Research Article

The Hidden Burden of Eskape Pathogens: A Hospital Based Antibiogram Study

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Abstract

Background: Infections caused by ESKAPE pathogens encompass a wide range of conditions, from superficial infections to life-threatening conditions. Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp (ESKAPE pathogens) are leading causes of many infections like bloodstream infection, wounds and surgical site infection, skin & soft tissue infection and endocarditis are notable for their antimicrobial resistance. Aim: This study aims to determine the prevalence of ESKAPE pathogen and analyze the resistance patterns, offering valuable guidance for optimized therapeutic management. Methods: A prospective, observational, cross-sectional study was conducted from January to December 2025 in the Bacteriology section of the Department of Microbiology. A total of 18,372 clinical specimens, including blood, urine, body fluids, pus, sputum and tissue samples, were processed using standard microbiological techniques. Isolates were identified, and antibiotic susceptibility was assessed following the Clinical and Laboratory Standards Institute (CLSI) guidelines. Results: Among 18,372 samples, 8,280 (45%) were culture-positive, with ESKAPE pathogens detected in 4452(53.5%) culture-positive isolates. Klebsiella pneumoniae 1572(35.3%) was the most frequently isolated organism, followed by Pseudomonas aeruginosa 1184 (26.5%) and Acinetobacter baumannii 796(17.8%). Methicillin-resistant S. aureus (MRSA) was found in 48 % of isolates. Among Gram-negative bacteria, 26 % were multidrug-resistant (MDR), but the large majority remained susceptible to colistin (96–100%). Limitations: Study was carried out in a single center and lacked long-term follow-up, the study may not reflect regional differences in antimicrobial resistance pattern, patient demographics, or variation in healthcare practices. Additionally, it does not evaluate long term treatment outcomes or recurrence rates. Conclusion: ESKAPE pathogens are the major causes of infection such as Blood stream infection,Urinary tract infection and skin & soft tissue infection. Their robust resistance mechanisms make treatment difficult. The increasing occurrence of multidrug-resistant Gram-negative bacteria underscores the importance of ongoing surveillance,appropriate antibiotic use and innovative treatment strategies to effectively control antimicrobial resistance.

Keywords: ESKAPE pathogen, MDROs, blood, body fluids, urine, and exudates (tissue, tracheal aspirate, pus swab), Extended-Spectrum β-Lactamase (ESBL)

1. Introduction

Modern healthcare is increasingly challenged by the growing threat of antimicrobial resistance, especially in hospital-acquired infections. A particularly concerning group of pathogens is collectively referred to as the ESKAPE group (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp.) These organisms are known for their high potential to cause healthcare-associated infections (HAIs) and their significant resistance to available antimicrobial treatment [1].

Infections caused by ESKAPE pathogens have profound clinical and economic implications. Patients with HAIs have significantly longer hospital stays–an average of 20.3 days compared to 8.7 days for non-infected patients [2]. These infections are also associated with increased mortality. Evidence suggests that HAIs significantly raise the risk of death, especially among patients with additional clinical risk factors such as central venous catheters, mechanical ventilation, or immunosuppression [2].

Mechanisms of drug resistance fall into several broad categories, including drug inactivation/alteration, modification of drug binding sites/targets, changes in cell permeability resulting in reduced intracellular drug accumulation, and

biofilm formation [3–5]. The rise of ESKAPE pathogens is driven by excessive antibiotic use, prolonged hospital stay, and intensive care management based on host immunity, with septicaemia and bacteraemia being more common in immunocompromised individuals(6).

Addressing this challenge requires strict infection control, judicious antibiotic use, and exploration of alternative treatments [7–9].

