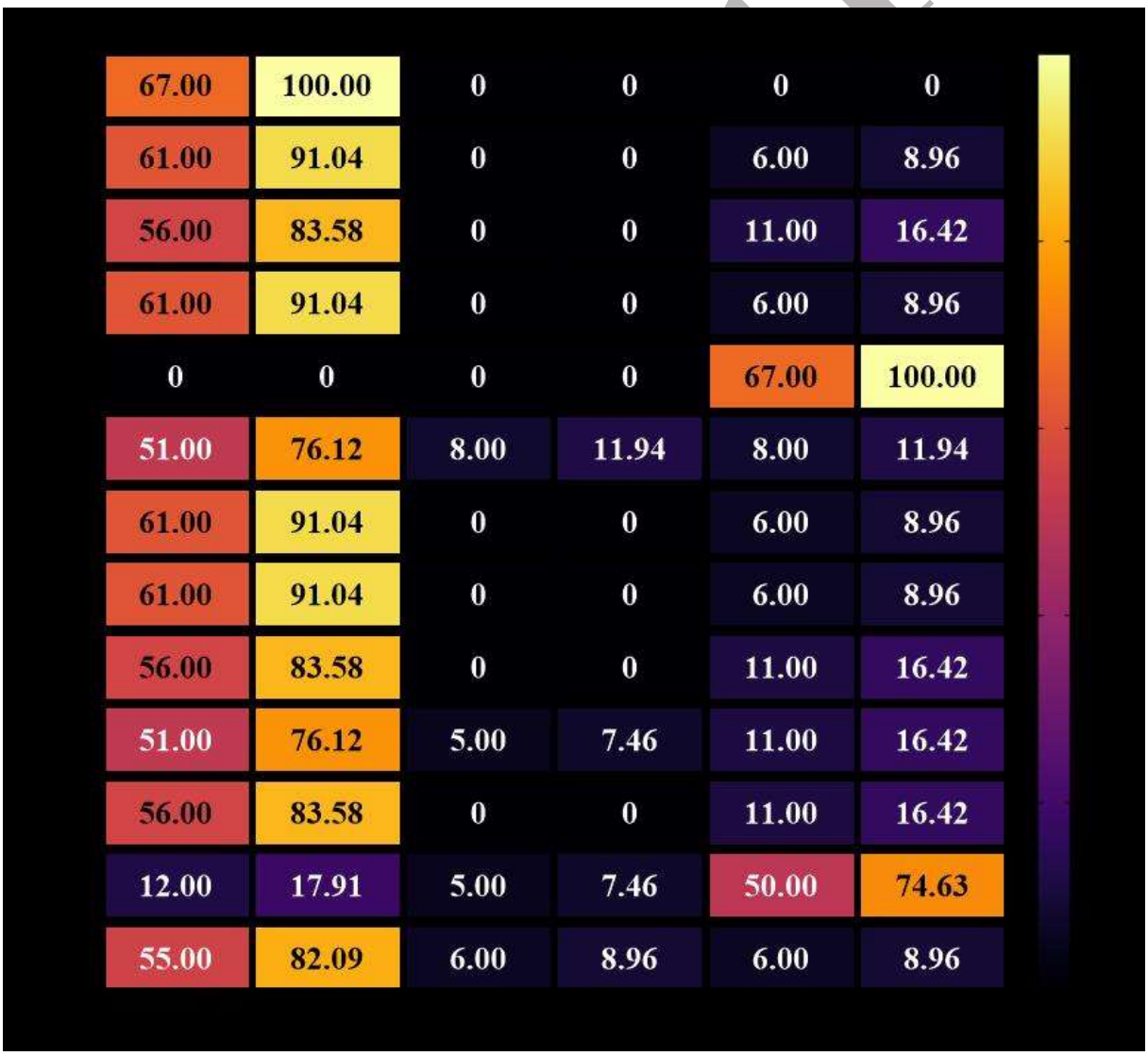

Figure 4. The heat map elucidates the levels of sensitivity (resistant, intermediate, and sensitive) of A. baumannii to several tested antimicrobial drugs.

