

Bacteriological Profile and Antimicrobial Susceptibility Pattern of ESKAPE Pathogens Isolated from Intensive Care Units of a Tertiary Care Hospital

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Abstract: Background: The rapid emergence and global dissemination of antimicrobial resistance (AMR) represent a severe threat to contemporary healthcare systems, particularly within Intensive Care Units (ICUs). The "ESKAPE" pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species) are the primary drivers of healthcare-associated infections (HAIs) capable of evading conventional antimicrobial agents. Objectives: To evaluate the prevalence, clinical specimen distribution, and antimicrobial susceptibility profiles of ESKAPE pathogens isolated from patients admitted to various ICUs at a tertiary care hospital in Hyderabad, India. Materials and Methods: A prospective, cross-sectional study was conducted in the Department of Microbiology at KIMS, Hyderabad, over a 12-month period (April 2024 to March 2025). Clinical specimens (blood, urine, respiratory aspirates, exudates) from ICU patients aged 18–80 years with an ICU stay ≥ 48 hours were processed. Bacterial identification and antimicrobial susceptibility testing (AST) were performed using the Vitek 2 Compact automated system. Results: Out of 5,247 processed clinical samples, 1,596 demonstrated significant microbial growth, yielding an overall culture positivity rate of 30.41%. ESKAPE pathogens constituted the majority, accounting for 55.2% ($n = 881$) of all positive cultures. The mean age of the infected population was 52.35 ± 17.25 years, with a pronounced male predominance (65.2%). The Medical ICU (MICU) contributed the highest proportion of ESKAPE isolates (60.6%), followed by the Surgical ICU (SICU) at 30.4%. Blood specimens were the most frequent source of ESKAPE strains (40.1%). Gram-negative bacilli strongly predominated (75.9%), led by *Pseudomonas aeruginosa* (41.8%), *Staphylococcus aureus* (21.7%, with 52.4% oxacillin resistance/MRSA), and *Acinetobacter baumannii* (16.5%). Widespread resistance was observed against fluoroquinolones, cephalosporins, and β -lactam/ β -lactamase inhibitor combinations. Carbapenem resistance exceeded 57% globally among Gram-negative isolates, though tigecycline (86.8% overall susceptibility) and glycopeptides (vancomycin 100% susceptibility in staphylococci) retained strong in vitro activity. Conclusion: This study highlights a critical burden of multidrug-resistant (MDR) ESKAPE pathogens within adult ICUs. The high prevalence of carbapenem resistance and emerging resistance to last-line therapies underscores the imperative for continuous local institutional surveillance, strict infection control measures, and aggressive antimicrobial stewardship programs.

Keywords: ESKAPE Pathogens, Antimicrobial Resistance, Intensive Care Unit, Antibigram, Carbapenem Resistance, Vitek 2.

1. Introduction

The rapid emergence and global expansion of antimicrobial resistance (AMR) pose a fundamental challenge to modern clinical medicine. Antimicrobial agents that previously guaranteed therapeutic success are systematically losing efficacy, transforming routine hospital-acquired conditions into life-threatening scenarios. This therapeutic crisis is acutely concentrated within Intensive Care Units (ICUs), where critically ill patients face prolonged hospitalizations, frequent exposures to invasive monitoring or life-support devices, and intense selective pressures exerted by broad-spectrum empirical therapies.

Among the problematic multidrug-resistant (MDR) phenotypes, the acronym **ESKAPE**- encompassing *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species- defines a high-priority cluster of pathogens. These organisms utilize an arsenal of

resistance mechanisms, including extended-spectrum β -lactamases (ESBLs), carbapenemases (such as NDM, KPC, and OXA variants), aminoglycoside-modifying enzymes, efflux pump overexpression, porin deletions, and robust biofilm architectures. Consequently, they account for a significant share of ventilator-associated pneumonia (VAP), catheter-associated urinary tract infections (CAUTIs), central line-associated bloodstream infections (CLABSIs), and deep surgical site infections.

