ORIGINAL RESEARCH PAPER
Volume - 15 | Issue - 02 | February - 2026 | PRINT ISSN No. 2277 - 8179 | DOI : 10.36106/ijsr
INTERNATIONAL JOURNAL OF SCIENTIFIC RESEARCH

PREVALENCE AND ANTIMICROBIAL SENSITIVITY PATTERN OF ESKAPE GROUP OF PATHOGENS IN BLOOD SAMPLES IN INTENSIVE CARE UNIT PATIENTS OF TERTIARY CARE HOSPITAL KOTA, SOUTH-EAST RAJASTHAN, INDIA

Microbiology

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ABSTRACT

Background: ESKAPE pathogens are responsible for the majority of nosocomial infections and are able to escape from the biocidal effect of antimicrobial agents. ICU's serve as epicenter of infections and health care associated infections occur at highest rates in the ICU patients when compared with those occurring in patients admitted in general wards, i.e 20- 30% of all ICU-admissions leading to an enormous impact on morbidity and mortality. Patients admitted to intensive care units (ICUs) are particularly at risk of acquiring infection due to multiple antibiotic resistant strains of notorious nosocomial pathogens including the ESKAPE group of pathogens. **Objectives:** This study was conducted to isolate ESKAPE microorganism from blood samples and its antimicrobial susceptibility and resistance pattern in ICU patients. **Methodology:** This observational study was conducted in the department of microbiology, Govt medical college Kota and attached hospital from 01/04/2024 to 31/03/2025 of blood samples of ICU patients of age above 18years to evaluate ESKAPE microorganism. **Results-** A total of 150 consecutive non duplicate blood specimens from ICU's were included in the study. Out of 150, 44 samples were blood samples in which 39 shows significant bacterial growth and prevalence of ESKAPE pathogens among these 44 blood samples were 32(72.73%). The distribution of pathogens of ESKAPE group was Staphylococcus aureus 22(50%) which was the predominant pathogen followed by Enterobacter species 4(9.10%), Acinetobacter baumannii 03(6.81%) and Enterococcus faecium 03(6.81%). **Conclusion-** The ESKAPE group of pathogens had a significantly higher prevalence (80.80%) when compared to the other bacterial pathogens in ICU's. The purpose of this study was to monitor the incidence and distribution of ESKAPE group of pathogens and their antimicrobial susceptibility and resistance pattern in critically ill patients with infections, admitted in ICU of a tertiary care hospital.

KEYWORDS

ESKAPE Pathogens, Nosocomial infections, Antimicrobial Agent, ICU, Antimicrobial Susceptibility and Resistance Pattern

INTRODUCTION

ESKAPE pathogens are responsible for the majority of nosocomial infections and are able to escape from the biocidal effect of antimicrobial agents.[1] The World Health Organization(WHO) has also recently included ESKAPE pathogens in the list of 12 bacteria that urgently need new methods and antibiotics.[2] Infectious Diseases Society of America (IDSA) has highlighted a group of antibiotic resistant bacteria as ESKAPE Pathogens because they effectively escape the effects of antibacterial drugs. ESKAPE is an acronym for the group of bacteria, encompassing both Gram positive and Gram negative species, made up of Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acenetobacter baumannii, Psuedomonas aeruginosa, and Enterobacter species.[3-5]

ESKAPE pathogens have a high potential for developing and acquiring drug resistance mechanisms: drug inactivation, modification of drug binding sites, decreased intracellular drug accumulation, and redefining paradigms in pathogenesis, transmission, and treatment.[6-7] Consequently, ICU's serve as epicenter of infections and Health care associated infections occur at highest rates in the ICU patients when compared with those occurring in patients admitted in general wards, i.e 20- 30% of all ICU-admissions leading to an enormous impact on morbidity and mortality. Patients admitted to intensive care units (ICUs) are particularly at risk of acquiring infection due to multiple antibiotic resistant strains of notorious nosocomial pathogens including the ESKAPE group of pathogens.[8] Listed ESKAPE pathogens have an increased occurrence of developing resistance towards 3rd generation cephalosporins and carbapenems. Dissemination of resistant bacteria within communities is an emerging global threat that deserves special attention.[9-11]

AIMS AND OBJECTIVES

To study the prevalence of ESKAPE (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneuoniae, Acinetobacter baumannii, Pseudomonas aeruginosa and Enterobacter species) group of pathogens and determine their Antimicrobial susceptibility and resistance pattern in blood samples of Intensive Care Unit Patients.