Acinetobacter baumannii is a bacterial pathogen known for causing nosocomial infections, primarily due to its high level of drug resistance (20, 21). Its ability to adhere to a variety of surfaces and medical devices significantly enhances its potential for colonization and transmission among hospitalized individuals (22). This bacterium can withstand a wide range of existing drugs by acquiring resistance factors and enhancing innate resistance mechanisms (23). *A. baumannii* exhibiting multidrug resistance causes severe infections and high fatality rates, especially in immunocompromised individuals (24, 25). According to our investigation, every isolate of A. baumannii showed resistance to a number of antibiotics. All exhibited sensitivity to CST and resistance to AK, aligning with results from previous Iranian investigations (26, 27). Zarifi et al. found that A. baumannii had significant resistance to all antibiotics except CST. The resistance rates for IMP, MEM, CAZ, cefotaxime, cefuroxime, ceftriaxone, CFP, ertapenem, and ampicillin/sulbactam were 97.9%, 98.1%, 96.4%, 97.9%, 99.3%, 97.9%, 97.9%, 98.6%, and 97.1%, respectively. CST had the highest efficacy as an antibiotic against A. baumannii, with a susceptibility rate of 97.9%, whereas AK exhibited a sensitivity of 27.1% (28).

Antibiotic resistance to monobactams, carbapenems, cephalosporins, and penicillin is provided by class A beta-lactamases. These lactamases may have a restricted spectrum of activity or acquire an expanded range of antibiotic efficacy via point mutations. Beta-lactamase enzymes, particularly class A, contribute to resistance against antibiotics such as monobactams, cephalosporins, carbapenems, and penicillins. These enzymes are often inhibited by agents like clavulanic acid (1). Additionally, the dissemination of ESBL genes among Gram-negative bacteria is facilitated by mobile genetic elements, such as plasmids (2). Regular monitoring of bacterial strains that produce extended-spectrum β-lactamases (ESBLs), coupled with the detection of associated genes such as blaTEM-92, blaSHV, blaGES-11, blaGES-14, blaPER-1, blaPER-7, and blaVEB-1, is vital for effective clinical management. Additionally, other significant enzymes in this group include the cefotaxime-expanding β-lactamase (CTX-M) family and the Klebsiella pneumoniae carbapenemase (KPC) enzymes (3).

Therefore, resistance to third-generation cephalosporins is heightened, corresponding with the production of genotypic ESBLs. The epidemiological variety of ESBL-encoding genes in A.

preprint

baumannii may indicate the continual emergence of novel ESBL strains. Upcoming research highlights the investigation of other ESBL-encoded genes. This research highlighted the need for more prudence in antibiotic use and the concerning rate of resistance.

As mentioned in the book, *A. baumannii* can acquire antibiotic resistance by altering the specific location where antibiotics are targeted, controlling the movement of medications across its cell membranes, and enzymatically changing antibiotics to render them ineffective. A. baumannii may augment antibiotic resistance not only via innate genetic pathways but also via other virulence-associated mechanisms. Mechanisms contributing to the resistance of A. baumannii include structural and functional adaptations, such as alterations in outer membrane proteins (e.g., porins) and components of the cell envelope (e.g., lipopolysaccharides and bacterial capsules). The development of resistance is further enhanced by various specialized mechanisms, including the action of enzymes such as phospholipases C and D, glycan-specific adamalysin-like protease CpaA, as well as processes like quorum sensing and biofilm production.

In conclusion, this study underscores the significant prevalence of ESBL-producing *A. baumannii* in clinical samples from Erbil City, contributing to the high resistance rates against critical antibiotics. The presence of blaSHV, blaTEM, and blaCTX genes highlights the genetic basis for this resistance, with the blaTEM gene being most prevalent. The findings call for careful antibiotic stewardship and enhanced surveillance to track resistance patterns and emerging ESBL strains. Future research should explore additional ESBL-associated genes to develop comprehensive strategies for managing and mitigating antibiotic resistance in *A. baumannii*.

One of the limitations of this study was the lack of control strains in the antimicrobial susceptibility testing section. Additionally, the study's findings are specific to the clinical settings in Erbil City, which may limit their generalizability to other regions with different antimicrobial resistance patterns. Future research should aim to incorporate a broader range of control strains and expand the geographical scope to enhance the validity and applicability of the results. Additionally, given the increasing challenge posed by antibiotic-resistant bacteria, research into alternative treatment strategies, such as bacteriophage therapy, could be of significant interest.

Acknowledgments

None

preprint

Author s contributions

Conceptualization and design: S.S.Q, P.A.H

Data acquisition: S.S.Q, S.H.A, R.M.HDrafting: M.A.A; P.A.H

Critical revision: S.S.Q; M.A.A; P.A.H

Conflict of interest

The authors confirm that there are no conflicts of interest associated with this study.

