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Antimicrobial resistance profiles of ESKAPE pathogens isolated in a microbiology laboratory in Somalia: a two-year retrospective study

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Abstract

Objective ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp.) are major causes of healthcare-associated infections and pose a serious public health threat because of their high antimicrobial resistance potential. This study evaluated the distribution, resistance profiles, and associated factors of ESKAPE pathogens isolated in Somalia.

Methods This retrospective single-center laboratory-based study was conducted at Mogadishu Somalia Türkiye Recep Tayyip Erdoğan Training and Research Hospital, a tertiary care center in Mogadishu, Somalia. Only culture-positive clinical specimens yielding ESKAPE pathogens between January 2024 and December 2025 were included. A total of 2,486 ESKAPE isolates were analyzed. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method according to CLSI criteria. Demographic and clinical data were analyzed using SPSS and R software. Associations between selected demographic and clinical factors and specific pathogens were evaluated using univariate binary logistic regression analysis.

Results Of the isolates, 1,442/2,486 (58.0%) were obtained from male patients, and the most common age group was 18–40 years [952/2,486 (38.3%)]. The most prevalent pathogens were *K. pneumoniae* [1,033/2,486 (41.6%)] and *S. aureus* [629/2,486 (25.3%)]. Overall, MDR and XDR phenotypes were detected in 1,633/2,486 (65.7%) and 687/2,486 (27.6%) isolates, respectively. The highest MDR and XDR rates were observed in *A. baumannii* [135/138 (97.8%) and 97/138 (70.3%)]. High resistance to ceftazidime [128/138 (92.8%)], cefepime [116/138 (84.1%)], ciprofloxacin [115/138 (83.3%)], trimethoprim-sulfamethoxazole [121/138 (87.7%)], and carbapenems [99/138 (71.7%)] was detected in *A. baumannii*. Susceptibility to vancomycin and linezolid remained largely preserved among Gram-positive pathogens. *A. baumannii* and *Enterobacter* spp. were significantly associated with ICU admission, while gender-related differences were observed for *P. aeruginosa* and *S. aureus*.

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Conclusion A high burden of antimicrobial resistance was observed among ESKAPE pathogens, particularly Gram-negative bacteria, with *A. baumannii* playing a central role. These findings provide important local surveillance data that may support empirical antibiotic selection, antimicrobial stewardship, and infection control strategies in Somalia.

Keywords ESKAPE pathogens, Healthcare-associated infections, Antimicrobial resistance, MDR, XDR, Somalia

Introduction

Antimicrobial resistance (AMR) is currently one of the most important global threats to human health and is associated with the inappropriate and excessive use of antibiotics, inadequate infection control practices, and increased antimicrobial exposure in healthcare systems [1]. In a comprehensive global analysis published in *The Lancet*, AMR was reported to have caused 1.27 million direct deaths and contributed to 4.95 million deaths across 204 countries and territories in 2019 [2]. Multidrug resistance (MDR) is increasing worldwide and complicating the treatment of infections. This situation often necessitates the use of reserve antibiotics, which may be more toxic or costly [3]. ESKAPE pathogens, including *Enterococcus faecium* (*E. faecium*), *Staphylococcus aureus* (*S. aureus*), *Klebsiella pneumoniae* (*K. pneumoniae*), *Acinetobacter baumannii* (*A. baumannii*), *Pseudomonas aeruginosa* (*P. aeruginosa*), and *Enterobacter* spp., are among the leading causes of healthcare-associated infections and constitute a substantial proportion of the global AMR burden [4, 5]. These pathogens are capable of developing multidrug resistance through mechanisms such as biofilm formation, enzymatic inactivation, and efflux pump systems, enabling their persistence and dissemination in healthcare environments [6, 7].

In 2017, the World Health Organization (WHO) published a priority pathogen list for research and development of new antibiotics, in which several ESKAPE pathogens were classified as critical-priority organisms [8]. In addition, the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) has emphasized the strengthening of antimicrobial resistance surveillance and the generation of standardized data across countries as a global necessity [9, 10]. Global data indicate that the burden of AMR is particularly higher in countries with limited diagnostic capacity and weaker healthcare infrastructure [11]. In Somalia, prolonged internal conflicts, population displacement, inadequate healthcare infrastructure, limited microbiology laboratory capacity, and uncontrolled antimicrobial use have created favorable conditions for the emergence and dissemination of resistant pathogens [12, 13]. AMR constitutes a substantial mortality burden in the country, with approximately 8,400 direct deaths and 32,700 associated deaths reported in 2019 [12].