This research aims to investigate the frequency of infections caused by ESKAPE pathogens and characterize the antimicrobial susceptibility patterns of ESKAPE pathogens to support and guide effective clinical management

2. Methods

A prospective, observational, cross-sectional study was conducted over 1 year (January–December 2025) in the Bacteriology section, Department of Microbiology at our institute. All clinical specimens including blood,body fluids,pus,pus swabs,tissues,urine,tracheal aspirates and other exudates were collected from various departments over a period of one year. From both outpatients and inpatients with clinical features suggestive of infection, specimens were collected under strict aseptic precautions using sterile containers and were promptly transported to Department of Microbiology for further processing.

All clinically significant specimens were included in the study. Specimens were cultured using 5% sheep blood and MacConkey agar, and incubated at 37°C for 24 hours, with prolonged incubation as needed. Specimens showing polymicrobial growth were excluded from the study. Bacterial isolates were identified using standard conventional microbiological methods. Antibiotic susceptibility testing (AST) was performed by the modified Kirby-Bauer disc diffusion method, E-strips, and VITEK 2 COMPACT, following CLSI guidelines. Methicillin resistance was assessed via the cefoxitin disc diffusion method, while extended-spectrum beta-lactamase production in *Klebsiella* species was detected using the cephalosporin/clavulanate combination disc method.

Demographic and clinical data were recorded in Microsoft Excel, ensuring confidentiality. Data analysis was performed using IBM SPSS version 27 software. To ensure accuracy and reliability, quality control was maintained using *Escherichia coli* ATCC 25922 (non-Extended-Spectrum β-Lactamase (ESBL) producer) and *Klebsiella pneumoniae* ATCC 700603 (ESBL producer).

3. Results:

Of the 18,372 clinical samples processed, 8,280 (45.06%) yielded bacterial growth, while 10,092 (54.93%) showed no growth, commensal growth, or mixed growth. Among culture-positive samples, ESKAPE pathogens were identified in 4452 (53.76%) samples, predominantly from urine , pus and infected tissue samples . Females (69.8%) outnumbered males (30.1%), with the most affected age group being 41–60 years (33.6%). The distribution of culture results is shown in Fig. 2.

Klebsiella pneumoniae 1572(35.3%) was the most frequently isolated ESKAPE pathogen, followed by *Pseudomonas aeruginosa* 1184, (26.5%), Acinetobacter baumannii 796 (17.8%), Staphylococcus aureus 528(11.8%), *Enterococcus faecium* 336(7.54%)and *Enterobacter spp* 36(0.8%) [Table 1]. In our study, the majority of ESKAPE pathogen-associated specimens were urine, reflecting predominantly uncomplicated urinary tract infection (47.1%), followed by exudates (44.0%) from skin and soft-tissue infections including folliculitis, impetigo, wound infection, infected burn wounds, ulcers, diabetic foot infections, deep-seated ulcers, and severe presentations such as scalded skin syndrome (SSS) and toxic shock syndrome (TSS). Bloodstream infection accounted for 6.73% of specimens and body fluids for 2%. The distribution of ESKAPE pathogens is shown in Fig. 3.

S. aureus showed high susceptibility to vancomycin, teicoplanin, and nitrofurantoin (98%), followed by tigecycline (96%). Methicillin-resistant *S. aureus* (MRSA) was detected in 424 isolates. Additionally, *Enterococcus* spp. showed high susceptibility to teicoplanin and nitrofurantoin(98%)[Table 2].

Among Gram-negative isolates, Klebsiella pneumoniae showed higher sensitivity to amikacin (94%), and P. aeruginosa showed high sensitivity to meropenem (96%). *A. baumannii* showed sensitivity to Piperacillin tazobactam (92%) ESBL

production was observed in 58% of *K. pneumoniae* isolates . Out of 3588 Gram-negative isolates, 932 isolates (26.0%) were multidrug-resistant (MDR), 97% susceptible to colistin, while 2656 (74.0%) were non-MDR [Table 3].

