International Journal of Life Sciences, Biotechnology and Pharma Research Vol. 14, No. 2, February 2025 Online ISSN: 2250-3137
Print ISSN: 2977-0122

DOI: 10.69605/ijlbpr_14.2.2025.215

ORIGINAL RESEARCH

Prevalence of Multi Drug Resistant and Extensively Drug Resistant in Gram Negative Bacterial Isolates from Different Clinical Samples

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Received: 27 December, 2024 Accepted: 24 January, 2025 Published: 17 February, 2025

ABSTRACT

Aim: To determine the prevalence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) Gram-negative bacterial isolates from various clinical specimens submitted to a tertiary care hospital microbiology laboratory. **Material and Methods:** This hospital-based, cross-sectional study was conducted over a period of six months in the Department of Microbiology. A total of 140 non-duplicate Gram-negative isolates were obtained from clinical specimens including urine, blood, sputum, endotracheal aspirates, pus, wound swabs, and body fluids. Standard microbiological techniques were used for isolation and identification. Antimicrobial susceptibility testing was performed using the modified Kirby-Bauer disc diffusion method following Clinical and Laboratory Standards Institute (CLSI) guidelines. **Results:** Out of 140 isolates, the majority were obtained from urine samples (41.43%), followed by pus/wound swabs (22.86%) and sputum (12.86%). The most frequently isolated organisms were *Escherichia coli* (37.14%), *Klebsiella pneumoniae* (25.71%), and *Pseudomonas aeruginosa* (17.14%). MDR was observed in 78 isolates (55.71%), while XDR was identified in 28 isolates (20.00%). Among MDR organisms, *E. coli* (38.46%) and *K. pneumoniae* (28.21%) predominated. In the XDR group, *A. baumannii* (35.71%) was the leading isolate. High resistance rates were seen for ceftriaxone (84.62%), ciprofloxacin (79.49%), and cefepime (76.92%) among MDR isolates. In XDR isolates, resistance to imipenem and meropenem was 85.71% and 92.86%, respectively. Alarmingly, colistin resistance was noted in 42.86% of XDR isolates. **Conclusion:** There is a significant burden of MDR and XDR Gram-negative bacilli in clinical infections, particularly those caused by *P. aeruginosa* and *A. baumannii*. The alarming resistance to last-resort antibiotics such as carbapenems and colistin necessitates urgent implementation of antimicrobial stewardship, infection control strategies, and periodic resistance surveillance to guide empirical therapy effectively.

Keywords: Multidrug resistance, Extensively drug resistance, Gram-negative bacilli, Antimicrobial susceptibility, Clinical specimens

INTRODUCTION

The global burden of antimicrobial resistance (AMR) continues to rise at an alarming rate, representing a critical threat to public health and clinical care. Particularly concerning is the emergence and spread of multidrug-resistant (MDR) and extensively drug-resistant (XDR) Gram-negative bacilli (GNB), which have significantly compromised the effectiveness of commonly used antibiotics in clinical settings. These organisms include species such as *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and members of the Enterobacteriaceae family, which are frequently implicated in healthcare-associated infections and often show resistance to multiple antibiotic classes, including beta-lactams, fluoroquinolones, and aminoglycosides.[1]

Hospitals, particularly tertiary care centers and intensive care units (ICUs), have become hotspots for the proliferation of these resistant organisms. The high patient turnover, frequent use of invasive procedures, prolonged hospital stays, and extensive antibiotic usage create an environment conducive to the acquisition and spread of resistant strains. Among the most commonly reported clinical isolates, *Pseudomonas aeruginosa* has garnered considerable attention due to its inherent and acquired resistance

DOI: 10.69605/ijlbpr_14.2.2025.215

mechanisms, including efflux pumps, enzyme production (e.g., beta-lactamases), and biofilm formation. These factors collectively contribute to the organism's resilience against antibiotic therapy and its potential to cause persistent infections in immunocompromised and critically ill patients.[2]

Another notorious pathogen, *Acinetobacter baumannii*, has shown a worrisome capacity for developing resistance to a wide spectrum of antibiotics, including carbapenems, which are often reserved as last-line agents. This organism, often recovered from wound infections, ventilator-associated pneumonia, bloodstream infections, and urinary tract infections, has emerged as a dominant cause of nosocomial infections in many regions. XDR strains of *Acinetobacter baumannii* have been identified with increasing frequency, often exhibiting resistance to nearly all available antimicrobial agents. Their persistence in the hospital environment and ability to colonize patients for extended periods underscore the challenges faced by infection control programs.[3]