Current studies have demonstrated considerable antibiotic resistance among clinically important pathogens, particularly *E. coli*, *K. pneumoniae*, and *S. aureus*, with

notably high MRSA rates reported in Somalia [12, 14]. However, these data are largely derived from single-center and cross-sectional studies, and there is still a lack of systematic and continuous investigations evaluating the distribution of ESKAPE pathogens according to clinical specimen types and hospital units, as well as the prevalence of multidrug resistance in Somalia [12, 14]. Furthermore, a standardized and sustainable national antimicrobial resistance surveillance system has not yet been adequately established in the country [9, 10, 12].

This situation limits the accurate determination of the true burden of AMR and the local resistance patterns of ESKAPE pathogens in Somalia, thereby restricting the development of local antibiograms, strengthening of infection control practices, and implementation of antimicrobial stewardship strategies [10, 12, 14]. Therefore, generating local surveillance data through retrospective analyses is of critical importance, as it may reveal short-term resistance trends even under the existing laboratory capacity constraints, help fill the current local data gap, and provide a foundation for future surveillance systems.

In this context, this two-year retrospective study aimed to evaluate the antimicrobial resistance profiles and multidrug resistance (MDR) prevalence of ESKAPE pathogens isolated between 2024 and 2025 in a microbiology laboratory affiliated with a tertiary care hospital in Somalia; to determine the distribution of these isolates according to clinical specimen types and hospital departments; and to assess the potential contribution of the findings to local antimicrobial surveillance, infection control practices, and empirical treatment strategies.

Materials and methods

Study design and setting

This retrospective cross-sectional laboratory-based study was conducted in the Microbiology Laboratory of Mogadishu Somalia Türkiye Recep Tayyip Erdoğan Training and Research Hospital, a tertiary care center located in Mogadishu, Somalia. The hospital is one of the largest healthcare centers in the country, providing services to approximately 250,000–300,000 patients annually from Mogadishu and other regions of Somalia. Ethical approval for the study was obtained from the Ethics Committee of Mogadishu Somalia Türkiye Recep Tayyip Erdoğan Training and Research Hospital, and all patient data were anonymized to ensure confidentiality.

Study population

This study included culture-positive clinical specimens yielding ESKAPE pathogens, namely *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp., isolated between January 2024 and December 2025. A total of 2,486 ESKAPE isolates obtained from blood, cerebrospinal fluid (CSF), urine, wound, respiratory, and other clinical samples were included in the study. Patient demographic data (age, gender), specimen type, and antibiogram results were retrospectively obtained from laboratory records. Age was categorized into four groups for analysis: ≤ 17 years, 18–40 years, 41–64 years, and ≥ 65 years. Only the first isolate from each patient was included in the analysis, and duplicate isolates from the same patient were excluded. Only samples with confirmed bacterial growth and completed organism identification and antimicrobial susceptibility testing were included. Records with incomplete laboratory data, cultures with no growth, and contaminated samples were excluded from the study.

Microbiological analysis

Antimicrobial susceptibility results were interpreted according to CLSI M100 guidelines [15]. Specimens were inoculated onto 5% sheep blood agar (Laborlar, Türkiye), chocolate agar (Laborlar, Türkiye), and eosin methylene blue (EMB) agar (Laborlar, Türkiye) and incubated at 37 °C for 18–24 h.

Bacterial identification was performed using conventional manual phenotypic and biochemical methods, as automated identification systems such as API, VITEK or MALDI-TOF MS were not routinely available in the study laboratory during the study period. Identification was based on Gram staining, colony morphology, hemolytic characteristics, and standard biochemical reactions.