Table 1. Clinico-epidemiological details of ESKAPE pathogens (n=4452)

Category	Frequency, n (%)
Sex	
Male	1342 (30.1)
Female	3110 (69.8)
Age group (years)	
≤20	400 (8.9)
21–40	1200 (26.9)
41–60	1500 (33.6)
61–80	900 (20.2)
≥80	452 (10.1)
Type of specimen	
Blood	300 (6.73)
Exudate (pus/wound swab/tissue)	1960 (44.0)
Body fluids	92 (2.0)
Urine	2100 (47.1)
Organism isolated	
Staphylococcus aureus	528 (11.8)
Pseudomonas aeruginosa	1184 (26.5)
Klebsiella pneumoniae	1572 (35.3)
Acinetobacter baumannii	796 (17.8)
Enterococcus spp.	336 (7.54)
Enterobacter spp.	36 (0.8)

Figure -1, Gender Distribution among ESKAPE Pathogens

Figure 1. Gender Distribution among ESKAPE Pathogens (n=4452)

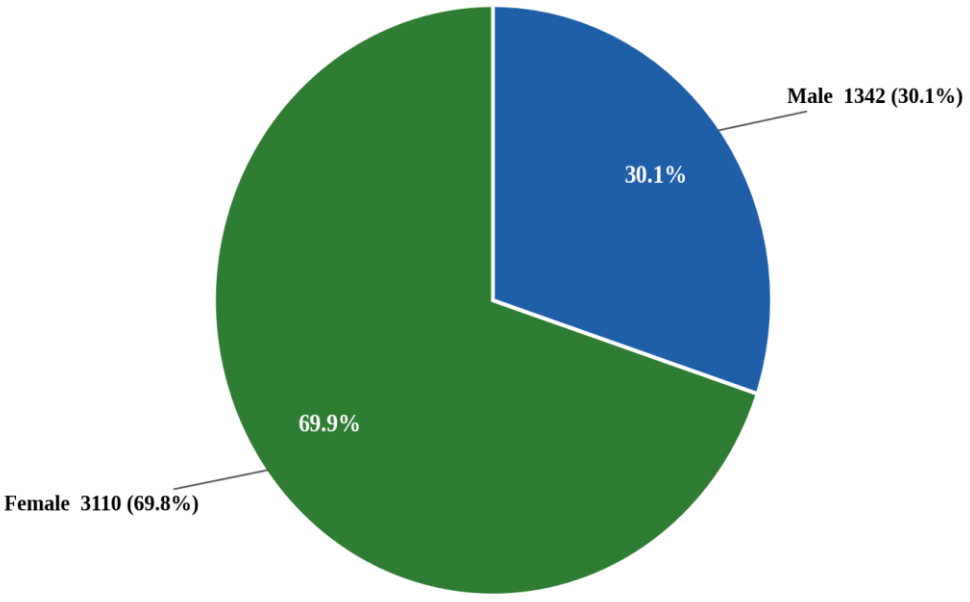

Figure-2: Distribution of Clinical sample culture Result

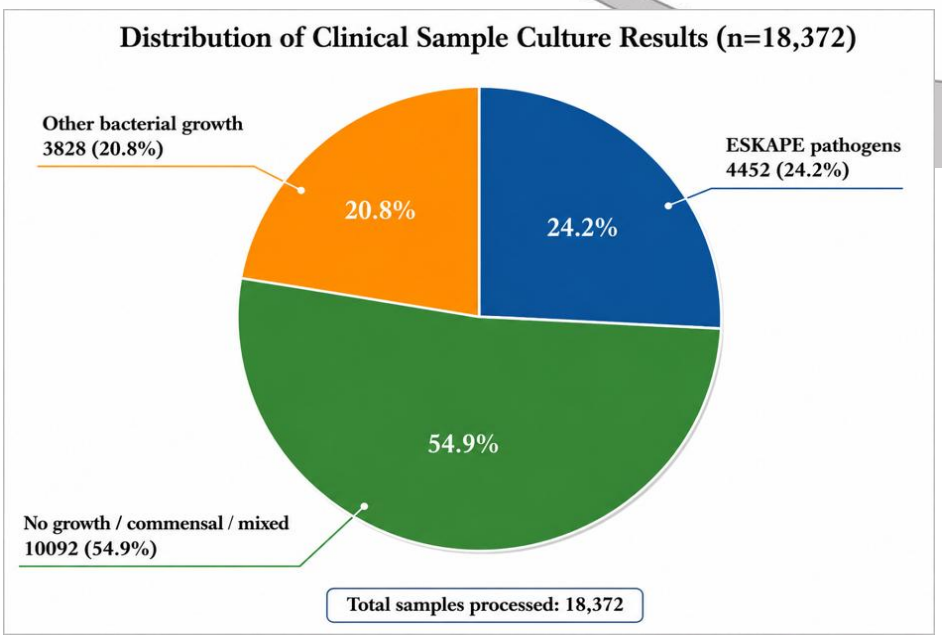

