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Original Research Article

SPECTRUM OF ESKAPE PATHOGENS AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERNS AT A TERTIARY CARE HOSPITAL IN TAMIL NADU

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ABSTRACT

Background: ESKAPE pathogens are important causes of bacterial infection and present substantial challenges because of antimicrobial resistance. Local surveillance is needed to describe their distribution and support appropriate empirical antibiotic selection. This study assessed ESKAPE pathogens and their antimicrobial susceptibility patterns at a tertiary care hospital in Tamil Nadu, India.

Materials and Methods: This retrospective laboratory study covered August 2025 to July 2026 at Swamy Vivekanandha Medical College Hospital and Research Institute. Clinical specimens were processed using standard microbiological methods. Organisms were identified by staining, colony characteristics, and biochemical tests. Antimicrobial susceptibility was assessed using disk diffusion and selected gradient diffusion tests, with interpretation based on Clinical and Laboratory Standards Institute guidelines issued in 2025.

Results: Among 4,777 specimens examined, 2,866 were reported as yielding ESKAPE organisms. These comprised 1,265 Staphylococcus aureus, 765 Klebsiella pneumoniae, 574 Pseudomonas aeruginosa, 145 Acinetobacter baumannii, 60 enterococci, and 57 Enterobacter isolates. Gram negative organisms accounted for 53.77% of isolates. Urine contributed 850 isolates, followed by wound or pus specimens with 810, blood with 706, and respiratory specimens with 500. Methicillin resistance was reported in 41.4% of S. aureus isolates, while one enterococcal isolate was vancomycin resistant. K. pneumoniae showed 78.5% resistance to ciprofloxacin and ampicillin with sulbactam. P. aeruginosa showed 70% resistance to ceftazidime and cefepime. Reported carbapenem resistance was 46.2% in K. pneumoniae and 39.5% in P. aeruginosa.

Conclusion: S. aureus was the most frequent isolate, while Gram negative organisms predominated collectively. Resistance to several commonly used antibiotics supports continued institutional surveillance, susceptibility guided treatment, and antimicrobial stewardship. These findings can inform local antibiotic policy when interpreted alongside clinical assessment and reliably collected susceptibility data and infection prevention practices.

Keywords: Antimicrobial resistance; ESKAPE pathogens; antimicrobial susceptibility; tertiary care hospital; surveillance.

INTRODUCTION

Antimicrobial resistance complicates the treatment of bacterial infections by reducing the reliability of commonly used antibiotics.[1,2] The ESKAPE group comprises Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and

Enterobacter species.[3] These organisms received particular attention because they combine clinical importance with the ability to evade antimicrobial treatment. The term provides a practical framework for studying resistant bacteria encountered in hospitals, although the frequency of individual organisms varies across institutions and patient populations.[4]

Infections caused by these pathogens can involve the bloodstream, urinary tract, respiratory tract, and surgical or other wounds. Their management becomes more difficult when resistance limits the antibiotics available for initial treatment. The Infectious Diseases Society of America highlighted the therapeutic challenges posed by ESKAPE organisms and the need for effective antibacterial development.[5] However, developing new drugs alone cannot replace accurate diagnosis, appropriate prescribing, and measures that prevent bacterial transmission within healthcare facilities.[6]

Resistance develops through several mechanisms, including antibiotic inactivation, modification of drug targets, reduced permeability, and active efflux.[7] Some organisms possess intrinsic resistance, whereas others acquire resistance through mutation or genetic exchange.[8] These processes can produce different susceptibility patterns even among isolates of the same species. Consequently, identifying a bacterium does not establish which antibiotic will be effective against it. Laboratory susceptibility testing remains essential for interpreting the clinical significance of resistance and supporting treatment decisions for individual patients.

Antibiotic exposure and inappropriate use contribute to selection pressure, while limitations in diagnostic services and infection prevention can make resistance harder to control.[9] These problems require coordinated responses involving clinicians, microbiologists, pharmacists, and hospital administrators.[10] Surveillance is particularly useful when its findings are translated into practical prescribing guidance and reviewed alongside local antibiotic consumption.[11] Such information can support stewardship programmes by identifying frequently encountered organisms and antibiotics whose activity has become unreliable in a particular setting.

