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Antibiotic Susceptibility Profile of ESKAPE Pathogens From Blood Culture in A Tertiary Care Hospital

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HIGHLIGHTS

1. ESKAPE pathogens showed high resistance to commonly used antibiotics
2. Klebsiella pneumoniae and Acinetobacter spp. were the most frequent isolates.
3. Colistin and tigecycline remained effectiveagainstmostmultidrug-resistantstrains.
4. Rising carbapenem resistance was noted, especially in Pseudomonas and Acinetobacter.
5. Continuous surveillance and strict antibiotic stewardship are urgently needed.

Key words:
ESKAPE pathogens
Antimicrobial resistance
Blood culture
Antibiotic susceptibility
Nosocomial infections

ABSTRACT

Introduction: ESKAPE pathogens Enterococcus faecium, Staphy lococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp. are leading culprits of hospital-acquired infections globally. Their remarkable ability to develop resistance through beta-lactamase production, efflux pumps, biofilm formation, and genetic mutations presents a serious challenge to patient care and infection control. These pathogens contribute to increased morbidity, mortality, and healthcare costs, especially in critical care settings. Aim and **Objective:** The primary aim of this study was to evaluate the antimicrobial susceptibility patterns of ESKAPE pathogens isolated from blood cultures in a tertiary care setting. Specific objectives were to isolate and identify ESKAPE organisms using standard laboratory methods, determine their antibiotic susceptibility patterns, and compare resistance trends among them. **Materials and Methods:** A prospective observational study was conducted in the Department of Microbiology, Pt. B.D. Sharma PGIMS, Rohtak. Blood culture specimens yielding ESKAPE pathogens from 200 admitted patients were included. Identification and susceptibility testing were performed using conventional and automated systems, following CLSI guidelines. Inclusion criteria covered patients of all ages and departments, while exclusions included prior prolonged antibiotic use or incomplete data. **Results:** Acinetobacter baumannii (28%) and Klebsiella pneumoniae (25%) were predominant among isolates. Gram-negative pathogens exhibited high resistance to cepha losporins and fluoro quinolones, with better susceptibility to colistin and carbapenems in selected strains. Among gram-positive isolates, Enterococcus faecium and Staphylococcus aureus demon strated resistance to ampicillin and ciprofloxacin, while linezolid and vancomycin retained efficacy. **Conclusion:** This study highlights the high burden of multidrug-resistant ESKAPE pathogens in bloodstream infections. Rapid identification, strict antibiotic stewardship, and effective infection control strategies are vital to limit the spread of resistant strains and improve patient outcomes.

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INTRODUCTION

ESKAPE pathogens, an acronym representing Enterococcus faecium, Staphylococcus aureus, Klebsiella pneu moniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter species, have emerged as the primary culprits behind hospital-acquired infections and the global escalation of antimicrobial resistance (AMR). These six bacteria are highly proficient at evading the effects of commonly used antibiotics, often rendering conventional treat ment approaches ineffective. Their resistance mech anisms are multifaceted, including the production of beta-lactamases that degrade beta-lactam antibiotics, the utilization of efflux pumps that actively remove antibiotics from their cells, the formation of biofilms that shield them from immune defenses and antimicrobial agents, and the acquisition of genetic mutations or resistance genes through horizontal gene transfer. As a result, they demonstrate resistance to a broad range of antibiotics such as aminog lycosides, fluoroquino lones, and carba penems, which greatly limits therapeutic options for infected patients [1].

These pathogens are predominantly encountered in healthcare settings and are responsible for a significant proportion of hospital-acquired infections, with estimates indicating they account for up to 60% of such cases globally [2]. Their presence is particularly concerning in critical care units, where they contribute to infections such as pneumonia, sepsis, surgical site infections, and urinary tract infections. Methicillin resistant Staphylococcus aureus (MRSA), for example, continues to cause severe infections, including bloodstream infections and pneumonia, leading to thousands of deaths annually [3]. Similarly, Klebsiella pneumoniae strains resistant to carbapenems have been linked to mortality rates between 40% and 50%, particularly when causing severe infections like sepsis or ventilator-associated pneumonia [4]. Acinetobacter baumannii is particularly notorious for causing outbreaks in intensive care settings, and its infections are associated with mortality rates as high as 60%. Pseudomonas aeruginosa, known for affecting immuno-compromised individuals, frequently causes bacte remia and pneumonia, with reported mortality rates reaching up to 30% in serious cases. These alarming statistics reflect not only the clinical severity of infections caused by ESKAPE pathogens but also their contribution to associated with loss of productivity, increased caregiver burden, prolonged hospita lization and increased healthcare burdens [5].