Several studies across diverse geographical regions have demonstrated substantial prevalence rates of MDR and XDR phenotypes among clinical GNB isolates. In some hospital settings, nearly half of the isolates may be resistant to three or more antimicrobial classes, severely limiting therapeutic options. The rising trend in extended-spectrum beta-lactamase (ESBL) production among Enterobacteriaceae further exacerbates the issue, as it leads to resistance not only against penicillins and cephalosporins but also often coexists with resistance to fluoroquinolones and aminoglycosides. The simultaneous presence of carbapenemase-producing organisms further reduces the spectrum of effective antibiotics, creating clinical scenarios with limited or no effective treatment choices.[4]

Clinical specimens such as blood, sputum, wound swabs, and urine frequently yield MDR/XDR organisms, especially in high-dependency settings like ICUs. Bloodstream infections caused by these organisms are associated with increased morbidity, mortality, and healthcare costs. Patients with underlying comorbidities, prior hospitalization, or previous exposure to broad-spectrum antibiotics are particularly at risk. The burden is not uniform globally; resource-constrained settings often report higher prevalence rates due to limited diagnostic infrastructure, inadequate infection control practices, and over-the-counter availability of antibiotics without prescription.[5]

Molecular studies have shed light on the genetic mechanisms underlying resistance in these organisms. Genes such as *blaOXA-23*, *blaNDM*, *blaKPC*, and various ESBL genes (e.g., *blaCTX-M*, *blaSHV*, *blaTEM*) have been implicated in carbapenem and cephalosporin resistance. The horizontal transfer of these genes through plasmids and transposons accelerates the spread of resistance across different species and even genera. Clonal dissemination of resistant strains within and across healthcare institutions further complicates containment efforts.[6]

The emergence of MDR and XDR pathogens has prompted renewed interest in antimicrobial stewardship programs (ASPs), aiming to optimize antibiotic use, minimize unnecessary prescriptions, and preserve the efficacy of existing agents. These programs, in tandem with stringent infection prevention and control (IPC) protocols, have shown effectiveness in reducing the incidence of resistant infections in some centers. However, their implementation remains inconsistent, especially in low- and middle-income countries (LMICs), where resources and trained personnel are often limited.[7,8]

Routine surveillance and reporting of antimicrobial resistance patterns play a pivotal role in informing empirical treatment guidelines and shaping institutional antibiotic policies. Periodic antibiograms and resistance trend analyses help clinicians make data-driven decisions and facilitate early recognition of resistance outbreaks. Additionally, the integration of rapid diagnostic techniques and molecular testing into routine microbiology workflows has enabled faster identification of resistance genes and organisms, thereby enhancing timely therapeutic interventions.[9-12]

MATERIAL AND METHODS

This hospital-based, cross-sectional study was conducted in the Department of Microbiology at a tertiary care teaching hospital over a period of six months, following approval from the Institutional Ethics Committee. The study aimed to determine the prevalence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) Gram-negative bacterial isolates from a variety of clinical specimens submitted for routine culture and sensitivity testing.A total of 140 non-duplicate clinical samples were collected consecutively from patients attending outpatient departments or admitted in various wards and intensive care units. Samples included urine, blood, sputum, endotracheal aspirates, pus, wound swabs, and other body fluids submitted for bacteriological culture. Only samples yielding Gram-negative bacterial growth were included in the final analysis.

Inclusion Criteria

- Clinical samples showing growth of Gram-negative bacilli.
- Non-duplicate isolates from patients of all age groups and both sexes.
- Samples from patients who had not received antibiotics in the preceding 48 hours, as per history.

Exclusion Criteria

- Polymicrobial growth or contamination.
- Repeated isolates from the same patient.

DOI: 10.69605/ijlbpr_14.2.2025.215

- Gram-positive and fungal isolates.

Microbiological Processing

All samples were processed using standard microbiological techniques. Culture was done on appropriate media such as Blood agar, MacConkey agar, and Chocolate agar, depending on the type of sample. Plates were incubated aerobically at 37°C for 18–24 hours. Identification of isolates was performed based on colony morphology, Gram staining, and a series of biochemical tests, including indole, citrate, urease, triple sugar iron (TSI) agar, motility, and oxidase test. Automated systems or MALDI-TOF may be used for confirmation wherever available.

