The ESRF Research Journal for Undergraduate Medical Students

Original Article

Volume 3 Issue 1 (Jul-Dec) 2025

Submission: 18th September,2025

Acceptance: 26th October, 2025

DOI: 10.5281/zenodo.17478020

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Available from: https://esrfrjums.co.in/index.php/main/article/view/76

Magnitude of ESKAPE Pathogens and Their Antimicrobial Resistance in a Tertiary Care Hospital

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Abstract

Background: Antimicrobial resistance (AMR) among healthcare-associated pathogens poses a critical global threat, with the ESKAPE group of organisms (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species) being major contributors. Despite extensive global data, limited comparative studies across different wards is available. This study identifies this gap by observing the antibiotic sensitivity patterns of ESKAPE pathogens from the varied clinical samples collected from the critical and non-critical wards in the hospital.

Methods: A cross-sectional descriptive study was conducted over six months in the Department of Microbiology, Nil Ratan Sircar Medical College and Hospital, Kolkata. Out of 2736 samples processed in the Microbiology department, 375 clinically significant ESKAPE pathogens from adult ICU, NICU, PICU, and adult non-ICU wards were analysed.

Results: Incidence of ESKAPE pathogens are about 14%, among them *Klebsiella pneumoniae* was the most common isolate, predominantly from non-ICU sputum and urine samples, showing high sensitivity to gentamicin. *Pseudomonas aeruginosa* was frequent in ICU samples especially sputum samples, demonstrating high resistance to first line drugs and *Pseudomonas* isolated from non-ICU wards showed sensitivity to ciprofloxacin. *Acinetobacter baumannii* predominated in PICU and NICU. *Enterococcus faecium* and *Staphylococcus* isolates exhibited highest sensitivity to vancomycin.

Conclusion: The study highlights the incidence of ESKAPE pathogens and their antibiogram. Ward-specific antibiograms are essential to optimize empirical therapy, reduce treatment failures, and improve patient outcomes. Regular surveillance and updated antimicrobial stewardship programs are crucial to combat evolving resistance trends.

INTRODUCTION

Antimicrobial resistance (AMR) poses a significant threat to medical science, contributing to rising mortality rates. According to infectious disease society of America (IDSA), the primary culprits behind healthcare-associated infections are the ESKAPE pathogens — *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species — all known for their high propensity to develop resistance.[1] They are capable of escaping the biocidal activity of antibiotics. Several studies have reported a marked increase in resistance to last-resort antibiotics such as polymyxin B, particularly in Indian hospitals.[2,3]

This crisis is further aggravated by the over-the-counter availability and widespread misuse of antibiotics without appropriate sensitivity testing.[4] As a result, hospitalisation and mortality rates have surged, placing an increased burden on the healthcare system.[5] Numerous global studies emphasize the critical nature of AMR, especially focusing on ESKAPE pathogens within hospital settings[6,7].

However, there is a noticeable gap in research from the post-COVID era, where resistance among hospital-acquired infections is expected to rise.[8] Moreover, there is a scarcity of comparative studies across different hospital wards, an important perspective that could offer more clinically relevant

Keywords: Antimicrobial resistance, ESKAPE, resistant pathogens, clinical microbiology

Published by: Eureka Scientech Research Foundation, Kolkata.

Online access: https://esrfrjums.co.in

insights into current trends in antimicrobial sensitivity, particularly (but not limited to) ESKAPE organisms.[9]

This study aims to address this gap by analysing the antimicrobial sensitivity patterns of ESKAPE pathogens from diverse clinical samples collected across critical and non-critical care units in a tertiary care hospital. The objective is to identify any significant shifts in resistance patterns that could guide the refinement of treatment protocols and improve patient outcomes.

MATERIALS AND METHODS

Study type and design: Descriptive Study with cross sectional design

Study setting: Department of Microbiology, Nil Ratan Sircar Medical College and Hospital

Study period: 6 months from August 2024 to January 2025.

Study population: The study included patients of all age groups admitted to different hospital units, including adult and paediatric critical care units and general wards, who had submitted clinical samples for microbiological analysis.

