RESEARCH PAPER

Antibiotic Susceptibility Profiles Of Bacterial Isolates Obtained From Diverse Clinical Specimens Of ICU Patients

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ABSTRACT

The present study was assess the antimicrobial susceptibility patterns of bacterial isolates obtained from various clinical specimens of patients admitted to Intensive Care Units (ICUs). Among the 550 clinical samples analyzed, 178 reported positive bacterial growth. These isolates were recovered from ten different categories of clinical specimens collected across seven distinct ICUs. Total 178 isolates, 55 (30.89%) were identified as gram-negative bacilli producing β-lactamase enzymes, including ESβL, AmpC β-lactamase, and combined ESβL+AmpC producers. Gram-negative bacilli were the predominant pathogens isolated, with Klebsiella pneumoniae (53 isolates) being the most frequent, followed by Pseudomonas aeruginosa (29 isolates). Colistin sulphate and polymyxin-B demonstrated the highest efficacy against gram-negative bacilli, followed by tigecycline, amikacin, meropenem, and imipenem. For gram-positive cocci, vancomycin, teicoplanin and linezolid were the most effective agents, with rifampicin, mupirocin, lincomycin, clindamycin, and daptomycin showing good activity. Antifungal susceptibility testing revealed flucytosine as the most effective drug against yeast isolates, followed by amphotericin-B and voriconazole. This investigation provides valuable insight into the prevailing antimicrobial susceptibility patterns of pathogens isolated from ICU patients in tertiary care hospitals. Routine monitoring of antibiotic sensitivity trends can play a crucial role in reducing the incidence of hospital acquired infections as well as limiting the spread of antimicrobial resistance.

Keywords: Antibiotic, Sensitivity, Intensive care unit (ICU), Resistance

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INTRODUCTION

Antimicrobial resistance has become a major global concern, as increasing resistance among bacterial populations compromises the effectiveness of available treatments and poses serious threats to patient health across all levels of medical care. Consequently, continuous evaluation of locally prevalent pathogens and their antimicrobial susceptibility patterns is crucial for clinicians to make informed treatment decisions and achieve better clinical outcomes. Research indicates that the judicious and rational use of antibiotics plays a key role in slowing the development and spread of resistance. Ongoing antimicrobial susceptibility surveillance provides critical insights for appropriate infection management and helps reduce the overall healthcare burden. Such evidence-based data support the optimization of antibiotic regimens and reinforce strategies aimed at preventing antimicrobial resistance at local, regional, and national scales (Thakur et al.,2025).

This investigation was conducted to analyze the antimicrobial susceptibility profiles of commonly isolated bacterial pathogens obtained from patients admitted to Intensive Care Units (ICUs). Infections developing in ICU settings are largely healthcare-associated, with reported occurrence rates several times higher than those observed in general hospital wards (Micek et al., 2025; Ak et al., 2002). Patients with critical illness are particularly susceptible to acquiring hospital-related infections, which are frequently attributed to microorganisms exhibiting antimicrobial resistance. Patterns of infection and their anatomical distribution vary according to the specific ICU environment, and the dominance of certain pathogens is closely linked to the site of infection (Micek et al., 2025; Dj et al., 1999). Moreover, a subset of serious infections arises opportunistically, affecting both hospitalised and community-based individuals, especially those with compromised immune function (Micek et al., 2025; Bergogne-Berezin, 2001). The increasing prevalence of resistant pathogens in ICU settings has consequently led to frequent revisions of antimicrobial treatment strategies for managing these infections (Micek et al., 2025).

The getting bigger worldwide incidence of resistance to broad-spectrum β-lactam antibiotics represents a significant clinical challenge, largely attributed to Gram-negative bacilli capable of producing extended-spectrum β-lactamases (ESβL) and AmpC β-lactamases. The presence of these enzymatic resistance mechanisms severely restricts available treatment options and makes the effective management of infections increasingly complex. Antibacterial agents have traditionally played a central role in the treatment of bacterial infections; however, over time, numerous bacterial species have evolved adaptive mechanisms that diminish drug efficacy, resulting in varying degrees of resistance to multiple antimicrobial classes (Jackson et al., 2026).

MATERIALS AND METHODS

Microbiological analysis was performed on ten categories of clinical specimens obtained from patients admitted across seven different Intensive Care Units. The collected samples comprised blood, endotracheal aspirates, urine, swabs from wounds, pus,

and bedsores, as well as a variety of body fluids including drain fluid, ascetic fluid, pleural fluid, abdominal fluid, peritoneal fluid, pericardial fluid and PCN fluid. Additional specimens such as broncho alveolar lavage, pus, tissue samples, cerebrospinal fluid, and catheter tips were also included in the study. All samples were cultured on MacConkey agar, blood agar, and nutrient agar plates using a four-quadrant streaking method to achieve discrete colony formation. Isolated colonies were then subcultured to obtain pure growth, which was further analyzed through Gram staining and conventional biochemical tests for definitive identification.

ANTIBIOTIC SENSITIVITY TEST

All culture-positive samples were evaluated for bacterial proliferation, and the isolates obtained were subsequently analyzed for their antimicrobial susceptibility patterns. Antibiotic sensitivity testing was carried out using the standard Kirby–Bauer disk diffusion technique on Mueller–Hinton agar. The interpretation of results followed the Clinical and Laboratory Standards Institute (CLSI) 2023 recommendations, as described by (Mihrete et al. 2026)**.**