The economic impact of infections caused by these pathogens is considerable. Management often neces sitates the use of high-cost antibiotics such as polymyxins or tigecycline, which may have toxic side effects and limited efficacy. Prolonged hospital stays and the requirement for intensive care significantly increase the cost of treatment, with the average expenditure per infected patient exceeding tens of thousands of dollars [6]. Moreover, the indirect costs and long-term disability further compound the societal impact. The global dimension of antimicrobial resistance means that resistant strains can cross borders rapidly, facilitated by travel and commerce. Consequently, the World Health Organization (WHO) has designated ESKAPE pathogens as priority organisms for the development of new antibiotics and thera peutic interventions [7].

In light of these challenges, alternative and innovative therapeutic strategies are being explored. The rapid pace of resistance development has outstripped the rate of new antibiotic discovery, compelling researchers to investigate non-traditional treatment avenues. These include bacteriophage therapy, antimicrobial peptides, CRISPR-Cas systems designed to target bacterial DNA, and host-directed therapies aimed at enhancing the immune response. Vaccines and immune modulators also hold promise in reducing the incidence and severity of infections [8]. However, these strategies are still in early stages and require significant research and validation before they can be implemented widely. In parallel, preventive strategies remain crucial. Antibiotic stew - ardship programs are essential to regulate the use of antimicrobials, minimize misuse, and preserve the effectiveness of existing drugs. Infection control practices such as hand hygiene, surface disinfection, proper catheter management, and patient isolation are fundamental in preventing nosocomial spread [9].

Blood cultures remain indispensable in the diagnosis of bloodstream infections, especially those caused by ESKAPE organisms. They offer definitive pathogen identification and allow for the determination of antimicrobial susceptibility profiles, which is critical for guiding effective and targeted treatment [10]. While empirical therapy is often initiated with broad-spectrum antibiotics, blood culture results enable de-escalation to narrower-spectrum agents, reducing side effects and lowering the risk of resistance development. Moreover, monitoring blood cultures during treatment helps detect persistent infections or complications such as infected intravascular devices or abscesses, prompting necessary interventions. In the context of sepsis, timely pathogen identification through blood cultures significantly improves survival outcomes. Additionally, the detection

of multidrug resistant organisms through blood cultures supports hospital infection control policies and informs epidemiological surveillance, thereby contributing to public health planning and response [11].

ESKAPE pathogens pose a critical challenge to healthcare due to their evolving resistance to multiple antibiotics, including vancomycin, methi cillin, carbapenems, and even newer agents like ceftazidime-avibactam. Resistance varies by region and infection site, complicating treatment. A global response is essential, involving robust survei -llance, antibiotic stewardship, public education, and strict regulation of antimicrobial use, especially in low-resource settings. International collaboration is vital to monitor resistance trends and develop effective therapies. These coordinated efforts are crucial to limit the spread of antimicrobial resistance, ensure appropriate treatment options remain available, and protect global health systems from the escalating burden of drug-resistant infections [2, 7].

The aim of this study is to evaluate the antimicrobial susceptibility patterns of ESKAPE pathogens isolated from blood culture samples. The objecti vesinclude isolating and identifying ESKAPE pathogens using conventional and automated methods, deter mining their antimicrobial susceptibility through these methods, and comparing the susceptibility patterns of the isolated pathogens.

MATERIALS AND METHODS

This prospective observational study was conducted in the Department of Microbiology at Pt. B.D. Sharma PGIMS, Rohtak, to assess the antibiotic susceptibility patterns of ESKAPE pathogens isolated from blood culture samples of patients admitted across hospital departments. A minimum of 200 isolates were included, with the sample size calculated using the formula $N = Z^2PQ/E^2$, assuming a 15% prevalence and 5% margin of error. Inclusion criteria encompassed patients of all ages and genders with clinically suspected systemic infections and blood cultures positive for ESKAPE pathogens. Exclusions included contaminated samples, incomplete records, or prior prolonged antibiotic use. Ethical approval and data confidentiality were ensured.