Inclusion criteria:

- All clinically significant isolates belonging to ESKAPE pathogens obtained from patient samples during the study period
- Samples with complete demographic and clinical details

Exclusion criteria

- Non-ESKAPE organisms
- Contaminated or duplicate samples
- Isolates with incomplete data or deemed clinically insignificant

Sample size: Sample size was calculated using the formula for estimation of proportion

$$n = \frac{Z^2_{1-\alpha/2} * p\,(1-p)}{d^2}$$

Where,

$Z^2_{1-\alpha/2}$ = critical value of the Normal distribution at α/2

p = proportion of ESKAPE pathogens in samples from a hospital

d = margin of error

Using p = 0.182 (based on the proportion of ESKAPE pathogens in samples from a hospital based on the study by Singh et al).[10] 1-p=0.818, and d = 0.04, the calculated sample size is 372, rounded off to 375. So, the final sample size is 375.

Sampling technique: Clinical samples were collected aseptically using standard protocol after proper consent and sent to Microbiology department for culture sensitivity testing. Samples were inoculated in routine culture media and incubated overnight. Culture plates showing growth were subjected to Gram stain and other biochemical tests for identification. Antimicrobial susceptibility testing (AST) was performed using the Kirby-Bauer disk diffusion method as per CLSI guidelines 2024. Some of the culture positive samples were put on automated VITEK system for identification and AST. Variables recorded included age, gender, ward/unit, sample type, bacterial species, and AST profile were collected from the records. This study was conducted after ethical clearance from institute ethic committee vide memo no *NRSMC/IEC/250/2024* dated 18.7.2024.

Data analysis: Laboratory data were entered into an electronic database and analyzed using SPSS v29 to determine distribution patterns and resistance trends across different wards and sample types.

RESULTS

The highest isolation rate was for *Acinetobacter baumannii* in NICU and PICU wards, reaching 100% of samples in both settings. In adult ICU, *Pseudomonas aeruginosa* predominated (91.3%), while *Klebsiella pneumoniae* (67.4%) was the most common in adult non-ICU. Other notable isolates included *Enterococcus faecium* (9.4%), *Pseudomonas aeruginosa* (10.5%), and *Enterobacter spp.* (4.9%) in adult non-ICU, indicating a wide range of resistant organisms even outside intensive care units. **(Table 1)**

In adult ICU, sputum yielded *Pseudomonas aeruginosa* in 50% and *Klebsiella pneumoniae* in 4.3% of samples, with CSF and urine contributing smaller proportions. "Other" sample types accounted for 34.8% isolation of *Pseudomonas aeruginosa*. **(Table 2)**

In adult non-ICU, the most frequent organism from sputum was *Klebsiella pneumoniae* (32.2%), and from urine, *Klebsiella pneumoniae* and *Enterococcus faecium* (both 3.8%). Blood cultures most often identified *Staphylococcus aureus* (1.9%) and MRSA (0.7%), highlighting the spectrum of resistance even within bloodstream infections. **(Table 3)**

Antibiotic sensitivity percentages showed substantial resistance among gram-negatives. *Acinetobacter baumannii* showed notable sensitivity to colistin (78%), polymyxin B (82%), and moderate sensitivity to ampicillin-sulbactam (68%), but very low sensitivity to amikacin (26%) and ceftriaxone (4%). *Pseudomonas aeruginosa* remained sensitive to colistin (77%), polymyxin B (75%), and moderately to piperacillin-tazobactam (68%). *Klebsiella pneumoniae* showed sensitivity to colistin (71%), polymyxin B (69%), and moderate sensitivity to ampicillin-sulbactam, cefepime, and ceftazidime (58–60%) with poor sensitivity to tobramycin and ciprofloxacin (16–45%). **(Table 4a)**

Enterococcus faecium displayed high sensitivity to vancomycin (78%) and linezolid (80%), as well as gentamicin (54% high-level resistance). *Staphylococcus aureus* isolates were most sensitive to linezolid (70%) and vancomycin (68%), with moderate sensitivity to erythromycin, clindamycin, and cotrimoxazole (65–70%). Sensitivity

to gentamicin, ampicillin, and tobramycin was relatively (12–32%). **(Table 4b)**