Figure-3:Distribution of ESKAPE Pathogens

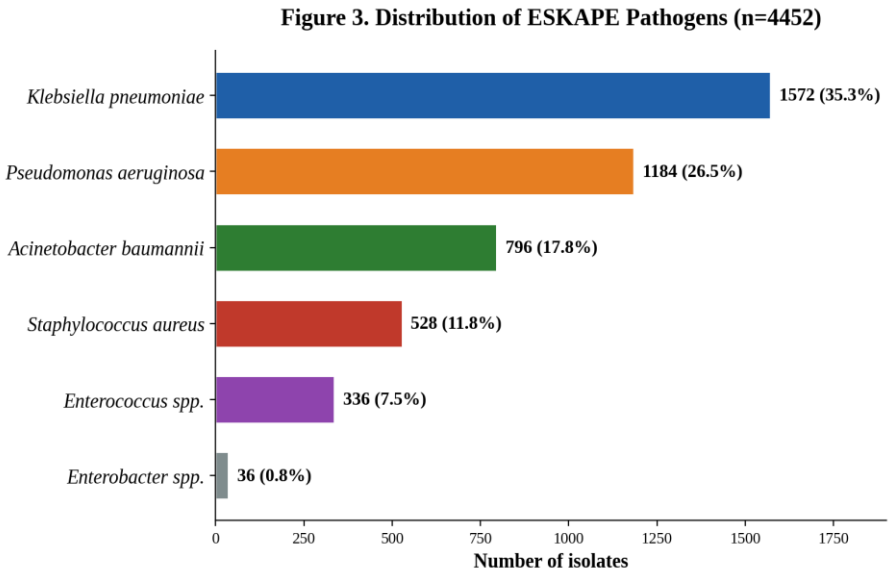

Table 2: Antibiotic sensitivity pattern of gram-positive isolates (n=864) (IR = intrinsic resistance, NT = not tested)

Antibiotic	*S. aureus* (n=528)	*Enterococcus* spp. (n=336)
Vancomycin (E-strip)	471 (98%)	NT
Cefoxitin	230 (48%)	Not tested
Teicoplanin	471 (98%)	330 (98%)
Linezolid	423 (88%)	322 (96%)
Erythromycin	439 (83%)	135 (40%)
Clindamycin	433 (90.1%)	IR
Co-trimoxazole	326 (67.7%)	NT
Penicillin	104 (20%)	201 (60%)

High-level gentamicin	422 (80%)	NT
Levofloxacin	370 (60%)	236 (70%)
Ciprofloxacin	386 (73%)	232 (69%)
Tetracycline	475 (90%)	205 (61%)
Tigecycline	506 (96%)	322 (96%)
Nitrofurantoin	518 (98%)	296 (98%)

Table 3: Antibiotic sensitivity pattern of gram-negative isolates (n=3588) (IR = intrinsic resistance, NT = not tested)