For Gram-positive bacteria, catalase, coagulase and PYR tests were used when appropriate. For Gram-negative bacteria, oxidase, triple sugar iron (TSI), citrate utilization, indole, motility, urease, and lactose fermentation characteristics on EMB agar were evaluated. Species identification was established according to conventional microbiological algorithms routinely used in the laboratory.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed on Mueller–Hinton agar (Laborlar, Türkiye) using the Kirby–Bauer disk diffusion method. Commercial antibiotic disks were used (Bioanalyse, Türkiye), and the plates were incubated at 37 °C for 18–24 h. Inhibition zone diameters were measured, and the results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) [15] criteria. Isolates

were classified as susceptible, intermediate, or resistant according to CLSI breakpoints. For statistical analysis, isolates categorized as intermediate were considered resistant.

Antibiotic groups and susceptibility testing panel

The antibiotic panel was selected according to the bacterial species isolated, routine laboratory practices, CLSI recommendations [15], and local antimicrobial stewardship protocols. Not all antibiotics were tested against all bacterial species.

For Gram-negative bacteria, the tested antibiotics mainly included beta-lactams [ampicillin (10 µg), amoxicillin-clavulanate (20/10 µg), ampicillin-sulbactam (10/10 µg), piperacillin-tazobactam (100/10 µg), cefepime (30 µg), ceftazidime (30 µg), ceftriaxone (30 µg), and meropenem (10 µg)], aminoglycosides [gentamicin (10 µg) and amikacin (30 µg)], fluoroquinolones [ciprofloxacin (5 µg) and levofloxacin (5 µg)], and trimethoprim-sulfamethoxazole (1.25/23.75 µg).

For Gram-positive bacteria, depending on the organism, penicillin (10 U), cefoxitin (30 µg), erythromycin (15 µg), clindamycin (2 µg), gentamicin (10 µg), high-level gentamicin (120 µg), ciprofloxacin (5 µg), tetracycline (30 µg), rifampicin (5 µg), trimethoprim-sulfamethoxazole (1.25/23.75 µg), linezolid (30 µg), vancomycin (30 µg), teicoplanin (30 µg), daptomycin (30 µg), and fusidic acid (10 µg) were tested.

Antimicrobial susceptibility testing was primarily performed using the Kirby–Bauer disk diffusion method. However, vancomycin and daptomycin susceptibility testing for Gram-positive organisms was performed using the E-test method (Bioanalyse, Türkiye) according to CLSI recommendations, and results were interpreted in accordance with CLSI M100 guidelines.

Quality control testing was performed weekly and whenever a new batch of media or antibiotic disks was introduced, using standard ATCC reference strains including *S. aureus* ATCC 25,923, *P. aeruginosa* ATCC 27,853, and *E. faecium* ATCC 29,212.

Antimicrobial resistance classification

Multidrug-resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) phenotypes were classified according to the internationally accepted criteria proposed by Magiorakos et al. [16] developed through a joint initiative of the European Centre for Disease Prevention and Control (ECDC) and the Centers for Disease Control and Prevention (CDC). MDR was defined as non-susceptibility to at least one agent in three or more antimicrobial categories. XDR was defined as susceptibility to only one or two antimicrobial categories, whereas PDR was defined as non-susceptibility to all tested antimicrobial agents. XDR and PDR classifications were based on

the antimicrobial categories routinely tested in the study laboratory according to local laboratory protocols and CLSI recommendations.

Statistical analysis

Statistical analyses were performed using IBM SPSS Statistics (version 23) and R software. The distribution of continuous variables was assessed using the Shapiro–Wilk test. Normally distributed data were presented as mean $\pm$ standard deviation, while non-normally distributed data were expressed as median (IQR). Categorical variables were presented as counts and percentages. For comparisons between groups, the chi-square or Fisher's exact test was used for categorical variables, and the Student's t-test or Mann–Whitney U test was applied for continuous variables, as appropriate. For multiple group comparisons, ANOVA or the Kruskal–Wallis test was used. Univariate binary logistic regression analysis was performed to evaluate associations between selected demographic and clinical variables and specific pathogens. Odds ratios (ORs) with 95% confidence intervals (CIs) were calculated. All tests were two-tailed, and a p-value < 0.05 was considered statistically significant. Records with incomplete demographic or laboratory information were excluded prior to statistical analysis. Therefore, all analyses were conducted using a complete-case approach, and no imputation procedures were performed for missing data.