Antimicrobial susceptibility testing was conducted for all isolates using a comprehensive panel of β-lactam and non-β-lactam agents. The β-lactam antibiotics tested comprised penicillins, including oxacillin (1µg); cephalosporins such as cefotaxime (30 µg) and cefepime (30µg); carbapenems, namely imipenem (10 µg) and meropenem (10 µg); and the monobactam aztreonam (30 µg). In addition, β-lactam/β-lactamase inhibitor combinations - including ampicillin–sulbactam (10/10 µg), piperacillin–tazobactam (100/10 µg), cefepime–tazobactam (30/10 µg), and cefoperazone–sulbactam (75/10 µg) - were evaluated. The non-β-lactam group included aminoglycosides, fluoroquinolones, glycylcyclines, lincosamides, glycopeptides, polymyxins, oxazolidinones, rifamycins, lipopeptides, and topical agents, represented by amikacin (30 µg), levofloxacin (5 µg), tigecycline (15 µg), clindamycin (2 µg), lincomycin, vancomycin (30 µg), teicoplanin (30 µg), colistin sulfate, polymyxin-B (300 U), linezolid (30 µg), rifampicin, daptomycin, and mupirocin. Antifungal susceptibility was also assessed using amphotericin-B, flucytosine, voriconazole, and fluconazole, following previously established methodologies (Aniokete et al., 2025; Sinha et al., 2008).

The inhibition zones surrounding each antimicrobial disk were measured in millimeters and categorized as susceptible, intermediate, or resistant according to the interpretive criteria outlined by the Clinical and Laboratory Standards Institute (CLSI). Isolates designated as susceptible fulfilled the breakpoint requirements specified for the disk diffusion assay. Alongside conventional manual testing, bacterial isolates were further evaluated using the VITEK-2 Compact automated system for organism identification and antimicrobial susceptibility profiling. Blood culture specimens were incubated and

monitored using the BD BACTEC™ 9120 automated blood culture system (Pincus; BD Diagnostics). To ensure the reliability and precision of susceptibility results, standard reference strains were included as quality controls, namely *Escherichia coli* ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, *Staphylococcus aureus* ATCC 25923, and *Enterococcus faecalis* ATCC 29212, as previously reported (Sirad et al., 2025).

β-lactamase production assay

Gram-negative isolates obtained from the clinical samples were examined for the production of β-lactamases, including βL, ESBL, ESBL+AmpC, and AmpC enzymes. Initial screening for these resistance mechanisms was carried out using the Kirby–Bauer disc diffusion method in accordance with CLSI guidelines. Isolates showing indicative patterns were further subjected to confirmatory testing for ESBL production using the combined-disc (double-disc synergy) technique. For each isolate, the zone of inhibition was measured on Mueller–Hinton agar. An organism was categorized as ESBL-producing when the inhibition zone around at least one antibiotic–inhibitor combination disc exceeded the corresponding antibiotic disc (without tazobactam, sulbactam, orclavulanic acid) by ≥5 mm (Geletaetal., 2024; Mobasherizadeh et al., 2012).

Data analysis

Antibiotic susceptibility data were analyzed using the chi-square statistical test, and associations yielding a p-value of 0.05 or lower were regarded as statistically significant.

RESULTS

From a total of 550 clinical specimens, 178 culture-positive bacterial isolates were recovered. These isolates were derived from ten different types of samples, including blood, endotracheal secretions (ET), urine, various swabs, body fluids, broncho alveolar lavage (BAL), pus, tissue, cerebrospinal fluid (CSF), and catheter tips. The samples were collected from patients admitted to seven different ICUs. Among these, 74 isolates (41.57%) originated from CCU-1, 44 (24.72%) from CCU-2, 41 (23.03%) from the Neuro-ICU, 7 (3.93%) from the Neonatal ICU, 5 (2.81%) from the Medical ICU, 4 (2.25%) from the Surgical ICU, and 3 (1.69%) from the Pediatric ICU. The study population consisted of 102 male patients (57%) and 76 female patients (43%) (Figure 1). The majority of blood, urine, swab, body fluid, BAL, pus, and CSF specimens originated from CCU-1, whereas most ET samples were obtained from the Neuro-ICU. Tissue samples predominately came from CCU-2, while catheter tip samples were mainly collected from the NICU (Table 1)

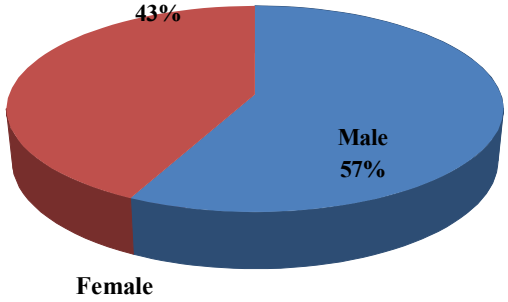

Figure 1: Number of Male Patients and Female Patients

Various clinical samples taken from different types of ICUs

Samples	CCU-1	CCU-2	Neuro ICU	NICU	MICU	SICU	PICU	Total	Percentage
Blood	24	6	6	2	0	0	2	40	22.47 %
ET	9	10	15	0	2	0	0	36	20.22 %

Samples	CCU-1	CCU-2	Neuro ICU	NICU	MICU	SICU	PICU	Total	Percentage
Urine	14	7	7	0	2	0	0	30	16.85 %
Swab	8	8	5	1	0	4	0	26	14.60 %
Body fluid	8	7	1	1	0	0	0	17	9.55 %
BAL	6	3	6	0	0	0	0	15	8.43 %
Pus	3	0	1	0	1	0	1	6	3.37 %
Tissue	1	2	0	0	0	0	0	3	1.69 %
CSF	1	1	0	1	0	0	0	3	1.69 %
Tip	0	0	0	2	0	0	0	2	1.12 %
Total	74	44	41	7	5	4	3	178	
Percentage	41.57 %	24.72 %	23.03 %	3.93 %	2.81 %	2.25 %	1.69 %		

From all total clinical specimens, blood samples represented 40 isolates (22.47%), ET secretions 36 isolates (20.22%), urine samples 30 isolates (16.85%), swabs 26 isolates (14.16%), body fluids17 isolates (9.55%), BAL samples 15 isolates (8.43%), pus 6 isolates (3.37%), tissue 3 isolates (1.69%), CSF3 isolates (1.69%), and catheter-tip

samples 2 isolates (1.12%) (Table1).