Funding

No financial support was received for this research.

preprint

References

1. Lin MF, Lan CY. Antimicrobial resistance in Acinetobacter baumannii: From bench to bedside. World journal of clinical cases. 2014;2(12):787-814. https://doi.org/10.12998/wjcc.v2.i12.787
2. Abdar MH, Taheri-Kalani M, Taheri K, Emadi B, Hasanzadeh A, Sedighi A, et al. Prevalence of extended-spectrum beta-lactamase genes in Acinetobacter baumannii strains isolated from nosocomial infections in Tehran, Iran. GMS hygiene and infection control. 2019;14:Doc02. https://doi.org/10.3205/dgkh000318
3. Abd El-Baky RM, Farhan SM, Ibrahim RA, Mahran KM, Hetta HF. Antimicrobial resistance pattern and molecular epidemiology of ESBL and MBL producing Acinetobacter baumannii isolated from hospitals in Minia, Egypt. Alexandria Journal of medicine. 2020;56(1):4-13. https://doi.org/10.1080/20905068.2019.1707350
4. Wong D, Nielsen TB, Bonomo RA, Pantapalangkoor P, Luna B, Spellberg B. Clinical and Pathophysiological Overview of Acinetobacter Infections: a Century of Challenges. Clinical microbiology reviews. 2017;30(1):409-47. https://doi.org/10.1128/cmr.00058-16
5. Freire MP, de Oliveira Garcia D, Garcia CP, Campagnari Bueno MF, Camargo CH, Kono Magri ASG, et al. Bloodstream infection caused by extensively drug-resistant Acinetobacter baumannii in cancer patients: high mortality associated with delayed treatment rather than with the degree of neutropenia. Clinical microbiology and infection : the official publication of the European Society of Clinical Microbiology and Infectious Diseases. 2016;22(4):352-8. https://doi.org/10.1016/j.cmi.2015.12.010
6. Morris FC, Dexter C, Kostoulias X, Uddin MI, Peleg AY. The Mechanisms of Disease Caused by Acinetobacter baumannii. Frontiers in microbiology. 2019;10:1601. https://doi.org/10.3389/fmicb.2019.01601
7. Moosavian M, Ahmadi K, Shoja S, Mardaneh J, Shahi F, Afzali M. Antimicrobial resistance patterns and their encoding genes among clinical isolates of Acinetobacter baumannii in Ahvaz, Southwest Iran. MethodsX. 2020;7:101031. https://doi.org/10.1016/j.mex.2020.101031
8. Khoshnood S, Heidary M, Mirnejad R, Bahramian A, Sedighi M, Mirzaei H. Drug-resistant gram-negative uropathogens: A review. Biomedicine & pharmacotherapy = Biomedecine & pharmacotherapie. 2017;94:982-94. https://doi.org/10.1016/j.biopha.2017.08.006
9. Jiang W, Yang W, Zhao X, Wang N, Ren H. Klebsiella pneumoniae presents antimicrobial drug resistance for β-lactam through the ESBL/PBP signaling pathway.

Preprint

Experimental and therapeutic medicine. 2020;19(4):2449-56. https://doi.org/10.3892/etm.2020.8498

10. Dirar MH, Bilal NE, Ibrahim ME, Hamid ME. Prevalence of extended-spectrum β-lactamase (ESBL) and molecular detection of blaTEM, blaSHV and blaCTX-M genotypes among Enterobacteriaceae isolates from patients in Khartoum, Sudan. The Pan African medical journal. 2020;37:213. https://doi.org/10.11604/pamj.2020.37.213.24988
11. Ibrahim ME, Algak TB, Abbas M, Elamin BK. Emergence of bla (TEM), bla (CTX-M), bla (SHV) and bla (OXA) genes in multidrug-resistant Enterobacteriaceae and Acinetobacter baumannii in Saudi Arabia. Experimental and therapeutic medicine. 2021;22(6):1450. https://doi.org/10.3892%2Fetm.2021.10885
12. Azizi M, Mortazavi SH, Etemadimajed M, Gheini S, Vaziri S, Alvandi A, et al. Prevalence of Extended-Spectrum β-Lactamases and Antibiotic Resistance Patterns in Acinetobacter baumannii Isolated from Clinical Samples in Kermanshah, Iran. Jundishapur J Microbiol. 2017;10(12):e61522. https://doi.org/10.5812/jjm.61522
13. Hamasalih R, Abdulrahman Z. Antibiofilm potency of ginger (Zingiber officinale) and quercetin against Staphylococcus aureus isolated from urinary tract catheterized patients. Applied Ecology & Environmental Research. 2020;18(1):219-36. http://dx.doi.org/10.15666/aeer/1801_219236
14. Humphries R, Bobenchik AM, Hindler JA, Schuetz AN. Overview of Changes to the Clinical and Laboratory Standards Institute Performance Standards for Antimicrobial Susceptibility Testing, M100, 31st Edition. Journal of clinical microbiology. 2021;59(12):e0021321. https://doi.org/10.1128/jcm.00213-21
15. Bakr KI, Abdul-Rahman SM, Muhammad Hamasalih R. Molecular detection of β-lactamase genes in Klebsiella pneumoniae and Escherichia coli isolated from different clinical sources. Cellular and molecular biology (Noisy-le-Grand, France). 2022;67(4):170-80. https://doi.org/10.14715/cmb/2021.67.4.19
16. Feizabadi MM, Fathollahzadeh B, Taherikalani M, Rasoolinejad M, Sadeghifard N, Aligholi M, et al. Antimicrobial susceptibility patterns and distribution of blaOXA genes among Acinetobacter spp. Isolated from patients at Tehran hospitals. Japanese journal of infectious diseases. 2008;61(4):274-8.
17. Ting C, Jun A, Shun Z. Detection of the common resistance genes in Gram-negative bacteria using gene chip technology. Indian journal of medical microbiology. 2013;31(2):142-7. https://doi.org/10.4103/0255-0857.115230