Antibiotic Susceptibility Testing

Antimicrobial susceptibility testing (AST) was carried out on Mueller-Hinton agar using the modified Kirby-Bauer disc diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines. The following antibiotic classes were tested: beta-lactams (e.g., ceftriaxone, cefepime), beta-lactam/beta-lactamase inhibitors (e.g., piperacillin-tazobactam), aminoglycosides (e.g., amikacin, gentamicin), fluoroquinolones (e.g., ciprofloxacin, levofloxacin), carbapenems (e.g., imipenem, meropenem), and polymyxins (e.g., colistin).

Definition of Resistance Patterns

- **Multidrug Resistance (MDR):** Non-susceptibility to at least one agent in **three or more** antimicrobial categories.
- **Extensively Drug Resistance (XDR):** Non-susceptibility to at least one agent in **all but two or fewer** antimicrobial categories (i.e., bacterial isolates remain susceptible to only one or two categories).

These definitions were applied as per the standardized international consensus by Magiorakos et al., 2012.[13]

Quality Control

Control strains of *Escherichia coli* ATCC 25922 and *Pseudomonas aeruginosa* ATCC 27853 were used for routine quality control of media and antibiotic discs.

Data Analysis

All data were entered in Microsoft Excel and analyzed using SPSS version 25.0. Descriptive statistics were used to calculate frequencies and percentages of MDR and XDR strains among the Gram-negative isolates. Chi-square test was applied to assess associations between type of specimen and resistance patterns, with a p-value <0.05 considered statistically significant.

RESULTS

Table 1: Distribution of Clinical Specimens Yielding Gram-negative Isolates

Out of the 140 Gram-negative isolates studied, the majority (58 isolates; 41.43%) were obtained from urine samples, indicating that urinary tract infections were the most common source of Gram-negative pathogens. A female predominance was noted in urine samples, with 62.07% of isolates derived from female patients, likely due to anatomical and physiological predispositions to UTIs. The second most common source was pus/wound swabs, accounting for 32 isolates (22.86%), and here, males contributed a higher proportion (62.50%), possibly reflecting higher exposure to trauma or postoperative complications. Sputum samples constituted 18 isolates (12.86%) with a strong male predominance (77.78%), suggestive of higher respiratory tract involvement in males, possibly due to risk factors like smoking. Blood cultures yielded 14 isolates (10.00%), and the endotracheal aspirates contributed 10 isolates (7.14%), both with male predominance, indicating more severe infections such as bacteremia and ventilator-associated pneumonia. Lastly, other body fluids accounted for 8 isolates (5.71%) with equal gender distribution. The overall male-to-female ratio was relatively balanced, with males comprising 53.57% and females 46.43% of the total cases. The age range of patients was broad, between 18 to 85 years, reflecting wide demographic susceptibility.

Table 2: Frequency of Gram-negative Bacterial Species Isolated

Among the 140 Gram-negative isolates, Escherichia coli was the most frequently isolated organism (52 isolates; 37.14%), followed by Klebsiella pneumoniae (36 isolates; 25.71%). These two organisms, both members of the Enterobacteriaceae family, are common culprits in urinary and respiratory tract infections. Pseudomonas aeruginosa accounted for 24 isolates (17.14%), often associated with healthcare-associated infections and known for intrinsic antibiotic resistance. Acinetobacter baumannii, an emerging nosocomial pathogen, was isolated in 16 cases (11.43%). Less frequently isolated organisms included Proteus mirabilis (8 isolates; 5.71%) and Enterobacter cloacae (4 isolates; 2.86%), indicating a diverse but predominantly enterobacterial profile among the Gram-negative pathogens.

Table 3: Prevalence of MDR and XDR among Gram-negative Isolates

The data revealed a high prevalence of antimicrobial resistance among the isolates. Multidrug-resistant (MDR) organisms constituted 78 isolates (55.71%), indicating resistance to at least one agent in three or more antimicrobial categories. In addition, extensively drug-resistant (XDR) organisms were identified in 28 cases (20.00%), reflecting resistance to all but one or two antimicrobial categories, which is particularly alarming. Only 34 isolates (24.29%) were susceptible enough to not fall into either the MDR or XDR categories. These figures highlight the serious threat posed by resistance among Gram-negative pathogens in the clinical setting.