The World Health Organization bacterial priority pathogens list further emphasizes the public health importance of resistant bacterial infections and the need for targeted prevention and research.[12,13] Nevertheless, broad international priorities cannot describe the susceptibility profile of every hospital. Differences in referral patterns, specimen selection, patient characteristics, and laboratory practices influence local findings. Institutional data therefore complement wider surveillance by providing information directly relevant to the patients and services represented in the laboratory records.

Assessment by specimen type also helps explain the overall distribution of organisms. A hospital receiving many wound specimens may report a different bacterial profile from one with predominantly urinary or respiratory submissions. Likewise, pooled resistance percentages may conceal clinically relevant differences between species.[14] Describing both organism distribution and antibiotic susceptibility offers a clearer account of the local microbiological pattern.[15] The present retrospective study therefore examined ESKAPE organisms recovered from clinical specimens at a tertiary care hospital in Tamil Nadu between August 2025 and July 2026. Its objectives were to identify the organisms represented, describe their distribution across specimen categories, and assess the reported antimicrobial susceptibility patterns to inform institutional surveillance and antibiotic policy. Such surveillance is most useful when results are interpreted within their context.

MATERIALS AND METHODS

Study design and setting: This retrospective laboratory study was conducted in the Department of Microbiology at Swamy Vivekanandha Medical College Hospital and Research Institute, Tamil Nadu, India. Records from August 2025 to July 2026 were reviewed. The laboratory examined 4,777 clinical specimens during the study period.

Eligibility and organism identification: Clinically significant isolates belonging to the ESKAPE group were included. Non ESKAPE organisms and contaminated specimens were excluded. Specimens included urine, wound or pus samples, blood, and respiratory samples. Processing followed standard microbiological techniques. Identification was based on Gram staining, colony morphology, motility, oxidase and catalase reactions, and a panel of biochemical tests.

Antimicrobial susceptibility testing: Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar. Results were interpreted according to the 2025 Clinical and Laboratory Standards Institute guidelines.[16] Tested agents represented beta lactams, aminoglycosides, macrolides, clindamycin, glycopeptides, carbapenems, fluoroquinolones, cotrimoxazole, and nitrofurantoin, as applicable to the organism and specimen.

Methicillin resistance in S. aureus was screened using a 30 µg cefoxitin disk. The source protocol classified inhibition zones of 21 mm or less as resistant. Gradient diffusion testing was described for selected confirmatory investigations, including vancomycin resistance and carbapenem resistance. Extended spectrum beta lactamase production was investigated using cephalosporin screening and combination disk testing with clavulanic acid.

Descriptive analysis: Organism and specimen distributions are presented as counts and percentages. Percentages for organism distribution were calculated using 2,866 reported isolates as the

denominator. Specimen specific distributions were calculated using the corresponding specimen category totals. Antibiotic resistance percentages are reported as supplied in the study records; no inferential comparisons were performed.

RESULTS

Of 4,777 specimens examined, 2,866 were reported as yielding ESKAPE organisms, corresponding to 60.00%. The reported dataset comprised 1,541 Gram negative isolates (53.77%) and 1,325 Gram positive isolates (46.23%). Urine contributed 850 isolates (29.66%), wound or pus specimens 810 (28.26%), blood 706 (24.63%), and respiratory specimens 500 (17.45%).

S. aureus accounted for 1,265 isolates (44.14%), followed by K. pneumoniae with 765 (26.69%), P. aeruginosa with 574 (20.03%), A. baumannii with 145 (5.06%), enterococci with 60 (2.09%), and Enterobacter species with 57 (1.99%). [Figure 1] summarizes the organism distribution.

K. pneumoniae was the most frequent organism in urine (422/850; 49.65%) and respiratory specimens (214/500; 42.80%). S. aureus predominated in wound or pus specimens (722/810; 89.14%) and blood cultures (401/706; 56.80%). The distribution by specimen type is presented in [Table 1].