This study was reported in accordance with the STROBE Statement guidelines for observational studies.

Results

Among 8,393 clinical specimens processed in the microbiology laboratory during the study period, 2,486 (29.6%) culture-positive isolates were identified as ESKAPE pathogens.

The overall distribution of ESKAPE pathogens ($n = 2486$) showed that *K. pneumoniae* was the most frequently isolated organism (41.6%, 95% CI: 39.6–43.5), followed by *S. aureus* (25.3%, 95% CI: 23.6–27.0) and *P. aeruginosa* (20.1%, 95% CI: 18.5–21.7). The prevalences of *A. baumannii*, *E. faecium*, and *Enterobacter* spp. were 5.6% (95% CI: 4.7–6.5), 4.1% (95% CI: 3.3–4.9), and 3.4% (95% CI: 2.7–4.1), respectively (Fig. 1).

During the study period, 1,292/2,486 (52%) isolates were obtained in 2024 and 1,194/2,486 (48%) in 2025. Among ESKAPE-positive isolates, the highest proportion was observed in male patients [1,442/2,486 (58.0%)] and in the 18–40 years age group [952/2,486 (38.3%)]. The majority of isolates were obtained from inpatient wards [908/2,486 (36.5%)], followed by outpatient clinics [809/2,486 (32.5%)]. Of the isolates obtained from inpatient wards, 416/908 (45.8%) were from medical wards and 492/908 (54.2%) were from surgical wards. The most common specimen types were wound samples [811/2,486 (32.6%)] and urine samples [547/2,486 (22.0%)] (Table 1).

A statistically significant association was observed between age group and gender distribution. Male patients constituted a higher proportion of ESKAPE-positive isolates across all age categories, with the most pronounced predominance observed in the 18–40 years age group (64.1%). In contrast, the gender distribution was relatively more balanced in the older age groups (Table 2).

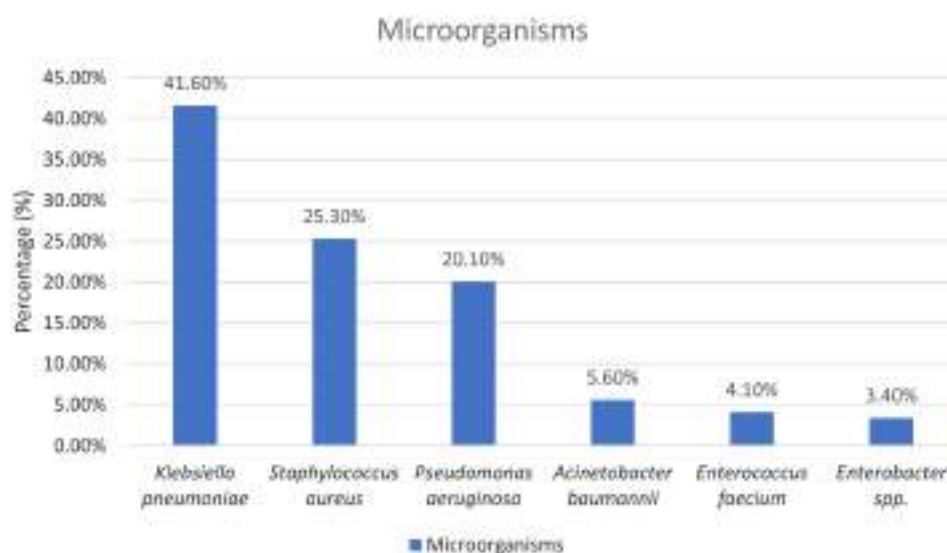


Fig. 1 Distribution of ESKAPE pathogens isolated during the study period

Table 1 Demographic, clinical, and microbiological characteristics of the study population