RESULTS

Table 1: Distribution of cases according to age

Age Group	No.	%
<1	37	18.5
1-20	30	15
21-40	31	15.5
41-60	44	22
61-80	55	27.5
>80	03	1.5
Total	200	100

The table shows that the highest number of cases (27.5%) occurred in the 61–80 age group, indicating increased vulnerability in older adults. Infants under 1 year also represented a significant proportion (18.5%), suggesting susceptibility at both age extremes. Middle-aged adults (41–60 years) accounted for 22%, reflecting a broad distribution across age groups.

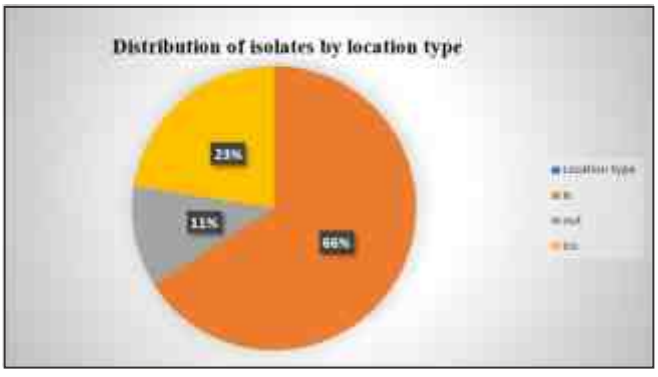

Figure 1: Distribution of isolates by location type

The majority of isolates originated from the "In" category (66%), followed by the "ICU" category (22.5%), while the "Out" category accounted for the lowest proportion (11.5%). This distribution highlights a higher prevalence of isolates in inpatient and critical care settings compared to outpatient areas.

Table 2: The distribution of isolates by department type

DEPARTMENT	NO.	%DISTRIBUTION
CTVS	10	5
Surgery	6	3
Pediatrics	35	17.5
Hemato/oncology	1	0.5
unknown	1	0.5
medicine	80	40
other	7	3.5
neonatology	35	17.5
nephrology	2	1
trauma	15	7.5
neurology	3	1.5
Urology	4	2
obgl/gyn	1	0.5

The highest number of isolates (40%) were reported from the medicine department, indicating it as the primary source of infection isolates. Pediatrics and neonatology departments contributed equally (17.5% each), highlighting significant infection rates in younger populations. Other departments showed relatively lower contributions, with hematology /oncology, OBG/GYN, and unknown sources accoun ting for only 0.5% each.

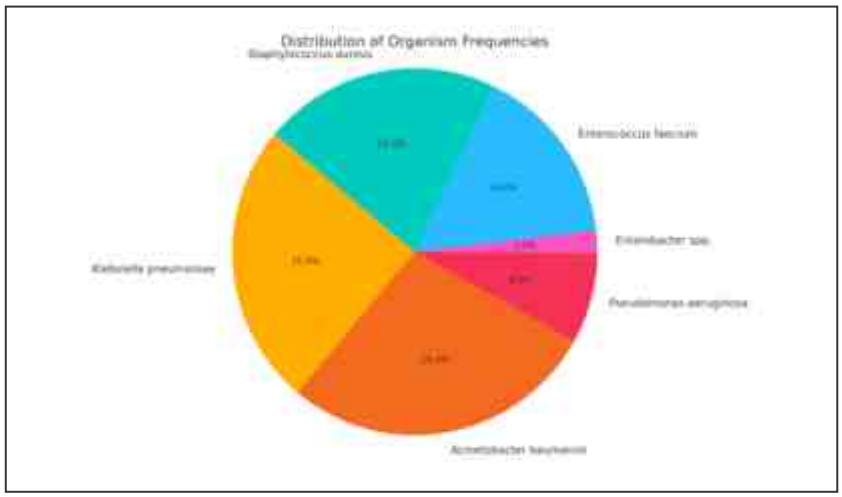

Figure 2: The distribution of the Organism frequencies

The distribution of bacterial isolates reveals that Acinetobacter species are the most prevalent, constituting 28% (56 isolates) of the total. Klebsiella species follow closely, accounting for 25% (501 solates). Notable proportions are also observed for Staphylococcus aureus at 16% and Enterococcus species at 14%, indicating their significant role among the isolated pathogens.