MATERIAL AND METHODS

Study type & Design – Observational & Cross sectional study
Study Period – 1year from 01.04.2024 to 31.03.2025 after approval from ethical committee (No.F.3()Acad/Ethical Clearance/Batch 2022/2023/47 date 06/10/2023)
Study Population – Intensive care unit patients in Tertiary care hospital
Type of Sample –Blood samples of ICU patients
Sample size – 150
Sample size was calculated by using formula as follows:
n=Z2 P (1-P)/d2

Inclusion Criteria

1. Patients aged above 18 years
2. Blood samples of ICU patients.
3. Those patients who are willing to give consent.

Exclusion Criteria

1. Patients aged less than18 years.
2. Subsequent samples from the same patient and duplicated were excluded in the study.
3. Those patients who are not willing to give consent.

Specimen Processing

The clinical specimens which were collected from patients admitted in the ICU's were processed as per standard guidelines using appropriate culture media and incubation conditions. Antimicrobial sensitivity testing (AST): As per CLSI 2024 guidelines, AST will be performed on Mueller-Hinton Agar using Kirby-Bauer disk diffusion metho.

All specimens were processed according to standard operating procedure of laboratory. The bacterial isolates were identified based on the standard identification test.

Statistical Analysis:- The Interpretation and analysis of the data were done by using Microsoft excel spread sheet. The quantitative data were expressed as numbers and percentage in a tabular form.

RESULTS

A total of 150 consecutive non duplicate specimens from ICU's were included in the study. The organisms were identified based on standard phenotypic identification test. Out of the total 150 samples, 44 are blood samples in which 20 (45.45 %) males and 24 were females (54.55 %) with ratio of 1/1.2. The age (in years) ranged from 18 to 80 years. About 52 % of the patients were in the age group of 41 to 60

years. Out of these 44 blood specimens from ICU patients, 39 (88.64%) specimens showed significant bacterial growth in which prevalence of ESKAPE pathogens among these 39 culture isolates are 32 (80.80 %) in which Gram positive bacteria are 28(87.5 %) as compared to Gram negative bacteria 04 (12.5 %) in this study.The distribution of pathogens of ESKAPE group is Staphylococcus aureus 22(68.75%) which is the predominant pathogen followed by Enterobacter species 4(12.50%), Acinetobacter baumannii 03(9.37%), and Enterococcus faecium 03(9.37%).

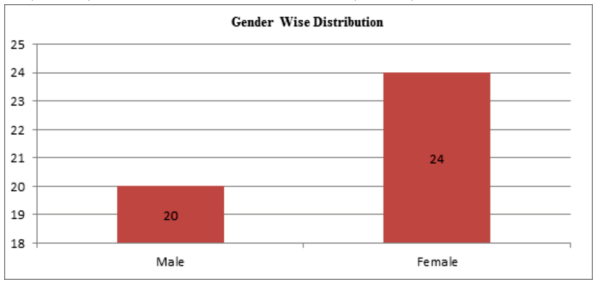

Fig. 01- Gender Wise Distribution of Blood Samples

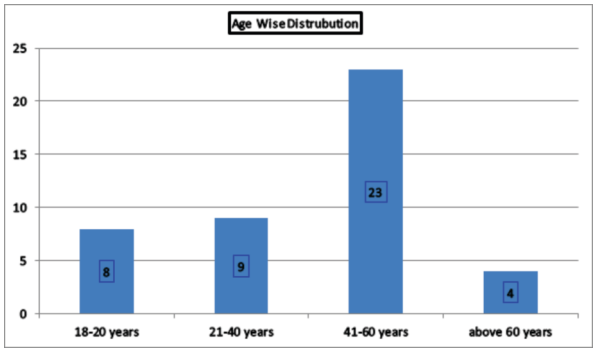

Fig. 02- Age Wise Distribution of Blood Samples

Table 01: Distribution of ESKAPE Pathogens vs Other Bacterial Pathogens in Blood Specimens (n=39)

ORGANISMS	Total Number of Isolates	Percentage (%)
ESKAPE group of pathogens	32	80.80 %
Other than ESKAPE Pathogens	07	19. 20 %
TOTAL	39	100%

Table 02: Organism Wise Distribution of ESKAPE Pathogens (n=32)

S.no	Organism	Total Number Isolated	Percentage (%)
1	Staphylococcus aureus	22	68.75 %
2	Enterobacter species	04	12.50 %
3	Acinetobacter baumannii	03	9.375 %
4	Enterococcus faecium	03	9.375 %
5	Pseudomonas aeruginosa	00	0.0 %
6	Klebsiella pneumonia	00	0.0 %
	TOTAL	32	100%

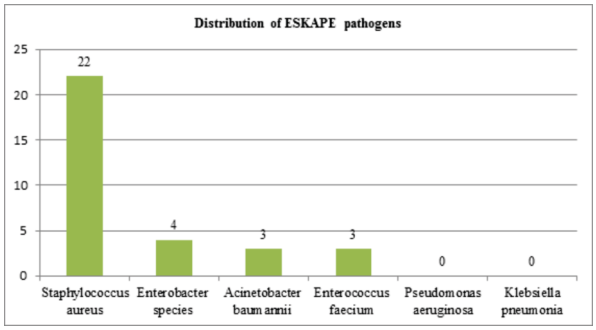

Fig 03: Organism Wise Distribution of ESKAPE Pathogens (n=32)