Developing nations face an exacerbated burden due to high baseline diagnostic thresholds, unregulated over-the-counter antibiotic availability, and varied institutional infection control compliance. India has emerged as a critical geographic focal point for AMR surveillance, frequently recording high baseline resistance frequencies in Gram-negative bacilli. Understanding the micro-epidemiological baseline of an institution is mandatory for designing accurate empirical regimens. Therefore, this prospective investigation was designed to systematically profile the bacteriological spectrum and

determine the precise institutional antibiogram of ESKAPE isolates across the intensive care units of a premier tertiary care hospital in Hyderabad, India.

2. Materials and Methods

2.1 Study Design and Setting

This prospective, cross-sectional institutional study was conducted over a 12-month period from April 2024 to March 2025 within the Department of Microbiology at the Krishna Institute of Medical Sciences (KIMS), Hyderabad, India. Institutional Scientific and Ethics Committee approvals were secured prior to implementation (Approval Letters: KIMS/SRC/202401-07 and KIMS/ECBMHR/2024/77-03).

2.2 Study Population and Selection Criteria

The study population comprised adult patients enrolled based on the following parameters:

- **Inclusion Criteria:** Patients aged 18–80 years, admitted to any dedicated adult ICU tier (Medical, Surgical, Neuro, or Coronary) for a minimum duration of 48 hours, presenting with clinically suspected healthcare-associated infections, and possessing documented comorbidities at admission. Informed consent was obtained from the patient or an authorized representative.
- **Exclusion Criteria:** Patients staying in the ICU for < 48 hours, individuals or legal representatives refusing informed consent, and all pediatric/neonatal patients (< 18 years).

2.3 Sample Size Calculation

The minimum statistical sample index was determined via the standard single proportion formula:

$$N = \frac{Z^2 \times P \times Q}{l^2}$$

Where Z represents the standard normal deviation at a 95% confidence threshold (1.96), P represents the historical institutional ICU baseline positivity rate (estimated at 17% or 0.17 based on preceding annual internal data), $Q = 1 - P$ (0.83), and l signifies the absolute allowable margin of error (0.05). The minimum calculated sample size was expanded to cross-verify clinical integrity, resulting in a minimum baseline target of 217 samples; ultimately, a total cohort of 5,247 cases was evaluated during the study window.

2.4 Specimen Collection, Processing, and Culture Verification

Diverse clinical specimens- comprising blood, sterile body fluids (ascitic, pleural, cerebrospinal fluid), midstream or catheterized urine, respiratory secretions (endotracheal aspirates [ETA], bronchoalveolar lavage [BAL], sputum), deep tissue biopsies, and wound exudates- were transferred in specialized transport media and processed under strict aseptic conditions.

- 1) **Blood and Sterile Fluids:** Specimens were immediately inoculated into BacT/Alert FA, FN, or PF automated culture bottles. Positive alerts triggered urgent Gram staining, followed by subculturing onto 5% Sheep Blood Agar (BA) and MacConkey Agar (MA).
- 2) **Respiratory Specimens:** Quantitative culture methods were utilized. Significant execution thresholds were maintained at $\geq 10^4$ CFU/ml for BAL and $\geq 10^5$ CFU/ml for ETA matrices on BA and MA lines.
- 3) **Urine Samples:** Specimens were inoculated onto Cystine-Lactose-Electrolyte-Deficient (CLED) agar systems using calibrated loops to calculate colony counts.
- 4) **Exudates and Tissue:** Samples were tracked through preliminary smear validation, enriched via thioglycolate broth pathways when necessary, and isolated on selective solid media.