Gram-negative organisms constituted the majority of isolates. *Klebsiella pneumoniae* was the most frequently recovered species with 53 isolates (29.76%), followed by *Pseudomonas aeruginosa* (29 isolates, 16.29%), *Escherichia coli* (22 isolates, 12.36%), *Enterobacter cloacae* (8 isolates, 4.49%), and *Acinetobacter baumannii* (7 isolates, 3.93%). Among gram-positive bacteria, methicillin-resistant *Staphylococcus aureus* (MRSA) was predominant (12 isolates, 6.74%), followed by *Enterococcus faecalis* (7 isolates, 3.93%), *Staphylococcus aureus* (4 isolates, 2.25%), and *Streptococcus pyogenes* (3 isolates, 1.69%).Fungal isolates included *Candida tropicalis* (16 isolates, 8.99%),*Candida glabrata* (7 isolates, 3.93%), *Candida albicans* (6 isolates, 3.37%), *Candida parapsilosis* (2 isolates, 1.12%), and *Cryptococcus neoformans* (2 isolates, 1.12%).The distribution of microbial isolates across different clinical specimens is summarized in Table 2. The highest numbers of *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and*Acinetobacter baumannii* were recovered from endotracheal (ET) samples. Urine samples predominantly yielded *Escherichia coli*, *Enterobacter cloacae*, *Enterococcus faecalis*, and *Candidaalbicans*. Blood specimens most commonly contained *Staphylococcus aureus, Streptococcuspyogenes, Candida tropicalis, Candida glabrata*, and*Candida parapsilosis*. Methicillin-resistant *Staphylococcus aureus* (MRSA) was mainly isolated from swab samples, while *Cryptococcus neoformans* was exclusively detected in cerebrospinal fluid (CSF) samples.

Table 2: Organisms isolated from various clinical samples

Organisms	Blood	ET	Urine	Swab	Body fluid	BAL	Pus	Tissue	CSF	Tip	Total	Percentage
K. pneumoniae	8	15	4	8	4	9	4	1	0	0	53	29.76 %
P. aeruginosa	2	11	3	6	1	4	1	0	0	1	29	16.29 %
E. coli	4	3	5	3	5	1	0	0	1	0	22	12.36 %
E. cloacae	2	0	6	0	0	0	0	0	0	0	8	4.49 %
A. baumannii	1	4	0	0	0	1	0	0	0	1	7	3.93 %
MRSA	3	1	0	4	2	0	0	2	0	0	12	6.74 %
E. faecalis	0	0	4	1	2	0	0	0	0	0	7	3.93 %
S.aureus	2	0	0	2	0	0	0	0	0	0	4	2.25 %
S. pyogens	2	0	0	1	0	0	0	0	0	0	3	1.69 %
C. tropicalis	10	2	2	0	1	0	1	0	0	0	16	8.99 %
C. glabrate	5	0	0	0	2	0	0	0	0	0	7	3.93 %
C. albicans	0	0	5	1	0	0	0	0	0	0	6	3.37 %
C. parapsilosis	1	0	1	0	0	0	0	0	0	0	2	1.12%
Crypto.neoformans	0	0	0	0	0	0	0	0	2	0	2	1.12 %
Total	40	36	30	26	17	15	6	3	3	2	178	
Percentage	22.47 %	20.22 %	16.85 %	14.61 %	9.55 %	8.43 %	3.37 %	1.69 %	1.69 %	1.12 %		

Prevalence of β-lactam producing organisms

All isolates were evaluated for the production of β-lactamase (βL), extended-spectrum β-lactamase (ESβL), ESβL combined with AmpC β-lactamase, and AmpC β-lactamase. Among the 178 total isolates, 55 (30.89%) Gram-negative bacteria demonstrated one or more of these β-lactamase mechanisms. Of these 55 β-lactamase-producing isolates, 29 (52.72%) were ESβL producers, 19 (34.54%) produced both ESβL and AmpC enzymes, 6 (10.90%) produced βL alone, and 1 (1.81%) showed AmpC β-lactamase activity (Figure 2). *Klebsiella pneumoniae* was the most common producer of ESβL, ESβL+AmpC, and βL, while *Escherichia coli* was identified as the primary AmpC β-lactamase producer. With respect to antimicrobial susceptibility, ESβL-producing isolates retained sensitivity to carbapenems and β-lactam/β-lactamase inhibitor combinations but showed resistance to third-generation cephalosporins. ESβL+AmpC producers were susceptible only to carbapenems. In contrast, βL-producing isolates remained sensitive to cephalosporins, carbapenems, monobactams, and β-lactam/β-lactamase inhibitor combinations. The AmpC-producing isolate exhibited susceptibility to carbapenems and the fourth-generation cephalosporin cefepime.