Table 1: Distribution of reported isolates by specimen type

Organism	Urine	Wound or pus	Respiratory	Blood	Total
S. aureus	42	722	100	401	1265
K. pneumoniae	422	28	214	101	765
P. aeruginosa	354	22	100	98	574
A. baumannii	3	33	54	55	145
Enterococci	27	3	0	30	60
Enterobacter spp.	2	2	32	21	57
Total	850	810	500	706	2866

Values are isolate counts. The source table labels enterococci as E. faecium, whereas the source narrative reports Enterococcus species.

Methicillin resistance was reported in 41.4% of S. aureus isolates. One of 60 enterococcal isolates was reported as vancomycin resistant (1.67%). Selected reported resistance percentages for K. pneumoniae and P. aeruginosa are presented in [Table 2 and Figure 2]. Detailed susceptibility results for A. baumannii and Enterobacter species were not provided.

Table 2: Selected reported antimicrobial resistance percentages

Organism	Antibiotic	Resistance (%)
K. pneumoniae	Ampicillin–sulbactam	78.5
K. pneumoniae	Ciprofloxacin	78.5
K. pneumoniae	Cotrimoxazole	56.9
K. pneumoniae	Imipenem	46.2
K. pneumoniae	Meropenem	46.2
K. pneumoniae	Piperacillin–tazobactam	46.2
P. aeruginosa	Ceftazidime	70.0
P. aeruginosa	Cefepime	70.0
P. aeruginosa	Imipenem	39.5
P. aeruginosa	Meropenem	39.5
P. aeruginosa	Piperacillin–tazobactam	39.5

Percentages reproduce the resistance results reported in the source narrative. The number tested for each antibiotic and the intermediate category were not supplied.

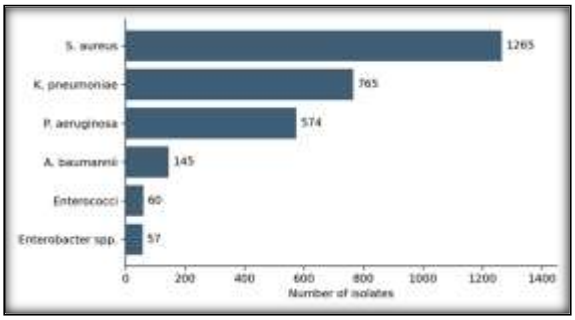

Figure 1: Distribution of the 2,866 reported isolates by organism. Enterococci are shown at genus level pending confirmation of species identification.

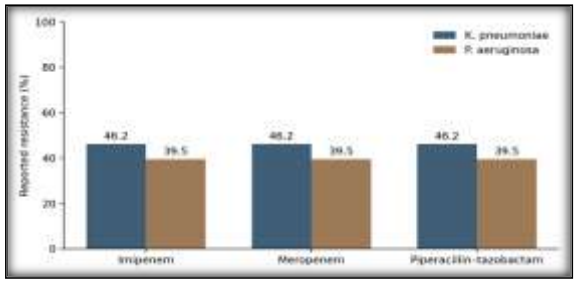

Figure 2: Reported resistance to imipenem, meropenem, and piperacillin–tazobactam in K. pneumoniae and P. aeruginosa. Antibiotic specific testing denominators require confirmation.

DISCUSSION

This retrospective study describes the distribution and reported antibiotic susceptibility of ESKAPE

organisms at a tertiary care hospital in Tamil Nadu. S. aureus was the most frequent individual organism, accounting for 44.14% of the 2,866 isolates. Gram negative organisms collectively represented 53.77%, with K. pneumoniae and P. aeruginosa contributing most of this group. These findings indicate that institutional surveillance should address both staphylococcal resistance and resistance among Gram negative bacilli, rather than relying on the overall predominance of either group.