preprint

18. Shahcheraghi F, Abbasalipour M, Feizabadi M, Ebrahimipour G, Akbari N. Isolation and genetic characterization of metallo-β-lactamase and carbapenamase producing strains of Acinetobacter baumannii from patients at Tehran hospitals. Iranian journal of microbiology. 2011;3(2):68-74.
19. Rezaee MA, Pajand O, Nahaei MR, Mahdian R, Aghazadeh M, Ghojazadeh M, et al. Prevalence of Ambler class A β-lactamases and ampC expression in cephalosporin-resistant isolates of Acinetobacter baumannii. Diagnostic microbiology and infectious disease. 2013;76(3):330-4. https://doi.org/10.1016/j.diagmicrobio.2013.04.003
20. Jahangiri S, Malekzadegan Y, Motamedifar M, Hadi N. Virulence genes profile and biofilm formation ability of Acinetobacter baumannii strains isolated from inpatients of a tertiary care hospital in southwest of Iran. Gene Reports. 2019;17:100481. https://doi.org/10.1016/j.genrep.2019.100481
21. Nowak P, Paluchowska PM, Budak A. Co-occurrence of carbapenem and aminoglycoside resistance genes among multidrug-resistant clinical isolates of Acinetobacter baumannii from Cracow, Poland. Medical science monitor basic research. 2014;20:9-14. https://doi.org/10.12659/msmbr.889811
22. Choi WS, Kim SH, Jeon EG, Son MH, Yoon YK, Kim JY, et al. Nosocomial outbreak of carbapenem-resistant Acinetobacter baumannii in intensive care units and successful outbreak control program. Journal of Korean medical science. 2010;25(7):999-1004. https://doi.org/10.3346/jkms.2010.25.7.999
23. Zeighami H, Valadkhani F, Shapouri R, Samadi E, Haghi F. Virulence characteristics of multidrug resistant biofilm forming Acinetobacter baumannii isolated from intensive care unit patients. BMC infectious diseases. 2019;19(1):629. https://doi.org/10.1186/s12879-019-4272-0
24. Howard A, O'Donoghue M, Feeney A, Sleator RD. Acinetobacter baumannii: an emerging opportunistic pathogen. Virulence. 2012;3(3):243-50. https://doi.org/10.4161/viru.19700
25. Poirel L, Bonnin RA, Nordmann P. Genetic basis of antibiotic resistance in pathogenic Acinetobacter species. IUBMB life. 2011;63(12):1061-7. https://doi.org/10.1002/iub.532
26. Vahdani P, Yaghoubi T, Aminzadeh Z. Hospital acquired antibiotic-resistant acinetobacter baumannii infections in a 400-bed hospital in Tehran, Iran. International journal of preventive medicine. 2011;2(3):127-30.
27. Saffari F, Monsen T, Karmostaji A, Azimabad FB, Widerström M. Significant spread of extensively drug-resistant Acinetobacter baumannii genotypes of clonal complex 92

preprint

among intensive care unit patients in a university hospital in southern Iran. J Med Microbiol. 2017;66(11):1656-62. https://doi.org/10.1099/jmm.0.000619

28. Vakili M, Zandi H, Eslami G. Prevalence of ESBLs in Acinetobacter baumannii isolated from intensive care unit (ICU) of Ghaem hospital, Mashhad, Iran. Journal of Pure and Applied Microbiology. 2017;11(2):811-9.

preprint

preprint