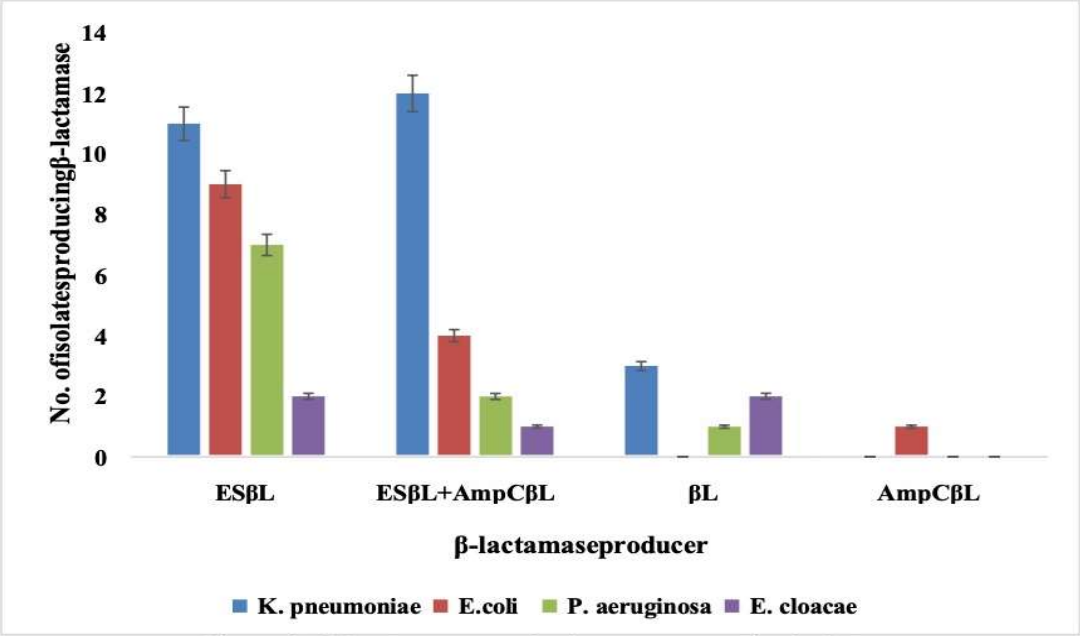

Figure 2: β-Lactamase producing gram negative isolates

Antibiotic sensitivity pattern of various organisms

Analysis of antimicrobial susceptibility showed that the gram-negative isolates exhibited variable sensitivity to different β-lactam antibiotics (Figure 3). Among the 55 isolates tested, Klebsiella pneumoniae, Escherichia coli, Pseudomonas aeruginosa, and Enterobacter cloacae demonstrated the highest susceptibility to Meropenem (100%), followed by Imipenem (96.36%). Moderate sensitivity was observed with Cefepime–Tazobactam (69.09%), Cefoperazone–Sulbactam (54.54%), Piperacillin–Tazobactam
(38.18%), and Ampicillin Sulbactam (34.54%). In contrast,only1 0.90%ofisolatesweresusceptibletoAztreonam,Cefotaxime,andCefepime.Ahighlevelofresistance wasnotedacrossmostgenerationsofcephalosporins;however,theuseofβ-lactam/β-lactamaseinhibitorcombinations improved the effectiveness of these drugs. These combinations function by blocking the bacterial enzymes that hydrolyze the β-lactam ring, thereby restoring the activity of β-lactam antibiotics and reducing resistance. The β-lactamase inhibitors thus enhance the efficacy of newer third-generation cephalosporins against resistant strains.

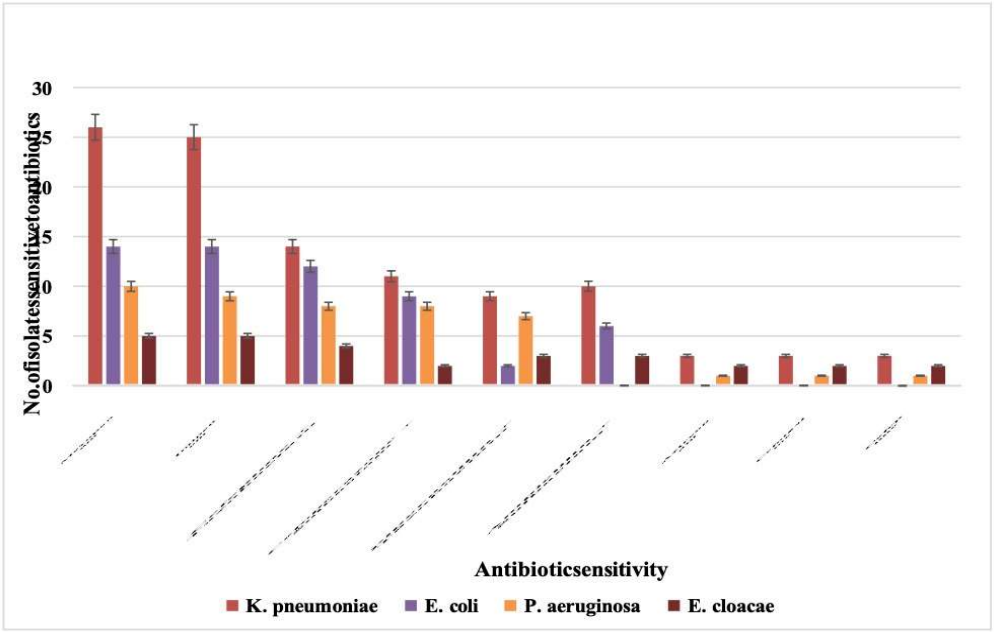

Figure3:Gram-negativeisolatessensitivetocertainβ-lactamantibiotics

Gram-negative isolates also demonstrated varying levels of susceptibility to non–β-lactam antibiotics. A total of 119 Gram-negative isolates showed sensitivity to these agents, as presented in Figure 4. Among the organismstested—including*K.pneumoniae,E.coli,P.aeruginosa,A.baumannii,*and*E.cloacae*—thehighestsusceptibilitywas observed with colistin sulfate (100%) and polymyxin-B (100%). Moderate levels of sensitivity were noted for tetracycline (75.63%), followed by amikacin (47.89%) and levofloxacin (28.57%). The bactericidal action of colistin sulfate and polymyxin-B results from their interaction with the outer and cytoplasmic membranes, leading todisruption of membrane integrity and altered permeability. Tetracycline exerts its effect by inhibiting bacterial protein synthesis, contributing to the observed susceptibility patterns