2.5 Phenotypic Identification and Antimicrobial Susceptibility Testing (AST)

Pure, isolated bacterial colonies were analyzed utilizing the automated Vitek 2 Compact platform (bioMérieux, Marcy-l'Étoile, France) using Gram-Negative (GN) and Gram-Positive (GP) Identification cards. AST profiles were concurrently generated using Vitek 2 automated cards (GP628, N405, and N406 configurations). The Minimum Inhibitory Concentrations (MICs) were converted into Susceptible (S), Intermediate (I), and Resistant (R) phenotypes adhering strictly to contemporary Clinical and Laboratory Standards Institute (CLSI) interpretative criteria.

2.6 Quality Control Protocols

Rigorous quality control measures were enforced using reference strains from the American Type Culture Collection (ATCC), including *Staphylococcus aureus* ATCC 25923, *Escherichia coli* ATCC 25922, and *Pseudomonas aeruginosa* ATCC 27853. Annual preventative maintenance and precision calibration of automated instrumentation were conducted by certified technical specialists.

2.7 Statistical Data Management

All experimental observations, demographic parameters, and susceptibility metrics were cross-tabulated within Microsoft Excel platforms and analyzed using IBM SPSS software suites. Categorical data profiles are presented as absolute frequencies and percentages. Continuous metrics are represented via mean values accompanied by standard deviations ($\pm$ SD).

3. Results

3.1 Culture Positivity Yield and Demographic Stratification

Out of 5,247 individual samples gathered across the target ICU settings, 3,651 samples were negative for significant bacterial growth, whereas 1,596 samples displayed confirmed pathognomonic development, yielding a clear baseline **culture positivity rate of 30.41%**. Within these positive isolates,

verified ESKAPE organisms formed the absolute statistical majority, accounting for **55.2% (n = 881)**, while non-ESKAPE variants comprised the remaining 44.8% (n = 715).

The overall demographic cohort had a mean age of 52.35 ± 17.25 years. Stratified analysis demonstrated that the highest concentration of positive cultures occurred within advanced age brackets: the 61–70 years demographic contributed 27.5% (n = 439) of total positive instances, followed by the 51–60 years segment at 22.7% (n = 362). An identical profile was recorded among the confirmed ESKAPE sub-population, where individuals older than 50 years comprised more than 60% of cases, peaking sharply in the 61–70 years tier at 27.8% (n =

245).

Gender metrics revealed a prominent male bias: males represented 64.2% (n = 1,025) of total positive cultures and **65.2% (n = 574) of the ESKAPE-positive subgroup**, establishing a clear male-to-female ratio of 1.87:1 within the critical care registry.

3.2 Spatial and Specimen-type Distribution Metrics

The distribution of pathogens across individual sub-specialized ICU environments and specimen matrices highlights specific institutional risk vectors (Table 1).

Table 1: Distribution of Isolates Across Intensive Care Units and Specimen Types

Parameter Layer	Total Culture Positive (n=1596)	ESKAPE-Positive Cohort (n=881)	ESKAPE-Negative Cohort (n=715)
ICU Stratification			
Medical ICU (MICU)	965 (60.5%)	534 (60.6%)	431 (60.3%)
Surgical ICU (SICU)	474 (29.7%)	268 (30.4%)	206 (28.8%)
Neuro ICU (NICU)	92 (5.8%)	55 (6.2%)	37 (5.2%)
Intensive Coronary Care (ICCU)	65 (4.1%)	24 (2.7%)	41 (5.7%)
Specimen Matrix Source			
Blood & Sterile Fluids	644 (40.4%)	353 (40.1%)	291 (40.7%)
Urinary Aspirates	377 (23.6%)	199 (22.6%)	178 (24.9%)
Other Matrices (Respiratory/Pus)*	575 (36.0%)	329 (37.3%)	246 (34.4%)

*Note: "Other Matrices" includes sputum, bronchial wash, endotracheal aspirates, deep pus swabs, tissue biopsies, cerebrospinal fluid, and ascitic fluid.