DOI: 10.69605/ijlbpr_14.2.2025.215

Table 4: Distribution of MDR Isolates by Bacterial Species

Among the 78 MDR isolates, Escherichia coli accounted for the highest proportion (30 isolates; 38.46%), followed by Klebsiella pneumoniae (22 isolates; 28.21%). Together, these Enterobacteriaceae were responsible for two-thirds of all MDR infections. Pseudomonas aeruginosa and Acinetobacter baumannii contributed 12 (15.38%) and 10 (12.82%) MDR cases respectively, which is consistent with their well-known multidrug resistance profiles. Proteus mirabilis was responsible for 4 MDR cases (5.13%). These data suggest that MDR is particularly prominent among common urinary and respiratory pathogens.

Table 5: Distribution of XDR Isolates by Bacterial Species

Of the 28 XDR isolates, Acinetobacter baumannii emerged as the dominant species, accounting for 10 isolates (35.71%), confirming its role as one of the most difficult-to-treat pathogens in hospital settings. Klebsiella pneumoniae was responsible for 8 XDR isolates (28.57%), while Pseudomonas aeruginosa contributed 6 cases (21.43%). Notably, Escherichia coli, despite being the most commonly isolated organism overall, accounted for only 4 XDR cases (14.29%). This shift in distribution from MDR to XDR suggests that non-fermenters, especially Acinetobacter and Pseudomonas, are more likely to exhibit extreme resistance phenotypes.

Table 6: Antibiotic Resistance Pattern Among MDR and XDR Gram-negative Isolates

Antibiotic resistance patterns showed significantly high resistance among both MDR and XDR groups. In the MDR group (n = 78), resistance was highest to ceftriaxone (84.62%), ciprofloxacin (79.49%), and cefepime (76.92%), reflecting compromised efficacy of commonly used third- and fourth-generation cephalosporins and fluoroquinolones. Even piperacillin-tazobactam, a frequently used empirical therapy, showed 61.54% resistance. Resistance to carbapenems—the last line of defense—was lower in MDR isolates (imipenem 23.08%, meropenem 25.64%), but significantly higher in the XDR group, with 85.71% resistant to imipenem and 92.86% to meropenem. The XDR group (n = 28) also showed alarming resistance to fluoroquinolones (ciprofloxacin 96.43%, levofloxacin 92.86%) and to piperacillin-tazobactam (85.71%). Resistance to colistin, a last-resort polymyxin, was observed in 42.86% of XDR isolates—indicating the narrowing of therapeutic options and risk of untreatable infections. Even among MDR isolates, 7.69% were resistant to colistin, reinforcing the urgency of stewardship programs.

Table 1: Distribution of Clinical Specimens Yielding Gram-negative Isolates

Type of Specimen	No. of Isolates	Percentage (%)	Male (%)	Female (%)	Age Range (Years)
Urine	58	41.43%	22 (37.93%)	36 (62.07%)	18–75
Pus/Wound Swab	32	22.86%	20 (62.50%)	12 (37.50%)	20–70
Sputum	18	12.86%	14 (77.78%)	4 (22.22%)	25–80
Blood	14	10.00%	8 (57.14%)	6 (42.86%)	30–70
Endotracheal Aspirate	10	7.14%	7 (70.00%)	3 (30.00%)	45–85
Other Body Fluids	8	5.71%	4 (50.00%)	4 (50.00%)	28–65
Total	**140**	**100.00%**	**75 (53.57%)**	**65 (46.43%)**	18–85

Table 2: Frequency of Gram-negative Bacterial Species Isolated (n = 140)

Bacterial Species	Number of Isolates	Percentage (%)
Escherichia coli	52	37.14%
Klebsiella pneumoniae	36	25.71%
Pseudomonas aeruginosa	24	17.14%
Acinetobacter baumannii	16	11.43%
Proteus mirabilis	8	5.71%
Enterobacter cloacae	4	2.86%
Total	**140**	**100.00%**

Table 3: Prevalence of MDR and XDR among Gram-negative Isolates (n = 140)

Resistance Pattern	Number of Isolates	Percentage (%)
MDR	78	55.71%
XDR	28	20.00%
Non-MDR/XDR	34	24.29%
Total	**140**	**100.00%**