Table 3: Antimicrobial Susceptibility Pattern of Gram-Negative Organism in Blood

Organism	Number of solates	AMK	AMP	AMC	ATM	FEP	CTX	CAZ	CRO	CIP	ETP	GEN	IPM	MEM	TZP	SXT	CXM	SAM
Klebsiella pneumoniae	50	28.2		30.4		54.3	44.2		74.6	27.2	81.3	32.7	64.8	77.8	27.9	11.4	64.3	
Acinetobacter baumannii	56	37.5						25.8		49.2	91.4	56.9	69.3	71.3	61	45.3		81.8
Pseudomonas aeruginosa	16	59.4			66.4			57.3		64.5		89.2	83.5	87.6	76.9			
Enterobacter spp.	04	24.5	86	63.7	21.4	29.5	37.6			31.2			10.4	52.3	34.8		43.1	

The antimicrobial susceptibility pattern shows Pseudomonas aeruginosa as highly sensitive to most antibiotics, especially piperacillin-tazobactam (89.2%) and meropenem (87.6%). Acinetobacter baumannii, though highly prevalent, exhibits low sensitivity to many agents except colistin (81.8%) and tigecycline (71.3%). *Klebsiella pneumoniae* shows moderate susceptibility, with higher resistance rates, posing a therapeutic challenge.

Table 4: Antimicrobial Susceptibility Pattern of Gram-Positive Organism in Blood

Organism	Number of isolates	AMP	AMX	CEF	GEN	TET	CIP	CTX	ERY	CLIN	CEFOXI	COT	CHLO	LEVO	NIT	VAN	LIN	TEI
Enterococcus faecium	32	82	26	46	42	51	47	43	35	53		44	95		76	87	98	47
Staphylococcus aureus	42	87	84	83	89	90	52	48	85	48	79	12	93	38	84	88	93	73

The susceptibility data indicate that Staphylococcus aureus shows high sensitivity to linezolid (93%) and chloramphenicol (79%), while showing poor response to penicillin (1%). Enterococcus faecium demonstrates significant resistance to most antibiotics but remains highly susceptible to linezolid (95%) and chloramphenicol (53%). These patterns suggest linezolid as a reliable option for treating Gram-positive bloodstream infections.

Table 5: Gram-negative & positive antibiotics

Code	Antibiotic	Code	Antibiotic	Code	Antibiotic
AMK	Amikacin	CRO	Ceftriaxone	TZP	Piperacillin/Tazobactam
AMP	Ampicillin	CIP	Ciprofloxacin	SXT	Trimethoprim/Sulfamethoxazo l e
ETP	Ertapenem	CXM	Cefuroxime	AMC	Amoxicillin/Clavulanic acid
ATM	Aztreonam	CTX	Cefotaxime	ME M	Meropenem
IPM	Imipenem	SAM	Ampicillin/Sulbacta m	FEP	Cefepime
GEN	Gentamicin	NIT	Nitrofurantoin	CAZ	Ceftazidime
TET	Tetracycline	CIP	Ciprofloxacin:	CEF	Cefazolin
TEI	Teicoplanin	ERY	Erythromycin:	FOX	Cefoxitin
RIF	Rifampicin	LIN	Linezolid	CLIN	Clindamycin:
CHL O	Chloramphenico l	LEV O	Levofloxacin	VAN	Vancomycin
COT	Cotrimoxazole				

This table provides the codes and full names of antibiotics used for susceptibility testing against Gram-negative and Gram-positive organisms. It includes a broad spectrum of antimicrobial classes such as beta-lactams (e.g., cefotaxime, meropenem), aminoglycosides (e.g., amikacin, gentamicin), and glycopeptides (e.g., vancomycin, teicoplanin). This coding system aids in the standardized reporting and interpretation of antibiograms in clinical micro biology.