3.3 Microorganism Spectrum and Prevalence Hierarchy

Gram-negative pathogens constituted the clear operational majority within the ESKAPE group, representing **75.9% (n = 669)**, while Gram-positive variants comprised 24.1% (n = 212). *Pseudomonas aeruginosa* was the most common isolate,

accounting for **41.8% (n = 368)** of the ESKAPE population, followed by *Staphylococcus aureus* at 21.7% (n = 191) and the *Acinetobacter baumannii* complex at 16.5% (n = 145). Detailed isolate specs, including explicit multi-drug-resistant (MDR) phenotypes determined during primary characterization, are delineated below (Table 2).

Table 2: Prevalence and Breakdown of Individual ESKAPE Pathogens

Rank	Target Pathogen Identity	Absolute Isolate Count (n)	Proportion Within Total ESKAPE Group (%)
1	<i>Pseudomonas aeruginosa</i> (Wild type & Mixed)	245	27.80%
2	<i>Pseudomonas aeruginosa</i> (Confirmed MDR)	123	14.00%
3	<i>Staphylococcus aureus</i> (Methicillin-Resistant / MRSA)	104	11.80%
4	<i>Klebsiella pneumoniae</i> (Standard profile)	91	10.30%
5	<i>Acinetobacter baumannii</i> complex	88	10.00%
6	<i>Staphylococcus aureus</i> (Methicillin-Sensitive / MSSA)	87	9.90%
7	<i>Acinetobacter baumannii</i> (Confirmed MDR)	35	4.00%
8	<i>Enterobacter cloacae</i> complex	31	3.50%
9	<i>Enterococcus faecium</i> (Standard profile)	23	2.60%
10	<i>Acinetobacter baumannii</i> (Non-resistant)	22	2.50%
11	<i>Enterobacter cloacae</i> (Isolated type)	20	2.30%
12	<i>Enterococcus faecium</i> (Vancomycin-Resistant / VRE)	12	1.40%
-	Total Cumulative ESKAPE Pool	881	100.00%

3.4 Comprehensive Antimicrobial Susceptibility Analysis

The overall susceptibility patterns across all clinical isolates

revealed substantial resistance levels against first-line and second-line broad-spectrum therapies (Table 3).

Table 3: Cumulative Antibiotic Susceptibility Profile Across All Tested Isolates

Antibiotic Agent tested	Intermediate (I) % (n)	Resistant (R) % (n)	Susceptible (S) % (n)	Total Evaluated (n)
Amikacin	1.5% (19)	53.3% (695)	45.3% (591)	1,305
Aztreonam	0.7% (4)	71.9% (407)	27.4% (155)	566
Benzylpenicillin	0.0% (0)	94.7% (215)	5.3% (12)	227
Cefepime	2.0% (25)	62.3% (776)	35.7% (444)	1,245
Cefoperazone/Sulbactam	3.0% (38)	55.7% (702)	41.3% (520)	1,260
Ceftazidime	2.9% (31)	63.7% (682)	33.4% (358)	1,071
Ceftriaxone	0.0% (0)	69.4% (177)	30.6% (78)	255
Ciprofloxacin	5.4% (83)	68.9% (1,054)	25.6% (392)	1,529
Colistin	92.6% (1,169)	7.4% (93)	0.0% (0)	1,262
Daptomycin	0.0% (0)	2.4% (4)	97.6% (164)	168
Imipenem	1.2% (15)	57.7% (727)	41.1% (518)	1,260
Levofloxacin	8.4% (106)	64.4% (809)	27.2% (342)	1,257
Linezolid	0.4% (1)	10.1% (23)	89.4% (203)	227
Meropenem	0.9% (11)	60.5% (762)	38.7% (487)	1,260
Piperacillin/Tazobactam	1.2% (15)	64.6% (824)	34.2% (436)	1,275
Teicoplanin	0.4% (1)	9.7% (22)	89.9% (204)	227
Tigecycline	9.9% (112)	3.3% (37)	86.8% (977)	1,126
Vancomycin	0.0% (0)	0.0% (0)	100.0% (1596)	1,596

3.5 Organism-Specific Cumulative Antibiograms

3.5.1 Gram-Positive Antibiograms (*E. faecium* and *S. aureus*)

Enterococcus faecium displayed high resistance rates to benzylpenicillin and fluoroquinolones, coupled with an

emerging vancomycin-resistant (VRE) burden. *Staphylococcus aureus* presented a clear methicillin-resistant (MRSA) bracket, though last-line lipopeptides and oxazolidinones retained definitive potency (Table 4).