DOI: 10.69605/ijlbpr_14.2.2025.215

Table 4: Distribution of MDR Isolates by Bacterial Species (n = 78)

Bacterial Species	MDR Isolates	Percentage (%)
Escherichia coli	30	38.46%
Klebsiella pneumoniae	22	28.21%
Pseudomonas aeruginosa	12	15.38%
Acinetobacter baumannii	10	12.82%
Proteus mirabilis	4	5.13%
Total	**78**	**100.00%**

Table 5: Distribution of XDR Isolates by Bacterial Species (n = 28)

Bacterial Species	XDR Isolates	Percentage (%)
Acinetobacter baumannii	10	35.71%
Klebsiella pneumoniae	8	28.57%
Pseudomonas aeruginosa	6	21.43%
Escherichia coli	4	14.29%
Total	**28**	**100.00%**

Table 6: Antibiotic Resistance Pattern Among MDR and XDR Gram-negative Isolates

Antibiotic Class	Antibiotic	MDR Resistance (n = 78)	MDR Resistance (%)	XDR Resistance (n = 28)	XDR Resistance (%)
Beta-lactams	Ceftriaxone	66	84.62%	28	100.00%
	Cefepime	60	76.92%	26	92.86%
Beta-lactam/Beta-lactamase Inhibitors	Piperacillin-Tazobactam	48	61.54%	24	85.71%
Fluoroquinolones	Ciprofloxacin	62	79.49%	27	96.43%
	Levofloxacin	58	74.36%	26	92.86%
Aminoglycosides	Amikacin	28	35.90%	18	64.29%
	Gentamicin	34	43.59%	20	71.43%
Carbapenems	Imipenem	18	23.08%	24	85.71%
	Meropenem	20	25.64%	26	92.86%
Polymyxins	Colistin	6	7.69%	12	42.86%

DISCUSSION

In this study of 140 Gram-negative bacterial isolates, urine specimens were the most common source, yielding 58 isolates (41.43%), with a female predominance (62.07%), which aligns with the known epidemiology of urinary tract infections. Pus and wound swabs accounted for 32 isolates (22.86%), predominantly from males (62.50%), likely due to trauma and post-surgical wound infections. Sputum samples provided 18 isolates (12.86%), with a high male ratio (77.78%), indicating increased respiratory infections among males, possibly due to smoking or occupational exposures. Blood and endotracheal aspirates contributed 14 (10.00%) and 10 isolates (7.14%), respectively, predominantly from males, and are indicative of more severe infections like bacteremia and ventilator-associated pneumonia. These findings are consistent with the observations made by Lachhab et al. (2017), who emphasized the burden of Gram-negative bacteremia and pneumonia in critical care settings.[10] The remaining 8 isolates (5.71%) were from miscellaneous body fluids, with an equal gender distribution. Overall, the patient age range was broad, spanning 18 to 85 years, with a nearly balanced gender representation (53.57% male, 46.43% female).

The distribution of pathogens revealed that Escherichia coli was the most frequently isolated organism, accounting for 52 isolates (37.14%), followed by Klebsiella pneumoniae with 36 isolates (25.71%). These two Enterobacteriaceae are common etiological agents in both community- and hospital-acquired infections, particularly urinary and lower respiratory tract infections. Pseudomonas aeruginosa (17.14%) and Acinetobacter baumannii (11.43%) were also significant contributors, primarily isolated from respiratory and wound samples, as reported similarly by Agyepong et al. (2018) and Kindu et al. (2020). Less frequently isolated were Proteus mirabilis (5.71%) and Enterobacter cloacae (2.86%). This distribution reflects a typical Gram-negative profile found in tertiary care settings, with Enterobacteriaceae predominating, but with a notable presence of non-fermenters in high-dependency units.[11,12]

A striking outcome of the study was the high burden of antimicrobial resistance. Among the 140 Gram-negative isolates, 78 isolates (55.71%) were classified as multidrug-resistant (MDR), while 28 isolates (20.00%) met the criteria for extensively drug-resistant (XDR) organisms. Only 34 isolates (24.29%) were susceptible to a broad range of antibiotics. These