Table 03: Antimicrobial Susceptibility Pattern of Staphylococcus Aureus (n=22)

Drugs	Total number of isolates	Percentage (%)
	Sensitive	Resistant	Sensitive	Resistant
Gentamicin	17	5	77.27	22.73
Ciprofloxacin	9	13	40.90	59.10
Cefoxitin	22	0	100	0
Trimethoprim + Sulphamethoxazole	17	5	77.27	22.73
Tetracycline	12	10	54.54	45.46
Azithromycin	10	12	45.46	54.54
Clindamycin	11	11	50	50
Linezolid	24	0	100	0
Vancomycin	24	0	100	0

Table 04: Antimicrobial Susceptibility Pattern of Enterobacter Species (n=04)

Drugs	Total number of isolates		Percentage (%)	
	Sensitive	Resistant	Sensitive	Resistant
Amoxacillin+Clavulanate	2	2	50	50
Amikacin	3	1	75	25
Piperacillin-Tazobactam	3	1	75	25
Ceftriaxone	1	3	25	75
Ciprofloxacin	3	1	75	25
Tobramycin	3	1	75	25
Trimethoprim-sulfamethoxazole	1	3	25	75
Imipenem	3	1	75	25
Cefepime	3	1	75	25
Doxycycline	1	3	25	75

Table 05: Antimicrobial Susceptibility Pattern of Acinetobacter Baumannii (n=03)

Drugs	Total number of isolates		Percentage (%)	
	Sensitive	Resistant	Sensitive	Resistant
Ampicillin-Sulbactam	1	2	33.33	66.67
Amikacin	2	1	66.67	33.33
Gentamicin	3	0	100	00
Ceftazidime	3	0	100	00
Piperacillin-Tazobactam	2	1	66.67	33.33
Ciprofloxacin	1	2	33.33	66.67
Tetracycline	2	1	66.67	33.33
Trimethoprim-sulphamethoxazole	1	2	33.33	66.67
Imipenem	3	0	100	0
Ticarcillin-Clavulanate	3	0	100	00
Doxycycline	1	2	33.33	66.67
Cefepime	1	2	33.33	66.67

Table No. 06: Antimicrobial Susceptibility Pattern of Susceptible Enterococcus Faecium (n=03)

Drugs	Total number of isolates		Percentage (%)	
	Sensitive	Resistant	Sensitive	Resistant
Amikacin	2	1	66.67	33.33
Ciprofloxacin	1	2	33.33	66.67
Piperacillin+Tazobactem	3	0	100	50
Amoxacillin+Clavulanate	1	2	33.33	66.67
Tetracycline	1	2	33.33	66.67
Linezolid	3	0	100	00
Vancomycin	3	0	100	00

DISCUSSION

Hospital acquired infections and multidrug resistance are global problems and many epidemiological studies are being carried out. The prevalence of infections caused by multidrug resistant pathogens are higher in developing countries with limited resources associated with the quality of care. Increasing drug resistance and the spread of multi drug-resistant (MDR) pathogens in the ICU's, results in limited therapeutic options and prolonged hospital stay. Bacterial species from the ESKAPE group (i.e. Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa and Enterobacter species) are the most frequently isolated resistant pathogens from ICU's posing potential threat to the clinical cure and survival of critically ill patients on device support. Out of 39 significant bacterial growth, prevalence of ESKAPE pathogens among these 39 culture isolates are 32 (%) which is significantly higher when compared to a study done by Jorge Martin

Llaca-Diaz et al[12] which showed a prevalence rate of ESKAPE pathogens at 64.5% but their study had shown a higher prevalence of Non ESKAPE pathogens at 35.5% when compared to the rate of Non ESKAPE pathogens at % in the present study. Gram positive bacteria constituted the majority of blood stream infections(70%) [Staphylococcus aureus was associated with 68.75% of blood stream infections which is slightly higher when compared to the study by Christoph. K Naberet al which showed a prevalence of about 52.4% but in the study done by Rajesh Ghanshani[13] in India. The present study showed significantly lower prevalence rate of 8.91%,when compared with studies done by Susa F Fraser etal[14] and Maria Virginia Villega etal[15] who reported a prevalence of about 11.3% and 23% respectively. Enterobacter species were associated with 12.5% of blood stream infections and 7.89% respiratory tract infection.