Antibiotic	***P. aeruginosa* (n=1184)**	***K. pneumoniae* (n=1572)**	***A. baumannii* (n=796)**	***Enterobacter* spp. (n=36)**
Cefotaxime	IR	676 (43%)	NT	IR
Ceftazidime	793 (67%)	NT	350 (44%)	NT
Cefepime	864 (73%)	723 (46%)	382 (48%)	IR
Ciprofloxacin	947 (80%)	943 (60%)	478 (60%)	17 (46%)
Levofloxacin	1018 (86%)	911 (58%)	462 (58%)	NT
Piperacillin-tazobactam	1114 (94.1%)	1037 (66%)	732 (92%)	26 (70%)
Co-trimoxazole	NT	817 (52%)	374 (47%)	23 (65%)
Amikacin	1053 (89%)	1478 (94%)	716 (90%)	25 (69%)
Gentamicin	1089 (92%)	1100 (70%)	732 (92%)	20 (55%)
Imipenem	1178 (94.8%)	1258 (80%)	645 (81%)	31 (86%)
Meropenem	1136 (96%)	1163 (74%)	557 (70%)	33 (91.5%)
Polymyxin B	1172 (99%)	NT	756 (95%)	NT
Colistin	1148 (97%)	1509 (96%)	780 (98%)	36 (100%)

4. Discussion

Overall burden of ESKAPE pathogens

This study screened 18,372 clinical specimens over one year, of which 8,280 (45.1%) yielded bacterial growth; ESKAPE pathogens accounted for 4,452 isolates, representing 53.8% of all culture-positive samples. Klebsiella pneumoniae was the predominant organism (35.3%), followed by Pseudomonas aeruginosa (26.5%), Acinetobacter baumannii (17.8%), Staphylococcus aureus (11.8%), Enterococcus spp. (7.5%), and Enterobacter spp. (0.8%). Gram-negative organisms together accounted for over four-fifths of ESKAPE isolates (80.6%), confirming the continuing dominance of resistant Enterobacterales and non-fermenters in hospital-associated infection in this setting, consistent with regional and global antimicrobial resistance surveillance data [1,3–5].

Demographic and clinical distribution

Female patients accounted for the majority of ESKAPE isolates (69.8% vs. 30.1% male), and the highest burden was observed in the 41–60-year age group (33.6%), followed by 21–40 years (26.9%), 61–80 years (20.2%), ≤20 years (8.9%), and ≥80 years (10.1%). This pattern likely reflects a combination of greater healthcare contact, comorbidities such as diabetes, and urinary tract instrumentation in middle-aged and older adults, together with a higher representation of urinary and gynaecological specimens characteristic of female outpatient and inpatient populations. Because isolate counts reflect laboratory recovery rather than true infection incidence, and because repeat isolates from the same patient were not excluded from this analysis, these findings should be interpreted as a description of the culture-positive workload rather than a formal incidence estimate.

Clinical specimen distribution

Urine was the leading specimen source (47.1%), consistent with the well-established role of Enterobacterales and *K. pneumoniae* in particular in community- and healthcare-associated urinary tract infection. Exudates (pus, wound swabs,

and tissue), associated with skin and soft-tissue infection, surgical-site infection, diabetic foot infection, and severe presentations such as scalded skin syndrome and toxic shock syndrome, accounted for a similarly large share (44.0%). Bloodstream isolates (6.7%) and body-fluid isolates (2.0%) were comparatively less common but clinically the most significant, given their association with severe sepsis and the need for prompt, susceptibility-guided therapy and source control.

Predominance of *Klebsiella pneumoniae*

K. pneumoniae was the single most frequently isolated ESKAPE pathogen in this series, in keeping with its recognised versatility across urinary, respiratory, bloodstream, intra-abdominal, and wound infections, and its propensity to acquire extended-spectrum β-lactamase (ESBL) and carbapenem-resistance mechanisms. In this cohort, ESBL production was identified in 58% of K. pneumoniae isolates, and resistance was correspondingly high to cefotaxime (57% resistant), cefepime (54%), co-trimoxazole (48%), ciprofloxacin (40%), and piperacillin-tazobactam (34%), while susceptibility remained high to amikacin (94%), meropenem (74%), and colistin (96%). A broadly similar resistance profile — high resistance to cefepime, cefuroxime, co-trimoxazole, piperacillin-tazobactam, ciprofloxacin, cefotaxime, cefazolin, and gentamicin has been reported previously among carbapenem-resistant Enterobacteriaceae isolated from urinary tract infection [15], reinforcing the need for carbapenem-sparing, susceptibility-guided prescribing wherever K. pneumoniae is suspected empirically.