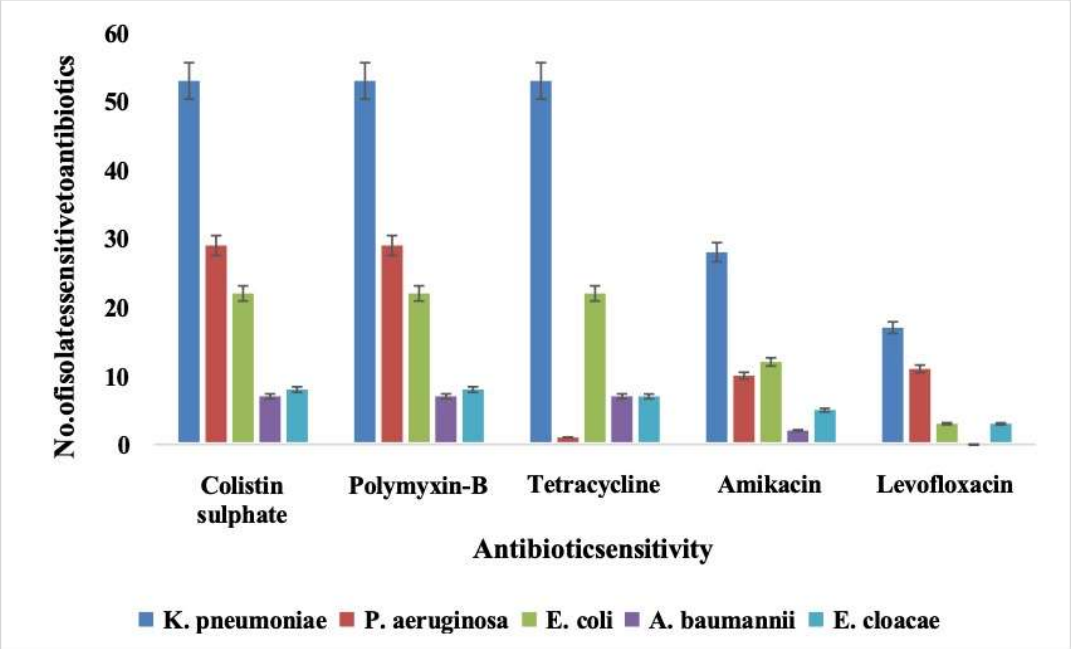

Figure4:Gram-negativeisolateswеresensitivetomultiplenon-β-lactamantibiotics.

A total of 26 gram-positive bacterial isolates demonstrated sensitivity to multiple antibiotics, as presented in Figure 5. Among the isolates—MRSA, E. faecalis, S. aureus, and S. pyogenes—the highest susceptibility wasobserved toward Vancomycin (100%), Teicoplanin (100%), and Linezolid (100%). These were followed by Rifampicin (92.30%), Mupirocin (53.84%), Lincomycin (50%), Clindamycin (50%), Daptomycin (50%), andOxacillin (15.38%). Vancomycin and Teicoplanin act by inhibiting peptidoglycan synthesis required for cell wall formation, while Linezolid blocks protein synthesis. Rifampicin exerts its effect by binding to the β-subunit of RNA polymerase, thereby preventing transcription. Through these mechanisms, the antibiotics effectively inhibit bacterial growth, resulting in observed susceptibility.

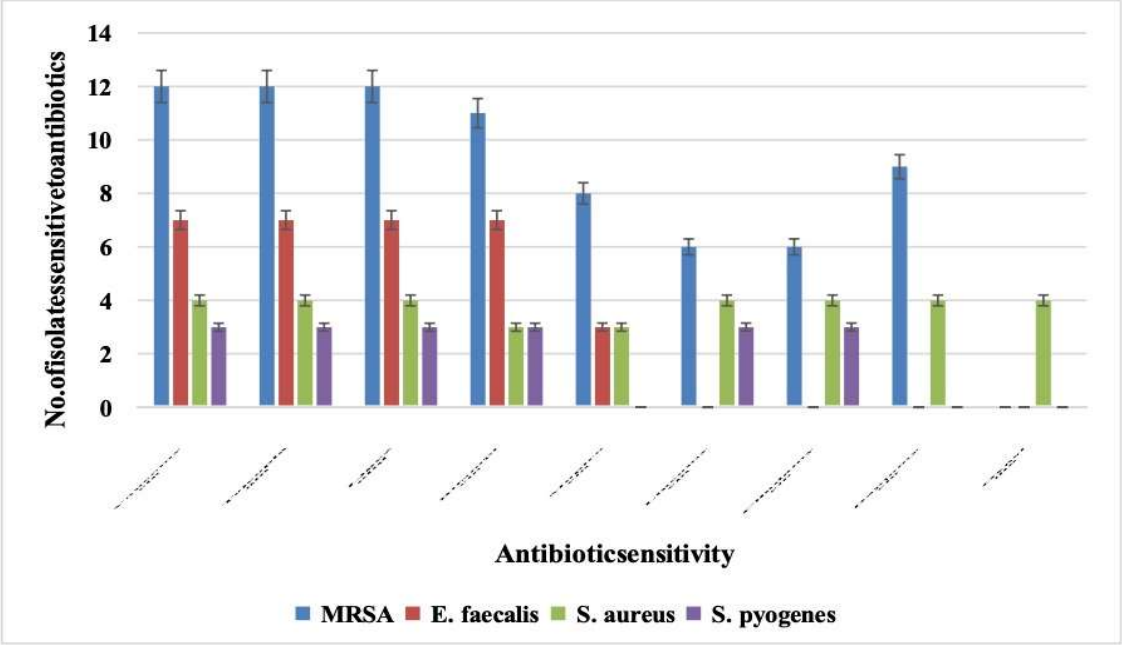

Figure5:Gram-positiveisolatessensitivetovariousantibiotics

A variety of antifungal agents were employed to control fungal infections in the human body. The fungal isolates demonstrated varying levels of susceptibility to these drugs, with a total of 33 strains responding to the antifungal treatments, as illustrated in Figure 6. Clinical isolates of *C. tropicalis, C. glabrata, C. albicans, C. parapsilosis,* and*Cryptococcus neoformans* showed the highest sensitivity to Flucytosine (100%), followed by Amphotericin-B (96.96%), Voriconazole (96.96%), and Fluconazole (42.42%). Theseantifungaldrugsexerttheiractionprimarilybyinteractingwithcomponentsofthefungalcellmembrane, thereby disrupting growth and rendering the fungi susceptible to treatment.