Table 4: Antibiogram Profiles for Gram-Positive ESKAPE Isolates

	Enterococcus faecium (n=35)	Staphylococcus aureus (n=191)
Antibiotic Agent	I% / R% / S%	I% / R% / S%
Benzylpenicillin	0.0% / 91.4% / 2.9%	0.0% / 93.7% / 4.7%
Oxacillin	NT	0.0% / 52.4% / 46.1%
Gentamicin (HLG)	NT	3.1% / 12.0% / 83.2%
Ciprofloxacin	0.0% / 91.4% / 2.9%	2.1% / 81.2% / 15.2%
Levofloxacin	0.0% / 91.4% / 2.9%	0.5% / 80.6% / 17.3%
Erythromycin	17.1% / 77.1% / 0.0%	6.3% / 41.9% / 50.3%
Clindamycin	NT	0.0% / 19.4% / 79.1%
Linezolid	2.9% / 17.1% / 74.3%	0.0% / 6.8% / 91.6%
Teicoplanin	2.9% / 31.4% / 60.0%	0.0% / 3.1% / 95.3%
Vancomycin	0.0% / 34.3% / 60.0%	0.0% / 0.0% / 98.4%
Tetracycline	0.0% / 82.9% / 11.4%	0.5% / 9.9% / 88.0%
Tigecycline	0.0% / 0.0% / 94.3%	0.0% / 0.0% / 96.3%
Cotrimoxazole	NT	0.0% / 15.2% / 83.2%

*NT = Not Tested / Not Applicable for routine reporting protocols.

3.5.2 Gram-Negative Antibiograms (*K. pneumoniae*, *A. baumannii*, *P. aeruginosa*, *Enterobacter* spp.)

The Gram-negative clusters demonstrated extensive resistance profiles, marked by high resistance rates to carbapenems,

extended-spectrum cephalosporins, and standard inhibitor combinations across *Klebsiella pneumoniae* and the *Acinetobacter baumannii* complex (Table 5).

Table 5: Antibiogram Profiles for Gram-Negative ESKAPE Isolates

Antibiotic Agent	<i>K. pneumoniae</i> (n=91) I% / R% / S%	<i>A. baumannii</i> (n=145) I% / R% / S%	<i>P. aeruginosa</i> (n=368) I% / R% / S%	<i>Enterobacter</i> spp. (n=51) I% / R% / S%
Piperacillin/Tazobactam	0.0 / 54.9 / 23.1	0.7 / 74.5 / 17.9	0.0 / 13.6 / 5.7	0.0 / 37.3 / 62.7
Cefoperazone/Sulbactam	0.0 / 45.1 / 25.3	2.1 / 68.3 / 25.5	5.4 / 37.2 / 54.3	13.7 / 21.6 / 64.7
Cefepime	0.0 / 50.5 / 19.8	4.8 / 71.7 / 20.0	4.9 / 36.1 / 53.5	0.0 / 29.4 / 70.6
Ceftazidime	1.1 / 31.9 / 18.7	0.7 / 73.8 / 18.6	1.1 / 35.6 / 49.5	0.0 / 25.5 / 41.2
Imipenem	2.2 / 42.9 / 25.3	0.0 / 73.1 / 22.8	0.3 / 44.8 / 51.6	3.9 / 23.5 / 72.5
Meropenem	0.0 / 44.0 / 26.4	0.0 / 75.9 / 21.4	2.4 / 44.0 / 48.1	2.0 / 29.4 / 68.6
Amikacin	0.0 / 46.2 / 33.0	4.1 / 68.3 / 23.4	3.5 / 38.0 / 52.4	0.0 / 25.5 / 74.5