The organism profile was closely related to specimen type. S. aureus predominated in wound or pus specimens and blood cultures, whereas K. pneumoniae was most frequent in urine and respiratory specimens. This distribution helps explain why the leading individual organism differed from the collectively predominant Gram category. Silva and colleagues also examined ESKAPE organisms across clinical specimens in Brazil, demonstrating the value of describing prevalence alongside susceptibility.[17] Comparisons between hospitals should nevertheless consider specimen composition, referral patterns, and laboratory inclusion criteria before interpreting differences as geographical effects.

Methicillin resistance was reported in 41.4% of S. aureus isolates. This proportion is similar to the 42% reported by the Indian Network for Surveillance of Antimicrobial Resistance in a multicentre study.[18] That comparison provides historical context but does not establish a temporal trend at the present hospital. Differences in patient populations and specimen sources can influence observed resistance proportions. Continued local monitoring is therefore needed to determine whether methicillin resistance remains stable or changes over subsequent surveillance periods.

One of 60 enterococcal isolates was reported as vancomycin resistant, corresponding to 1.67%. Although the absolute number was small, this finding supports attention to accurate identification and confirmatory susceptibility testing. Interpretation also depends on reliable species identification, since E. faecium specifically forms part of the ESKAPE acronym. Pooling enterococcal species can obscure differences in their distribution and susceptibility.[19] The observed proportion should therefore be interpreted cautiously because it is based on a small denominator and cannot describe the broader regional burden of vancomycin resistance.

K. pneumoniae showed reported resistance of 78.5% to ciprofloxacin and ampicillin with sulbactam, while resistance to imipenem, meropenem, and piperacillin with tazobactam was 46.2%. These findings suggest restricted activity of several commonly used agents. However, relatively lower resistance does not establish that an antibiotic is suitable for routine empirical treatment. Clinical decisions must also consider infection severity, site, patient factors, and individual susceptibility results. The study did not investigate resistance genes, so specific carbapenemase mechanisms cannot be assigned to these isolates.

P. aeruginosa showed 70% reported resistance to ceftazidime and cefepime, compared with 39.5% to the reported carbapenems and piperacillin with tazobactam. This pattern reinforces the need for organism specific interpretation. Resistance mechanisms described for ESKAPE bacteria include reduced permeability, efflux, and enzymatic inactivation, but phenotypic results alone cannot determine their contribution here. Moreover, resistance to several antibiotics does not by itself establish a standardized multidrug resistance classification. Such classification requires isolate level results across defined antimicrobial categories,[20] which were unavailable for this analysis.

The findings support regular institutional antibiograms, review of empirical prescribing policies, and communication between the microbiology laboratory and treating teams. Surveillance should report the number tested for each organism and antibiotic, distinguish susceptible, intermediate, and resistant categories, and apply consistent interpretive standards. Repeated isolates from individual patients should be handled explicitly to reduce distortion of resistance estimates. Linking laboratory findings with clinical information would further help distinguish colonization from infection and assess whether prescribing changes improve patient outcomes. Reporting specimen sources separately would make these summaries more useful for clinical teams. Consistent methods across successive surveillance periods would also help determine whether apparent changes reflect evolving resistance or differences in laboratory sampling.

Several limitations restrict interpretation. This was a retrospective study from one institution, and patient characteristics, prior antibiotic exposure, ward distribution, and clinical outcomes were not available. The relationship between 4,777 submitted specimens and 2,866 reported isolates requires verification, particularly regarding repeat samples and polymicrobial growth. Detailed susceptibility data were incomplete for A. baumannii, Enterobacter, and enterococci. The study therefore supports descriptive surveillance but cannot establish hospital acquired infection rates, resistance mechanisms, or the comparative effectiveness of antibiotics. Future surveillance should use standardized collection and reporting procedures. These improvements would strengthen the interpretation of future findings.

CONCLUSION

S. aureus was the most frequent organism in the reported dataset, while Gram negative bacteria collectively predominated. The reported methicillin resistance and resistance among K. pneumoniae and P. aeruginosa support continued local surveillance and susceptibility guided prescribing. Regular

antibiogram review, antimicrobial stewardship, and infection prevention should inform institutional responses to these findings.

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