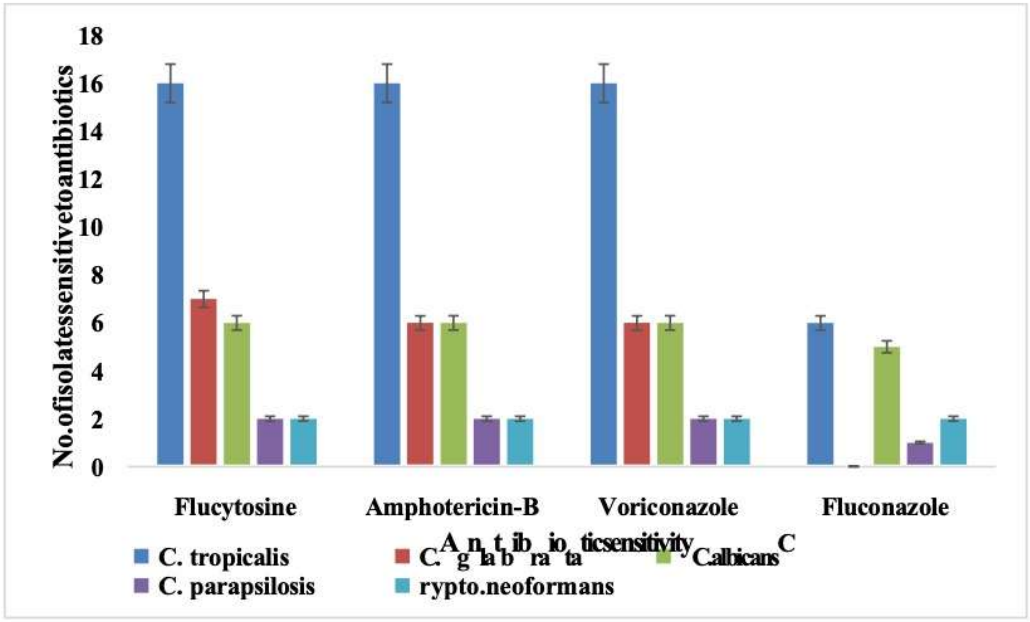

Figure6: Fungisensitivetovariousantibiotics

DISCUSSION

Antimicrobial resistance has become a significant global public health concern, particularly within hospital settings where the use of antibiotics is extensive. The issue is especially pronounced in Intensive Care Units (ICUs), as critically ill patients frequently depend on prolonged courses of broad-spectrumantimicrobialagents.Evidencefrommultiple studies indicates that hospital units with heavy antibiotic consumption tend to experience higher rates of resistant pathogens, leading to fewer effective treatment options, extended durations of hospitalization and less favorable patient outcomes (Micek et al., 2025).

The present investigation revealed a substantial occurrence of β-lactamase activity among Gram-negativebacterialisolates,with*Klebsiellapneumoniae*and *Escherichia coli* identified as the most frequently isolated pathogens. The ability of these organisms to produce β-lactamase enzymes contributes to the degradation and loss of activity of widely prescribed

third-generation cephalosporins, including cefotaxime, ceftazidime, and ceftriaxone (Rao et al., 2014). Significant clinical concern is the high prevalence of extended-spectrum β-lactamase (ESBL)-producing strains, which are commonly linked to resistance against several classes of non-β-lactam antimicrobials. This pattern of resistance poses considerable challenges for antimicrobial therapy and reduces the reliability of conventional empirical treatment regimens. Comparable observations have been documented in previous studies, which consistently report that ESBL-producing isolates demonstrate multidrug-resistant (MDR) characteristics (Bayaba et al., 2025).In one investigation, 250 *Escherichia coli*isolates were screened using the double disc synergy test and the AmpC disc method to detect ESβL- and AmpC β-lactamase production. During a three-month study period, ESβL activity was detected in 162 isolates (64.8%), AmpC β-lactamase production in 60 isolates (24%), and simultaneous production of both enzymes in 20 isolates (8%) (Albahar et al., 2023; Sinha et al., 2008).

In another large-scale analysis, 7,172 clinical specimens along with 1,725 samples obtained from carrier screening were processed for the identification of methicillin-resistant *Staphylococcus aureus*(MRSA) using conventional microbiological techniques. Of the 906 *S. aureus* isolates recovered, 250 clinical isolates (31.1%) and 39 carrier isolates (37.9%) were confirmed as methicillin resistant. Resistance among clinical MRSA strains was almost universaltopenicillin(99.6%)andampicillin(93.6%), whileapproximatelytwo-thirds(63.2%)alsoexhibited resistance to gentamicin, co-trimoxazole, cephalexin, erythromycin,andcefotaxime.Amongcarrierisolates, complete resistance to penicillin (100%) wasobserved, with substantial resistance to ampicillin (71.8%) and co-trimoxazole (35.9%). Multidrug resistance was identified in 63.6% of clinical MRSA isolates compared with 23% of carrier strains.Notably, nearly all isolates from both groups retained susceptibility to vancomycin (99.9%) (Rajaduraipandi et al. 2006). Consistent with previous reports, *E. coli*demonstrated the highest prevalence of ESBL production in this study, followed by AmpC β-lactamase producers and isolates producing bothESBL and AmpC enzymes. The coexistence of these resistance mechanisms reflects the dynamic evolution of bacterial defense strategies under sustained antibiotic pressure. In addition to Gram-negative pathogens,methicillin-resistant*Staphylococcusaureus*(MRSA) strains were also identified. These isolates showed resistance to commonly used antibiotics such as penicillin, ampicillin and gentamicin which finds from other hospital-based studies also (Brusselaers et al., 2011).