DISCUSSION

Out of 2736 samples that were sent for culture sensitivity, 679 (25%) samples showed significant growth, among them 375 (14%) were ESKAPE pathogens. It is about 55% of total culture positive isolates. One ominous finding from the adult ICU ward was the high isolation of *Pseudomonas aeruginosa*. It is a non-fermenter bacteria and has the ability to form biofilms on frequently used medical devices like catheters and ventilators, leading to hospital-acquired infections like catheter-associated urinary tract infection (CAUTI) and ventilator-associated pneumonia (VAP). Whereas in non-ICU, *Klebsilla pneumoniae* is the most common isolate. In PICU and NICU *Acinetobacter baumannii* is the most common isolated organism in various samples. Among the Gram-positive isolates *Staphylococcus* species were less in number and they showed a good percentage of sensitivity among the first line drugs.

Antimicrobial resistance (AMR) remains a major global health crisis, particularly in hospital settings[1,6]. In this study, we examined the antimicrobial resistance profiles of common pathogens isolated from various wards. ward-specific variations in resistance patterns is also seen among the same isolate.

The study revealed that *Klebsiella pneumoniae* was predominantly isolated from adult non-ICU samples mainly sputum and urine. *Klebsiella pneumoniae* isolated from sputum, blood, and urine showed high sensitivity to gentamicin, similar to findings by Herschel et al.[11] and isolates from ICU were mostly sensitive to Meropenem. ICU-derived *Klebsiella* isolates highlight hospital-acquired UTI as a major concern. *Enterobacter spp*. was mainly isolated from sputum samples of adult non-ICU wards, with maximum sensitivity to minocycline, consistent with earlier surveillance reports.[12]

Enterococcus faecium, isolated from sputum and urine in adult non-ICU wards, showed high sensitivity to Vancomycin. Its presence in sputum also suggests involvement in respiratory tract infections.[13] Adult ICU wards showed a high prevalence of *Pseudomonas aeruginosa*, a non-fermenter known for causing hospital-acquired infections like CAUTI and VAP, owing to its biofilm-forming ability.[14] Adult non-ICU wards also demonstrated significant involvement of this pathogen, especially from sputum samples. Isolates were sensitive to Ciprofloxacin but highly resistant to CLSI approved drugs. This altered sensitivity complicates treatment in ICU settings, severely limiting treatment options.[15]

In paediatric wards, especially PICU and NICU, *Acinetobacter baumannii* was abundantly isolated. The organism was fully sensitive to Polymyxin B however, ward-specific variation was noted. Such variation necessitates ward-specific protocols, especially for vulnerable groups like neonates.[16] Staphylococcus aureus and CONS were prevalent in adult ICU and non-ICU wards, predominantly from blood samples. Isolates from non-ICU wards showed good sensitivity to all first-line antimicrobials listed in CLSI guidelines.[17] Similarly, *Staphylococcus* species from sputum samples showed full sensitivity to first-line drugs suggesting these remain effective despite the organism's HAI potential.[18]

Limitations of this study include the use of data from a single tertiary care hospital, which limits its generalizability. Additionally, not all organisms were tested against the same antibiotic panels, making cross-comparison challenging and less ideal for accurately pinpointing resistance patterns.

CONCLUSION

The study clearly demonstrates the presence of AMR patterns among bacterial isolates across various wards of a tertiary care hospital, with particularly high rates of multidrug resistance in ICUs. Ward-specific sensitivity differences underscore the need for targeted antimicrobial stewardship and localized treatment protocols.

Developing ward and sample specific antibiograms can guide more effective empirical therapy, reducing hospital stays and improving bed turnover. Regular monitoring and updates of treatment strategies in response to evolving resistance trends are essential to reduce morbidity, mortality, transmission of resistant strains, and overall healthcare costs.

ACKNOWLEDGMENTS

The authors gratefully acknowledge the technical support provided by the Medical Technologists of the Department of Microbiology, Nil Ratan Sircar Medical College, during the course of this study.