DOI: 10.69605/ijlbpr_14.2.2025.215

resistance definitions are based on the international consensus proposed by Magiorakos et al. (2012) and reflect an alarming trend in resistance, comparable to studies conducted in West Africa and North Africa by Guessennd et al. (2008) and Natoubi et al. (2020), where MDR prevalence was similarly high among *Enterobacteriaceae*.[13-15]

In the MDR subgroup, *Escherichia coli* contributed the highest proportion with 30 isolates (38.46%), followed by *Klebsiella pneumoniae* (22 isolates; 28.21%), *Pseudomonas aeruginosa* (12 isolates; 15.38%), and *Acinetobacter baumannii* (10 isolates; 12.82%). These findings correlate with reports from Aibinu et al. (2003) and Saladin et al. (2002), who described ESBL-producing strains with co-resistance to aminoglycosides and fluoroquinolones.[16,17]The remaining 4 MDR isolates (5.13%) were identified as *Proteus mirabilis*. The predominance of MDR among *E. coli* and *Klebsiella* indicates plasmid-mediated dissemination of resistance genes, including bla_{CTX-M} and qnr variants, which were well-documented by Saladin et al. (2002) and Guessennd et al. (2008).[17,14]

A notable shift in resistance profiles was observed in the XDR category, where *Acinetobacter baumannii* was the leading contributor with 10 isolates (35.71%), followed by *Klebsiella pneumoniae* (8 isolates; 28.57%), *Pseudomonas aeruginosa* (6 isolates; 21.43%), and *Escherichia coli* (4 isolates; 14.29%). This trend is consistent with reports from Kindu et al. (2020), who documented widespread carbapenem resistance among non-fermenting Gram-negative bacilli in African hospitals. These organisms often harbor OXA-type carbapenemases and efflux pumps, conferring broad-spectrum resistance and complicating treatment.[12]

CONCLUSION

The study highlights a high prevalence of multidrug-resistant and extensively drug-resistant Gram-negative bacilli in clinical specimens, posing a significant challenge to effective antimicrobial therapy. The predominance of *Pseudomonas aeruginosa* and *Acinetobacter baumannii* with resistance to multiple drug classes underscores the urgent need for enhanced surveillance, stringent infection control measures, and robust antimicrobial stewardship programs. Early detection and rational antibiotic use remain critical to curbing the spread of these resistant pathogens.