Despite the high level of resistance observed, certain antimicrobial agents retained good activity against resistant isolates. Carbapenems particularly imipenem along with amikacin and nitrofurantoin demonstrated comparatively higher efficacy against ESBL-producing organisms (Fu et al., 2024). Similar susceptibility patterns have been reported in*Pseudomonas*, *Klebsiella*, and *E. coli* isolates from respiratory and urinary tract infections (Bayaba et al., 2025). Among fungal isolates, most *Candida* species showed high susceptibility to amphotericin B, reinforcing its continued importance in the treatmentof invasive fungal infections (Staniszewska et al.,2010).

Analysis of 178 culture-positive samples, bloodstream infections were the most frequent, followed by endotracheal aspirates, urine samples and wound swabs. This distribution reflects the high burden of nosocomialinfectionssuchassepticemia,ventilator-associated pneumonia, and catheter-associated urinary tract infections in ICU patients (Alnimr 2023). These infections are well recognized as major contributors to morbidity, mortality and healthcare utilization, particularly among patients requiring invasive proceduresandprolongedhospitalization(Aieshetal.,2023).

The predominance of Gram-negative bacilli observed in this study, including *E. coli*, *Klebsiella*,*Acinetobacter* and *Pseudomonas* species, aligns with global trends indicating a shift toward Gram-negative organisms as leading causes of ICU-acquiredinfections (Aiesh et al., 2023). The significantpresence of *Acinetobacter* and *Pseudomonas* sp. is especially concerning, as these organisms are frequently implicated in ventilator-associated pneumonia and bloodstream infections and often display extensive multidrug resistance (Alnimr 2023). In addition, the notable proportion of fungal isolates observed in this study emphasizes the vulnerability of critically ill and immunocompromised patients to opportunistic fungal infections, which can further increase morbidity and prolong hospital stays (Trelles et al., 2025).

Another study analyzing 440 clinical samples reported microbial growth in 269 cases (60.13%), comprising bacterial pathogens and *Candida* species. Respiratory tract infections were the most frequently diagnosed (47.95%), with urinary tract infections constituting the second most common category (25.3%). *Pseudomonas aeruginosa* was the leading isolate, followed by *Klebsiella pneumoniae*,*Escherichia coli*, and *Candida* species. More than half of the Gram-negative isolates exhibited multidrug resistance, particularly against third-generation cephalosporins such as cefotaxime, ceftriaxone, and ceftazidime, with resistance rates exceeding 60%.High levels of resistance were also observed for fluoroquinolones, including ofloxacin (65.9%) and ciprofloxacin (73.9%), whereas lower resistance rates were noted for amikacin (21.3%) and imipenem (26.1%). These findings highlight the substantial burdenofhospital-acquiredinfectionsandthegrowing challenge posed by multidrug-resistant organisms (Salvia et al., 2022; Akhtar, 2010).

In response, the development of newer antimicrobial agents, including siderophore cephalosporins, glycylcyclines, and novel aminoglycosides, offers renewed hope for the treatment of resistant infections (Basaran and Oksuz 2025). However, the successful integration of these agentsintoclinicalpracticerequirescarefulevaluation oftheirpharmacokineticandpharmacody

properties, along with strict stewardship to prevent the rapid emergence of resistance (Karvouniaris et al.,2023).

CONCLUSION

The findings of this study reveal a substantial prevalence of multidrug-resistant pathogens in Intensive Care Units, with Gram-negative bacteria emerging as the dominant contributors. Among these,*Klebsiellapneumoniae*,*Pseudomonasaeruginosa*,and*Escherichia coli* were most frequently isolated. A considerable number of these organisms were identified as producers of ESβL and AmpC β-lactamases, which largely accounted for the highlevels of resistance observed against commonly prescribed cephalosporins and other β-lactam antibiotics.Carbapenemscontinuedtodemonstratethe greatest effectiveness against β-lactamase-producing isolates, whereas colistin and polymyxin-B showed notable efficacy among alternative, non-β-lactam therapeutic agents. Gram-positive isolates exhibited high susceptibility to glycopeptides and oxazolidinones, while fungal pathogens were largely sensitive to flucytosine, amphotericin-B, and voriconazole. Collectively, these results highlight the importance of implementing continuous antimicrobial susceptibility surveillance programs and enforcing stringent infection control measures within ICU settings. Adoption of these approaches is essential to limit the

development and spread of resistant organisms, enhance clinical outcomes as well asreduce both the healthcare costs and disease burden associated with hospital-acquired infections in critically ill patients.

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CONFLICTOFINTEREST

Authorsdeclarednoconflictof interest.