Gentamicin	4.4 / 39.6 / 35.2	0.0 / 69.0 / 26.9	NT	0.0 / 27.5 / 72.5
Ciprofloxacin	5.5 / 57.1 / 16.5	0.7 / 72.4 / 22.8	2.4 / 43.8 / 47.8	15.7 / 31.4 / 52.9
Levofloxacin	4.4 / 24.2 / 14.3	2.8 / 70.3 / 21.4	2.7 / 39.7 / 44.6	2.0 / 11.8 / 52.9
Tigecycline	2.2 / 0.0 / 68.1	28.3 / 1.4 / 66.2	NT	0.0 / 11.8 / 88.2
Colistin	67.0 / 3.3 / 0.0	92.4 / 4.8 / 0.0	79.6 / 15.5 / 4.9	100.0 / 0.0 / 0.0
Cotrimoxazole	0.0 / 40.7 / 38.5	0.0 / 63.4 / 32.4	NT	0.0 / 35.3 / 64.7
Minocycline	5.5 / 13.2 / 24.2	12.4 / 51.7 / 29.0	NT	7.8 / 15.7 / 43.1

4. Discussion

4.1 Interpretation of Culture Positivity and Bacterial Distribution

This study identified a diagnostic culture positivity index of 30.41% across evaluated ICU specimens. This matches the findings of Jagadevi et al., who documented an identical 29.64% baseline recovery rate from a extensive multi-year clinical sample evaluation, indicating consistent microbiological yields in tertiary care facilities.

Within the positive cultures, the high prevalence of ESKAPE pathogens (**55.2%**) underscores their established role in healthcare-associated infections. This mirrors the findings of Emamie et al. (65.5% ESKAPE prevalence in bacteremia) and Singh et al. (65.2% blood culture isolation index), reinforcing the consensus that high-acuity tiers select heavily for these pathogens.

In contrast, general multi-ward studies, such as those by Pandey et al. and Sah et al., report lower baseline ESKAPE rates (18.96% and 32.1%, respectively). This discrepancy emphasizes that intensive care environments act as distinct ecological hubs for resistant strains, driven by invasive procedures and continuous antimicrobial exposure.

4.2 Demographic Risk Correlates

Demographic profiling identified advanced age (≥ 50 years) and male gender (65.2% of the ESKAPE cohort) as key factors associated with these infections. These findings align with Al Marzooqi et al., who reported that 76% of culture-positive critical care samples were from patients over 50 years of age, with a 62% male predominance. Similarly, De Prisco et al. reported that 70.6% of ESKAPE bloodstream infections occurred in patients aged ≥ 60 years, with a 59.9% male predominance.

The increased vulnerability observed in older patients likely stems from immunosenescence, higher rates of comorbidities, and cumulative exposure to healthcare interventions. The higher prevalence in males warrant further investigation into potential physiological or healthcare-utilization factors.

4.3 Analysis of Resistance Trajectories

4.3.1 Gram-Positive Resistance Challenges

The identification of 52.4% oxacillin resistance among *Staphylococcus aureus* isolates highlights a significant MRSA burden within our critical care framework. This rate is notably

higher than the 35.2% MRSA frequency reported by De Prisco et al., signaling elevated endemic transmission or intense selective pressures within our ICU sectors.

Similarly, the *Enterococcus faecium* cohort demonstrated critical resistance metrics, with vancomycin resistance reaching 34.3%. This surpasses the 20% VRE baseline reported by Pandey et al. and contrasts sharply with the complete vancomycin susceptibility noted by Nirmal et al.

These findings indicate substantial resistance pressure affecting Gram-positive alternatives within our facility. Nevertheless, the preserved susceptibility to linezolid (91.6% in *S. aureus*) and tigecycline (94.3% in *E. faecium*) supports their continued utility as definitive choices for structured Gram-positive coverage.