Variables	Category	n = 2,486	%
Year	2024	1292	52
	2025	1194	48
Gender	Male	1442	58
	Female	1044	42
Age group	≤ 17	505	20.3
	18–40	952	38.3
	41–64	561	22.6
	≥ 65	468	18.8
Hospital departments	Outpatient clinic	809	32.5
	Intensive care unit (ICUs)	756	30.4
	Inpatient ward	908	36.5
	(Internal services)	416	45.8
	(Surgical services)	492	54.2
	Emergency department	13	0.5
Sample type	Abscess	44	1.8
	Sputum	167	6.7
	Cerebrospinal fluid	11	0.4
	Tracheal aspirate culture	348	14.0
	Urine	547	22.0
	Blood	344	13.8
	Wound	810	32.6
	Peritoneal fluid/Pleural fluid	83	3.3
	Catheter	25	1.0
	Other (Ear, throat, vagina, nasal swab, joint fluid, drainage fluids, etc.)	107	4.3

ICUs: Intensive Care Units

Table 2 Distribution of ESKAPE-positive isolates according to age groups and gender

Age groups	Gender		Total n (%)
	Male n (%)	Female n (%)	
≤ 17 years	280 (55.4)	225 (44.6)	505 (20.3)
18–40 years	610 (64.1)	342 (35.9)	952 (38.3)
41–64 years	300 (53.5)	261 (46.5)	561 (22.6)
≥ 65 years	252 (53.8)	216 (46.2)	468 (18.8)
Total	1442 (58.0)	1044 (42.0)	2486 (100)

The distribution of ESKAPE pathogens differed significantly according to age, gender, year, clinical unit, and specimen type ($p < 0.001$ for all comparisons). In the age-based analysis, *K. pneumoniae* was the most frequently isolated pathogen across all age groups, particularly in the 18–40 [393/2,486 (15.8%)] and 41–64 [249/2,486 (10.0%)] age groups. *S. aureus* was more commonly detected in the ≤ 17 [168/2,486 (6.8%)] and 18–40 [268/2,486 (10.8%)] age groups. *P. aeruginosa* and *A. baumannii* showed a more balanced distribution across age groups.

In the gender-based analysis, pathogens were generally isolated at higher rates in males, with *K. pneumoniae* [600/2,486 (24.1%)] and *P. aeruginosa* [329/2,486 (13.2%)] being more frequently detected in male patients. A significant difference was observed in the distribution by years ($p < 0.001$); *Enterobacter* spp. showed an increase in 2025 [73/2,486 (2.9%)], whereas a decrease was noted in *A. baumannii*. The distribution of other pathogens remained relatively stable.

According to clinical units, *S. aureus* [297/2,486 (11.9%)] and *K. pneumoniae* [294/2,486 (11.8%)] were most frequently isolated in outpatient clinics, whereas *K. pneumoniae* was the most common pathogen in ICUs [345/2,486 (13.9%)] and inpatient wards [390/2,486 (15.7%)], respectively.

Based on specimen type, *K. pneumoniae* was more frequently isolated from urine [324/2,486 (13.0%)] and wound samples [230/2,486 (9.3%)], while *P. aeruginosa* was also commonly detected in urine [142/2,486 (5.7%)] and wound samples [126/2,486 (5.1%)]. *S. aureus* was predominantly isolated from wound [389/2,486 (15.6%)] and blood samples [107/2,486 (4.3%)]. In contrast, *A. baumannii* [49/2,486 (2.0%)] and *Enterobacter* spp. [27/2,486 (1.1%)] were predominantly associated with respiratory specimens, particularly tracheal aspirates (Table 3).

MDR, XDR, and PDR phenotypes showed a heterogeneous distribution among pathogens. The highest MDR rate was observed in *A. baumannii* [135/138 (97.8%)], followed by *Enterobacter* spp. [71/84 (84.5%)]

Table 3 Demographic and clinical characteristics of isolates (n, %)