REFERENCES

- Aiesh B M,Qashou R,Shemmessian G,Swaileh MW,AbutahaSA,SabateenA,BarqawiA K,AbuTahaAandZyoudSH(2023)Nosocomial infections in the surgical intensive care unit: an observational retrospective study from a large tertiary hospital in Palestine. BMC Infect Dis23(686):1-10.
- Ak S, M S, Anupurba S, and Bhattacharya P (2002). Antibiotic sensitivity pattern of the bacteria isolated from nosocomial infections in ICU. J Commun Dis 34(4):1-10.
- Akhtar N (2010) Hospital acquired infections in a medical intensive care unit. J Coll PhysiciansSurg Pak 20(6):386-390.
- Albahar F, Alhamad H Q, Abu Assab M I E,FarhaRA,AlawiL,KhaleelS(2023)Theimpact of antifungal stewardship on clinical and performance measures: a global systematicreview. Trop Med Infect Dis 9(1):8.
- Alnimr A (2023) Antimicrobial resistance in ventilator associated *Pneumonia*: predictive microbiology and evidence-based therapy. Infect Dis Therap 12:1527-1552.
- AnioketeUC,UzorS,OkoroiwuHU,IbenemeS C, Iroha I R (2025) Antibiotic susceptibility patterns of clinical isolates of *salmonella* species producing extended spectrum beta lactamases as predictor of multidrug resistance in a tertiary hospital, Southeastern Nigeria. BMC Infect Dis25(1833):1-24.
- Basaran S N and Oksuz L (2025) Newly developed antibiotics against multidrug-resistant andcarbapenem-resistantGram-negativebacteria: action and resistance mechanisms. ArchMicrobiol 207(5):1-9.
- BayabaS,FounouRC,TchouangueuF T,DimaniDB,MafoLD,NkengkanaOA,FounouL L and NoubomM (2025) High prevalence of multidrug resistant and extended spectrum β-lactamase producing *Escherichia coli*and *Klebsiella pneumonia* isolated from urinary tract infections in the west region, Cameroon. BMC Infect Dis 25(115):1-10.
- Bergogne-Berezin E (2001) Guidelines on antimicrobial chemotherapy for prevention and treatment of infections in the intensive care unit. J Chemoth 13(1):134–149.
- Brusselaers N, Vogelaers D and Blot S (2011)The rising problem of antimicrobial restance intheintensivecareunit.AnnIntenCare1(47):1-10.
- Dj W, Raasch R and Wa R (1999). Nosocomial infections in the ICU: the growing importance of antibiotic-resistant pathogens. *Chest* (115).
- Fu Y, Chen Y, Wang Y, Yao B, Li P, Yu Y(2024) Susceptibility of various gram-negative bacteria to antibacterial agents: Smart in China 2019-2020. BMC Microbiol 24(524):1-10.
- Geleta D, Abebe G, Tilahun T, Abdissa A, Mihret A, Cataldo R J, Workneh N, Negash A A and Beyene G (2024) Molecular and clinical insights into extended-spectrum β-lactamase genes of*Klebsiella pneumoniae* isolated from neonatal sepsis in Ethiopia. BMC Infect Dis 24(1442):1-10.
- Jackson C, Williamson J C and Smith J (2026) Filling the gaps: A review and update on beta-lactamase inhibitor combinations. Cur Infect Dis Rep 28(3):1-15.
- Karvouniaris M, Almyroudi M P, Abdul-Aziz M H, Blot S, Paramythiotou E, Tsigou E and Koulenti D (2023) Novel antimicrobial agents for gram negative pathogens. Antibiotics 12(4):1-8.
- Micek S T, Guillamet M C V, Reynolds D, Matuszak S, Kolodziej L and Koller M H (2025) Optimal antibiotic use in the intensive care unit. Critical Care 29(434):1-16.
- Mihrete K, Awoke T, Melake A, Sisay T and Abera B (2026) Bacterial pharyngitis, antimicrobialsusceptibility,andassociatedfactors among children at comprehensive specialized hospitals, Northwest Ethiopia. BMC Infect Dis26(235):1-10.
- Mobasherizadeh S, Shokri D, Zargarzadeh A H, JalalpoorS,EbneshahidiSAandSajadiM(2012) Antimicrobial resistance surveillance among hospitalized and non-hospitalized extend-spectrum beta-lactamase producing Escherichia coli from four tertiary-care hospitals in Isfahan, Iran 2008-2011. Afr J Microbiol Res 6(5):953-959.
- Rajaduraipandi K, Mani K R, Panneerselvam K, Mani M, Bhaskar M, Manikandan P (2006) Prevalence and antimicrobial susceptibilitypattern of methicillin resistant *Staphylococcus aureus*: A multicentre study. Ind J Med Microbiol24(1):34-38.
- Rao S P N, Rama P S, Gurushanthappa V, Manipura R and Srinivasan (2014) Extended-Spectrum Beta-LactamasesProducing *Escherichia coli*and*Klebsiella pneumoniae*: A multi-centric study across Karnataka. J Lab Physic 6(1):7-13.
- SalviaT,DolmaKG,DhakalOP,KhandelwalB,Singh L S (2022) Phenotypic detection of ESBL, AmpC, MBL and their co-occurrence among MDR*Enterobacteriaceae*isolates. J Lab Physic 14(3): 329-335.
- Sinha P, Sharma R, Rishi S, Sharma R, Sood S, PathakD(2008)Prevalenceofextendedspectrum beta lactamase and AmpC beta lactamase producers among *Escherichia coli* isolates in a tertiary care hospital in Jaipur. Ind J Pathol Microbiol 51(3):367-9. Sirad N, Atalay M A and Sagiroglu P (2025) EvaluationofBDPhoenixandVITEK2fordirect and routine antimicrobial susceptibility from positive blood culture bottles. Ind J MedMicrobiol 56(100906):1-10.
- Staniszewska M, Rozbicka B,Rajnisz A,Bocian E,WasinskaE,JakimiakB,Rohm-RodowaldE,KurzątkowskiWandTyskiS(2025) Susceptibility of Candida spp. Clinical isolates to antimycotics and dicinfectants. Cent Eur J Biol5:821-826.
- Thakur R, Dhar H, Wozniak T M, Mathew S (2025) Addressing the overlooked frontier in AMR research and surveillance. Front Public Health 13:1-5.
- TrellesM,MurilloJ,Fuenmayor-GonzálezL,Yu-Liu Y,Alexander-Leon H, Acebo J, CuicapuzaD,Morales M,Pena Cand García-Aguilera M F (2025) Prevalence of invasive fungal infection in critically ill patients: a systematic review and meta-analysis. BMC Infect Dis 25(896):1-10.