CONFLICT OF INTEREST

None Declared

FUNDING

The authors received no financial support for the research, authorship, and/or publication of this article.

Table 1: Ward wise distribution of isolated ESKAPE organisms (n=375)

WARD	ESKAPE ORGANISM ISOLATED FROM PATIENT SAMPLES	NO. OF SAMPLES n (%)
Adult ICU (n=46)	*Klebsiella pneumoniae*	3 (6.5)
	Pseudomonas aeruginosa	42 (91.3)
	Staphylococcus aureus	1 (2.2)
Adult non-ICU (n=267)	*Acinetobacter baumannii*	5 (1.9)
	Enterobacter sp	13 (4.9)
	Enterococcus faecium	25 (9.4)
	Klebsiella pneumoniae	180 (67.4)
	Pseudomonas aeruginosa	28 (10.5)
	Staphylococcus aureus	16 (6.0)
NICU (n=24)	*Acinetobacter baumannii*	24 (100)
PICU (n=38)	*Acinetobacter baumannii*	38 (100)

Table 2: Sample wise distribution of isolated ESKAPE organisms in adult ICU (n=46)

Sample	ESKAPE Organism isolated from patient samples	No of samples n (%)
CSF	*Pseudomonas aeruginosa*	2(4.3)
SPUTUM	*Klebsiella pneumoniae*	2(4.3)
	Pseudomonas aeruginosa	23 (50)
URINE	*Klebsiella pneumoniae*	1(2.2)
	Pseudomonas aeruginosa	1(2.2)
OTHERS	*Pseudomonas aeruginosa*	16 (34.8)
	Staphylococcus aureus	1(2.2)
Total		**46 (100)**

Table 3: Sample wise distribution of isolated ESKAPE organisms in ADULT NON-ICU (n=267)

SAMPLES	ESKAPE ORGANISM ISOLATED FROM PATIENT SAMPLES	NO. OF SAMPLES n (%)
SPUTUM	*Acinetobacter baumannii*	9 (3.4)
	Enterobacter sp	6 (2.2)
	Enterococcus faecium	4 (1.5)
	Klebsiella pneumoniae	86 (32.2)
	Pseudomonas aeruginosa	21 (7.9)
BLOOD	*Staphylococcus aureus*	5 (1.9)
	Staphylococcus aureus MRSA	2 (0.7)
URINE	*Enterobacter sp*	2 (0.7)
	Enterococcus faecium	9(3.4)
	Klebsiella pneumoniae	9(3.4)
OTHERS	*Acinetobacter baumannii*	3 (1.1)
	Enterobacter sp	3 (1.1)
	Enterococcus faecium	12 (4.5)
	Klebsiella pneumoniae	80 (29.9)
	Pseudomonas aeruginosa	7 (2.6)
	Staphylococcus aureus	3 (1.1)
	Staphylococcus aureus MRSA	5 (1.9)
	Staphylococcus aureus MSSA	1 (0.4)
Total		**267 (100)**

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Table 4a: Antibiotic sensitivity percentage (%) of Gram negative ESKAPE pathogens

Organism	Amp-Salbact	Piper-tazob	Cefepime	Ceftazidime	Mero-penem	Ciprof-loxacin	Tobramy-cin	Amikacin	Colistin	Gentami-cin	Polymyx-inB	Aztre-onam	Ceftriax-one
A.baumannii	68	67	69	71	64	16	10	26	78	27	82	57	4
P.aeruginosa	64	68	66	67	63	66	15	35	77	36	75	55	21
K.pneumoniae	58	59	60	57	62	45	16	36	71	58	69	52	57

Table 4b: Antibiotic sensitivity percentage (%) of Gram positive ESKAPE pathogens

Organism	Ampicillin	Vancomycin	Erythromycin	Clindamycin	Ciprofloxacin	Tobramycin	Linezolid	Gentamicin	Cotrimoxazole
S.aureus	21	68	66	65	44	12	70	32	70
Enterococcus faecium	52	78	-	-	-	-	80	54(high level)	-

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