DISCUSSION

ESKAPE pathogens—Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp. are major contributors to antibiotic resistance and hospital-acquired infec tions due to their biofilm formation, genetic adaptability, and horizontal gene transfer. Widesp - read antibiotic misuse in healthcare and agriculture, lack of rapid diagnostics, and slow antibiotic development have worsened this global crisis. WHO prioritizes ESKAPE pathogens, urging innovative therapeutics to counteract their growing resistance (12).

In our study, most infections occurred in older adults, with 27.5% in the 61–80 age group and 22% in the 41–60 group, and only 1.5% in those over 80, reflecting age-related susceptibility to hospital-acquired infections due to comorbidities and immune decline. Similarly, Qureshi S et al. (2025) reported a higher incidence in patients over 60 . Most isolates were from inpatients (66%) and ICU (22.5%), consistent with Mthombeni TC et al. (2024), who found 60% from ICU and 30% from wards –(13, 14).

In our study, most ESKAPE pathogen isolates originated from the Medicine department (40%), followed by Pediatrics and Neonatology (17.5% each), likely due to higher patient loads and hospitalization rates; the fewest isolates were from Hemato/Oncology, Obstetrics/Gynecology, and Unknown departments (0.5% each). Gupta M et al. (2024) reported a similar trend, with most isolates from internal medicine and pediatric units, and higher resistance in ICUs , while Ismail H et al. (2019) noted a predominance in medicine and surgical wards. Acinetobacter baumannii was most frequently isolated (28%), followed by Klebsiella pneumoniae (25%), Staphylococcus aureus (21%), and Enterococcus faecium (16%), reflecting their role in hospital-acquired infections. Similarly, Silva DM et al. (2017) found Acinetobacter (30%) and Klebsiella (24%) most prevalent, while Wei DD et al. (2020) confirmed Acinetobacter and Klebsiella as dominant, with

Pseudomonas aeruginosa and Enterococcus faecium also significant (15-18).

In our study, Acinetobacter baumannii showed low susceptibility to Ceftazidime and Meropenem but responded well to Sulfamethoxazole/ Trimethoprim and Ciprofloxacin, while Klebsiella pneumoniae was resistant to Ampicillin and Ceftriaxone but susce ptible to Meropenem and Amikacin. Pseudomonas aeruginosa was highly susceptible to carbapenems, and Enterobacter spp. showed mixed resistance. Similar patterns were reported by Namukonda S et al. and Prethii N . Enterococcus faecium showed high Ampicillin resistance (82%) and moderate Vancomycin resistance (47%), while Staphylococcus aureus remained susceptible to Vancomycin and Linezolid, consistent with Saipriya JB et al. (2018) and Emamie A et al. (2023)(19-22).

In our study, gram-positive bacteria showed notable resistance, with Enterococcus faecium resistant to Ampicillin (82%) and Piperacillin /Tazobactam (76%), and Staphylococcus aureus to Tetracycline (89%) and Ciprofloxacin (90%). However, both showed better susceptibility to Vancomycin (Enterococcus: 47%, Staphylococcus: 93%) and Linezolid (Enterococcus: 87%, Staphy lococcus: 93%). Similar resistance profiles were reported by De Prisco M et al. (2024) and Pandey R et al. (2024), who found high resistance in Enterococcus to Ampicillin and good susceptibility to Linezolid and Vancomycin, with Staphylococcus showing similar patterns "(23, 24).

CONCLUSION

This study underscores the critical threat posed by multidrug-resistant (MDR) ESKAPE pathogens, especially in ICU patients and those with extended hospital stays. High levels of carbapenem resistance in Acinetobacter and Klebsiella necessitate cautious use of last-resort antibiotics like colistin and tigecycline. MRSA remains challenging, though vancomycin and linezolid remain effective. Alarming resistance to fluoroquinolones and cephalosporins highlights the need for strict antibiotic guidelines. Rapid identification of resistance patterns through advanced diagnostics is vital for timely and appro priate empirical therapy. These findings call for robust infection control, stewardship, and surveil lance strategies to curb the growing antibiotic resistance crisis.

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