Staphylococcus aureus and Gram-positive resistance

S. aureus was the leading Gram-positive organism and the second most frequently isolated ESKAPE pathogen overall, reflecting its broad role in skin and soft-tissue infection, surgical-site infection, and bacteraemia. A substantial proportion of isolates were methicillin-resistant (MRSA) is 48% on cefoxitin screening underscoring the continued need for MRSA-directed empirical therapy, contact precautions, and antimicrobial stewardship alongside strategies targeting resistant Gram-negative organisms. Encouragingly, susceptibility to vancomycin, teicoplanin, and nitrofurantoin remained high (98%), and to tigecycline (96%), providing reliable options for confirmed MRSA infection. Enterococcus spp. showed a similar pattern, with high susceptibility to teicoplanin and nitrofurantoin (98% each), supporting their continued use as first-line options while glycopeptide resistance remains uncommon in this setting.

Multidrug resistance and comparison with other studies

Multidrug resistance (MDR) was identified in 932 of 3,588 Gram-negative isolates (26.0% by the reported counts), while colistin susceptibility remained high across all Gram-negative ESKAPE organisms (96–100%), providing a reassuring last-line option in this setting. This pattern declining carbapenem and fluoroquinolone susceptibility alongside preserved polymyxin activity mirrors the broader literature on MDR Gram-negative bacteria, recognised as one of the greatest threats to patients requiring prolonged hospitalisation or intensive care [13].

Our findings are broadly consistent with several comparator studies. A large population-based cohort study similarly found Enterobacterales to be a leading cause of bacteraemia [10], and a United States emergency-department study likewise reported Gram-negative predominance, particularly Escherichia coli, among all clinical specimens [11] — both in line with the Gram-negative, Klebsiella-led profile observed here. A five-year Hungarian survey of ESKAPE pathogens in the emergency department similarly emphasised substantial regional and setting-related variation in the relative frequency of individual ESKAPE organisms, even while confirming their combined clinical importance as a group [12]. In a hospital-wide series from Tanzania, pus was the leading specimen source for K. pneumoniae (23%), followed by urine [14]; in the present study urine was the predominant overall specimen, although organism-specific specimen breakdown was not performed here, so this comparison should be interpreted cautiously.

Taken together, these findings reinforce that local, isolate-level antibiogram surveillance remains essential to translate global ESKAPE and WHO priority-pathogen data [16] into actionable guidance for empirical therapy, infection-prevention practice, and antimicrobial stewardship in this setting. As with all single-centre microbiology surveys, organism distribution should be interpreted alongside clinical correlation, and the limitations outlined below should be considered when generalising these findings.

Limitations

The study was carried out at a single institution, so the results may not reflect variations in patient demographics, healthcare practices, or regional microbial resistance patterns. The study did not include long-term patient outcomes,

preventing an assessment of the sustained efficacy of interventions or potential relapses.

Conclusion

Our study provides insights into the prevalence, distribution, and antimicrobial resistance patterns of ESKAPE pathogens across clinical infections predominantly urinary tract infection, skin and soft-tissue infection, and bloodstream infection highlighting the burden posed by resistant pathogens and underscoring the need for comprehensive strategies to address this growing threat.

Ethical approval: Our Institution doesn't mandate ethical approval for prevalence study
Consent to Participate declaration: Not applicable
Consent to Publish declaration: Not applicable
Clinical trial number: Not applicable.
Availability of data and materials: The data supporting the findings of this study are available from the corresponding author on reasonable request, subject to institutional and patient-privacy requirements.

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