SUMMARY AND CONCLUSION

This study mainly focussed on the distribution of ESKAPE group of pathogens, their susceptibility pattern and resistance mechanisms. The ESKAPE group of pathogens had a significantly higher prevalence (80.80%) when compared to the other bacterial pathogens in ICU's. This knowledge not only aids in formulating antibiotic policies but additionally provides an insight on prevention of emergence and transmission of multidrug resistant organisms by adopting standard infection and prevention control practices. The prevalence of ESKAPE group of pathogens represent the stage of limited treatment options available for the treatment of patients in critical care units. Hence frequent surveillance studies should be done to assess the antimicrobial resistance prevalence rates in health care facilities, along with audits in antibiotic prescription practices and prevention & control measures. These surveillance studies aids in formulating hospital policies and guidelines in areas of infection control and antibiotic management practices.

DECLARATION

Limitation of Study

Clinical characteristics of the subjects were not taken into consideration in this study. Treatment outcome was not followed up in this study. Comorbidities and vulnerability of the patients were not assessed.

Financial Aid-None

Conflict of Interest: The authors have no conflict of interest.

Human and Animal Rights and Informed Consent: This article does not contain any studies with human or animal subjects performed by authors.

Bio-Safety: All standard precautions, bio-safety measures & Biomedical Waste Management in our study according to Biological Waste Management's Rules 2016 and it`s new amendment were observed.

Data Availability: All datasets generated of analyzed during this study are included in the manuscript.

Acknowledgments

I would like to thank all my colleagues in Microbiology as well as other supporting staffs for extending all help for the fulfillment of this endeavor

REFERENCES

1. Dixit A, Kumar N, Kumar S, Trigun V. Antimicrobial resistance: progress in the decade since emergence of New Delhi metallo-β-lactamase in India. Indian journal of community medicine: official publication of Indian Association of Preventive & Social Medicine. 2019 Jan;44(1):4.
2. Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, Pulcini C, Kahlmeter G, Kluytmans J, Carmeli Y, Ouellette M. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic resistant bacteria and tuberculosis. The Lancet Infectious Diseases. 2018 Mar 1;18(3):318-27.
3. N. Puvaca and R. Frutos, "Antimicrobial resistance in escherichia coli strains isolated from humans and pet animals," Antibiotics, vol. 10, p. 69, 2021.
4. World Health Organisation, Emergencies . Ten 0reats to Global Health in 2019, p. 1, World Health Organisation, Geneva, Switzerland, 2019
5. H. W. Boucher, G. H. Talbot, J. S. Bradley, and J. E. Edwards, "Bad bugs, no drugs: no eskape! an update from the infectious diseases society of america," Clinical Infecticious DIseases(IDSA), vol. 48, no. 1, pp. 1–12, January 2009.
6. J. N. Pendleton, S. P. Gorman, and B. F. Gilmore, "Clinical relevance of the ESKAPE pathogens," Expert Reviews Anti- Infective 0erapy, vol. 11, 2013.
7. N. Puvaca, J. Milenkovic, T. J. Coghill et al., "Antimicrobial activity of selected essential oils against selected pathogenic bacteria: in vitro study," Antibiotics, vol. 10, 2021.
8. Al-Musawi AM-S, Al-Charrakh A H, Al-Juwethry A H (2020): ESKAPE pathogens among pediatric patients in Iraq, Ann Trop Med & Public Health; 23(S16): SP231632.
9. A. H. Uc-Cahon, C. Gracida-Osorno, I. G. Luna-Chi, and G. M. Molina-Salinas, "High prevalence of antimicrobial resistance among gram-negative isolated bacilli in intensive care units at," a Tertiary-Care Hospital in Yucatan Mexico Medicina, vol. 55, 2019.
10. S. Santajit and N. Indrawattana, "Mechanisms of antimicrobial resistance in ESKAPE pathogens," BioMed Research International, vol. 2016, Article ID 2475067, 7 pages, 2016.
11. F. G. De Rosa, "From ESKAPE to ESCAPE, From KPC to CC," Clinical Infectious Diseases IDSA, vol. 60, p. 1289, 2015.
12. 2012 Jorge Martin Llaca-Diaz at el One-Year Surveillance of ESKAPE Pathogens in an Intensive Care Unit of Monterrey, Mexico Chemotherapy 2012;58:475–481
13. Bales P.M., Renke E.M., May S.L., Shen Y. and Nelson D.C. "Purification and characterization of biofilm-associated EPS exopolysaccharides from ESKAPE organisms and other pathogens". PLoS One. 2013; 8(6): 67950.
14. 2023 Vidushi Singh at el A study on the Prevalence of ESKAPE Pathogens Isolated from the Blood Culture Specimens of Various Intensive Care Units Patients, Int. J. Curr. Microbiol. App.Sci(2023) 12(03): 203-213
15. Rice LB: Progress and challenges in implementing the research on ESKAPE pathogens. Infect Control Hosp Epidemiol 2010;31(suppl 1):S7–S10