Age groups ($p < 0.001$)	<i>A. baumannii</i>	<i>Enterobacter</i> <i>spp.</i>	<i>E. faecium</i>	<i>K. pneumoniae</i>	<i>P. aeruginosa</i>	<i>S. aureus</i>
≤ 17	32 (1.3)	15 (0.6)	27 (1.1)	145 (5.8)	118 (4.7)	168 (6.8)
18–40	52 (2.1)	36 (1.4)	23 (0.9)	393 (15.8)	180 (7.2)	268 (10.8)
41–64	29 (1.2)	12 (0.5)	25 (1.0)	249 (10.0)	114 (4.6)	132 (5.3)
≥ 65	25 (1.0)	21 (0.8)	27 (1.1)	246 (9.9)	88 (3.5)	61 (2.5)
Gender ($p < 0.001$)						
Female	54 (2.2)	31 (1.2)	44 (1.8)	433 (17.4)	171 (6.9)	311 (12.5)
Male	84 (3.4)	53 (2.1)	58 (2.3)	600 (24.1)	329 (13.2)	318 (12.8)
Years ($p < 0.001$)						
2024	88 (3.5)	11 (0.4)	47 (1.9)	548 (22.0)	255 (10.3)	343 (13.8)
2025	50 (2.0)	73 (2.9)	55 (2.2)	485 (19.5)	245 (9.9)	286 (11.5)
Hospital departments ($p < 0.001$)						
Outpatient clinic	13 (0.5)	10 (0.4)	26 (1.0)	294 (11.8)	169 (6.8)	297 (11.9)
Intensive care unit	94 (3.8)	52 (2.1)	29 (1.2)	345 (13.9)	151 (6.1)	85 (3.4)
Inpatient ward	30 (1.2)	22 (0.9)	47 (1.9)	390 (15.7)	179 (7.2)	240 (9.7)
Emergency department	1 (0.0)	0 (0.0)	0 (0.0)	4 (0.2)	1 (0.0)	7 (0.3)
Sample type ($p < 0.001$)						
Abscess	0 (0.0)	2 (0.1)	1 (0.0)	8 (0.3)	6 (0.2)	27 (1.1)
Sputum	11 (0.4)	4 (0.2)	0 (0.0)	120 (4.8)	27 (1.1)	5 (0.2)
Cerebrospinal fluid	1 (0.0)	1 (0.0)	0 (0.0)	4 (0.2)	4 (0.2)	1 (0.0)
Tracheal aspirate culture	49 (2.0)	27 (1.1)	0 (0.0)	177 (7.1)	78 (3.1)	17 (0.7)
Urine	14 (0.6)	9 (0.4)	38 (1.5)	324 (13.0)	142 (5.7)	20 (0.8)
Blood	37 (1.5)	18 (0.7)	34 (1.4)	101 (4.1)	47 (1.9)	107 (4.3)
Wound	20 (0.8)	22 (0.9)	23 (0.9)	230 (9.3)	126 (5.1)	389 (15.6)
Peritoneal fluid/Pleural fluid	5 (0.2)	1 (0.0)	5 (0.2)	44 (1.8)	13 (0.5)	15 (0.6)
Catheter	1 (0.0)	0 (0.0)	0 (0.0)	6 (0.2)	4 (0.2)	14 (0.6)
Other (Ear, throat, vagina, nasal swab, joint fluid, drainage fluids, etc.)	0 (0.0)	0 (0.0)	1 (0.0)	19 (0.8)	53 (2.1)	34 (1.4)

and *K. pneumoniae* [764/1,033 (74.0%)]. The XDR phenotype was most prominent in *A. baumannii* [97/138 (70.3%)], while lower rates were detected in *Enterobacter* spp. [42/84 (50.0%)] and *K. pneumoniae* [362/1,033 (35.0%)]. XDR rates were lower in Gram-positive pathogens, including *E. faecium* [10/102 (9.8%)] and *S. aureus* [126/629 (20.0%)]. In *P. aeruginosa*, MDR [158/500 (31.6%)] and XDR [50/500 (10.0%)] rates were relatively lower. The PDR phenotype was rare across all pathogens, with the highest rate observed in *A. baumannii* [7/138 (5.1%)] (Fig. 2).

Using a classification in which both intermediate (I) and resistant (R) results were considered resistant at the antimicrobial-class level, the estimated MDR prevalence decreased from 61.8% in 2024 to 57.4% in 2025 ($p = 0.026$). In contrast, the estimated XDR prevalence declined from 33.4% to 30.7%, but this difference was not statistically significant ($p = 0.161$). Compared with 2024, isolates obtained in 2025 showed lower odds of being classified as MDR (OR = 0.83, 95% CI 0.71–0.98), whereas no significant temporal difference was observed for XDR (OR = 0.88, 95% CI 0.75–1.05) (Table 4).