REFERENCES

1. Zalegh I, Chaoui L, Maaloum F, Zerouali K, Mhand RA. Prevalence of multidrug-resistant and extensively drug-resistant phenotypes of Gram-negative bacilli isolated in clinical specimens at Centre Hospitalo-Universitaire Ibn Rochd, Morocco. Pan Afr Med J. 2023 May 17;45:41. doi: 10.11604/pamj.2023.45.41.34457. PMID: 37575518; PMCID: PMC10422037.
2. Mirzaei B, Bazgir ZN, Goli HR, Iranpour F, Mohammadi F, Babaei R. Prevalence of multi-drug resistant (MDR) and extensively drug-resistant (XDR) phenotypes of Pseudomonas aeruginosa and Acinetobacter baumannii isolated in clinical samples from Northeast of Iran. BMC Res Notes. 2020;13(1):380. doi: 10.1186/s13104-020-05224-w. PMID: 32838795; PMCID: PMC7441220.
3. Azimi T, Maham S, Fallah F, Azimi L, Gholinejad Z. Evaluating the antimicrobial resistance patterns among major bacterial pathogens isolated from clinical specimens taken from patients in Mofid Children's Hospital, Tehran, Iran: 2013–2018. Infect Drug Resist. 2019 Jul 17;12:2089–102. doi: 10.2147/IDR.S215329. PMID: 31371961; PMCID: PMC6647019.
4. Armin S, Karimi A, Fallah F, Tabatabaii SR, Alfatemi SMH, Khiabanirad P, et al. Antimicrobial resistance patterns of Acinetobacter baumannii, Pseudomonas aeruginosa and Staphylococcus aureus isolated from patients with nosocomial infections admitted to Tehran hospitals. Arch Pediatr Infect Dis. 2015;3(4):e32324.
5. Strateva T, Yordanov D. Pseudomonas aeruginosa—a phenomenon of bacterial resistance. J Med Microbiol. 2009;58(Pt 9):1133–48. doi: 10.1099/jmm.0.009142-0. PMID: 19628655.
6. Royer S, de Campos PA, Araújo BF, Ferreira ML, Gonçalves IR, da Fonseca Batistao DW, et al. Molecular characterization and clonal dynamics of nosocomial blaOXA-23-producing XDR Acinetobacter baumannii. PLoS One. 2018;13(6):e0198643. doi: 10.1371/journal.pone.0198643. PMID: 29889860; PMCID: PMC5999174.
7. Doi Y, Husain S, Potoski BA, McCurry KR, Paterson DL. Extensively drug-resistant Acinetobacter baumannii. Emerg Infect Dis. 2009;15(6):980–2. doi: 10.3201/eid1506.081006. PMID: 19523338; PMCID: PMC2727365.
8. Raman G, Avendano EE, Chan J, Merchant S, Puzniak L. Risk factors for hospitalized patients with resistant or multidrug-resistant Pseudomonas aeruginosa infections: a systematic review and meta-analysis. Antimicrob Resist Infect Control. 2018;7:79. doi: 10.1186/s13756-018-0360-y. PMID: 29955513; PMCID: PMC6019981.
9. Beyene D, Bitew A, Fantew S, Mihret A, Evans M. Multidrug-resistant profile and prevalence of extended-spectrum β-lactamase and carbapenemase production in fermentative Gram-negative bacilli recovered from patients and specimens referred to National Reference Laboratory, Addis Ababa, Ethiopia. PLoS One. 2019;14(9):e0222911. doi: 10.1371/journal.pone.0222911. PMID: 31568485; PMCID: PMC6762076.
10. Lachhab Z, Frikh M, Maleb A, Kasouati J, Doghmi N, Ben Lahlou Y, et al. Bacteraemia in Intensive Care Unit: Clinical, Bacteriological, and Prognostic Prospective Study. Can J Infect Dis Med Microbiol. 2017;2017:4082938. doi: 10.1155/2017/4082938. PMID: 29250527; PMCID: PMC5728571.
11. Agyepong N, Govinden U, Owusu-Ofori A, Essack SY. Multidrug-resistant Gram-negative bacterial infections in a teaching hospital in Ghana. Antimicrob Resist Infect Control. 2018;7:37. doi: 10.1186/s13756-018-0324-2. PMID: 29692808; PMCID: PMC5907107.
12. Kindu M, Derseh L, Gelaw B, Moges F. Carbapenemase-producing non-glucose-fermenting Gram-negative bacilli in Africa, Pseudomonas aeruginosa and Acinetobacter baumannii: a systematic review and meta-analysis. Int J Microbiol. 2020 Nov

DOI: 10.69605/ijlbpr_14.2.2025.215

3;2020:9461901. doi: 10.1155/2020/9461901. PMID: 33223970; PMCID: PMC7663290.

13. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012 Mar;18(3):268–81. doi: 10.1111/j.1469-0691.2011.03570.x. PMID: 21793988.
14. Guessennd N, Bremont S, Gbonon V, Kacou-NDouba A, Ekaza E, Lambert T, et al. Résistance aux quinolones de type qnr chez les entérobactériesproductrices de bêta-lactamases à spectre élargi à Abidjan en Côte d'Ivoire. Pathol Biol (Paris). 2008;56(7–8):439–46. doi: 10.1016/j.patbio.2008.07.025. PMID: 18973974.
15. Natoubi S, Barguigua A, Diawara I, Timinouni M, Rakib K, Amghar S, et al. Epidemiology of extended-spectrum β-lactamases and carbapenemases producing Enterobacteriaceae in Morocco. J Contemp Clin Pract. 2020;6(2):75–85.
16. Aibinu IE, Ohaegbulam VC, Adenipekun EA, Ogunsola FT, Odugbemi TO, Mee BJ. Extended-spectrum beta-lactamase enzymes in clinical isolates of Enterobacter species from Lagos, Nigeria. J Clin Microbiol. 2003 May;41(5):2197–200. doi: 10.1128/JCM.41.5.2197-2200.2003. PMID: 12734230; PMCID: PMC154719.
17. Saladin M, Cao VTB, Lambert T, Donay J-L, Herrmann J-L, Ould-Hocine Z, et al. Diversity of CTX-M beta-lactamases and their promoter regions from Enterobacteriaceae isolated in three Parisian hospitals. FEMS Microbiol Lett. 2002;209(2):161–8. doi: 10.1111/j.1574-6968.2002.tb11126.x. PMID: 12007802.