4.3.2 Gram-Negative Therapeutic Bottlenecks

The resistance profiles of Gram-negative ESKAPE isolates reveal narrow therapeutic windows. *Acinetobacter baumannii* complex isolates showed carbapenem resistance rates exceeding 73% for imipenem and 75% for meropenem. These metrics align with the 72–78% resistance levels reported by Al Marzooqi et al., but remain below the $> 96\%$ rates documented by Abukhalil et al. in highly resistant settings.

For *Klebsiella pneumoniae*, carbapenem resistance ranged between 42.9% and 44.0%, exceeding the 37–43% baseline cited by Emamie et al. The low susceptibility rates to amikacin (33.0%) and piperacillin/tazobactam (23.1%) further complicate empirical management.

Crucially, colistin evaluation revealed an overwhelming predominance of **"Intermediate" phenotypes (up to 92.4% in *A. baumannii*)**, following current CLSI interpretive criteria. This high rate of intermediate susceptibility, combined with emerging full colistin resistance (15.5% in *Pseudomonas aeruginosa*), restricts the reliability of polymyxins as standard salvage therapies.

Consequently, tigecycline remains one of the few viable options for non-pseudomonal Gram-negative infections, showing susceptibility rates of 68.1% for *K. pneumoniae* and 66.2% for *A. baumannii*.

4.4 Clinical Implications and Strategic Recommendations

The high prevalence of carbapenem resistance and multi-drug resistant (MDR) phenotypes among Gram-negative ESKAPE isolates highlights the limitations of traditional empirical regimens, such as carbapenems or β -lactam/ β -lactamase

inhibitor combinations. To address this challenge, several key strategies should be implemented:

- **Restructured Empirical Frameworks:** Revision of institutional treatment guidelines to limit the use of carbapenems for low-risk cases, preserving them for targeted indications based on local surveillance data.
- **Active Antimicrobial Stewardship:** Implementing prescription validation protocols, rapid de-escalation based on automated cultures, and mandatory infectious disease consultations for last-line agents like colistin, linezolid, and tigecycline.
- **Enhanced Infection Control Measures:** Strengthening hand hygiene compliance, enforcing contact precautions for confirmed MDR/VRE cases, and conducting routine environmental screening of high-touch surfaces within MICU and SICU settings.

4.5 Strengths and Limitations

This study provides a comprehensive look at ICU resistance patterns through a large sample size ($N = 5,247$) gathered over a full year across four specialized adult ICU sectors. The use of automated Vitek 2 systems ensured highly reproducible phenotypic results.

However, certain limitations should be noted: the study was conducted at a single tertiary care center, which may affect the generalizability of the findings to community-based settings. Additionally, neonatal cohorts were excluded, and molecular characterization of resistance genes (such as *bla*NDM, *bla*OXA, or *mecA*) was not performed. Clinical outcomes, including mortality rates and length of stay, were also not correlated with specific resistance phenotypes.

5. Summary and Conclusion

In conclusion, this investigation demonstrates a high burden of ESKAPE pathogens within adult intensive care units, accounting for 55.2% of all positive cultures. Gram-negative bacilli, particularly *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Klebsiella pneumoniae*, were the predominant isolates.

The study reveals widespread resistance to fluoroquinolones, third- and fourth-generation cephalosporins, and standard β -lactamase inhibitor combinations, alongside carbapenem resistance rates exceeding 57%. Among Gram-positive isolates, *Staphylococcus aureus* exhibited a 52.4% methicillin resistance rate, and *Enterococcus faecium* showed a 34.3% vancomycin resistance rate.

While last-line agents such as tigecycline, linezolid, vancomycin, and teicoplanin retain significant in vitro activity, the overall high prevalence of multi-drug resistance underscores the critical need for robust local surveillance, strict infection control practices, and systematic antimicrobial stewardship programs to manage infections within critical care environments.

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