When the antimicrobial susceptibility profile was evaluated, distinct resistance patterns were identified among ESKAPE pathogens (Table 5). In *A. baumannii* isolates, high resistance rates to broad-spectrum antibiotics were notable, with particularly elevated resistance to ceftazidime (92.8%), cefepime (84.1%), ciprofloxacin (83.3%), and trimethoprim-sulfamethoxazole (87.7%). In addition, carbapenem resistance was also high (71.7%).

In *K. pneumoniae*, marked resistance was observed against third-generation cephalosporins (67.8% for ceftazidime; 63.8% for ceftriaxone) and trimethoprim-sulfamethoxazole (65.1%). Although carbapenem susceptibility remained relatively preserved (75.4%), resistance rates were still considerable.

In *P. aeruginosa*, low resistance rates were detected for amikacin (14.2%) and meropenem (16.4%), whereas higher resistance was observed against cephalosporins. Among Gram-positive pathogens, *S. aureus* showed high resistance to penicillin (92.2%), while vancomycin (99.0%), teicoplanin (96.5%), and linezolid (98.9%) retained their effectiveness. Similarly, *E. faecium* demonstrated high susceptibility to linezolid (100%) and vancomycin (95.1%). The preserved activity of vancomycin and

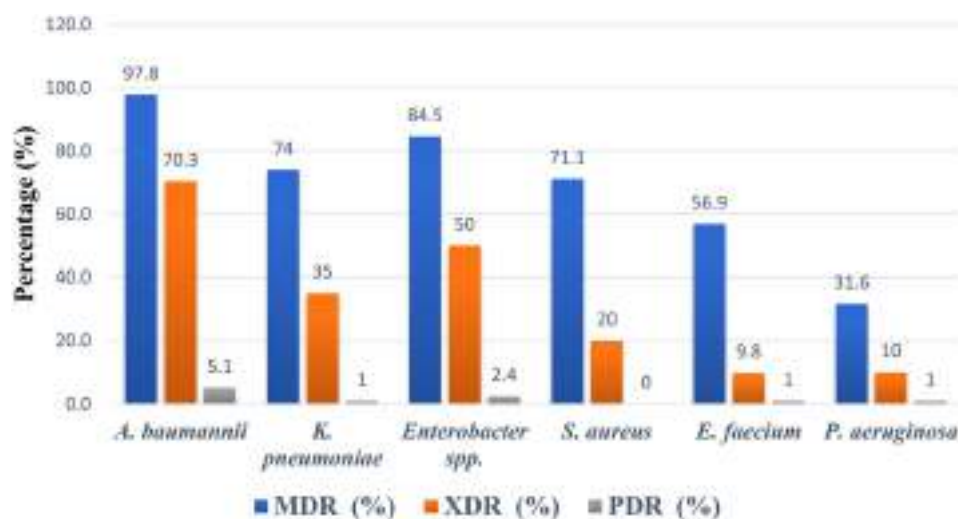


Fig. 2 Distribution of Multidrug-Resistant (MDR), Extensively Drug-Resistant (XDR), and Pan-Drug-Resistant (PDR) phenotypes across ESKAPE pathogens

Table 4 Temporal comparison of MDR and XDR prevalence among ESKAPE pathogens between 2024 and 2025

Variable	Years		p-value
	2024	2025	
MDR n/N (%)	799/1292 (61.8%)	685/1194 (57.4%)	0.026
XDR n/N (%)	431/1292 (33.4%)	366/1194 (30.7%)	0.161
Result	OR	%95 CI	p-değeri
MDR	0.83	0.71–0.98	0.023
XDR	0.88	0.75–1.05	0.149

linezolid is clinically important, as these agents remain key treatment options for severe infections caused by resistant Gram-positive pathogens. In *Enterobacter* spp., high resistance to β -lactam antibiotics was observed (Table 5). Despite the high MDR prevalence, susceptibility to certain reserve agents remained relatively preserved, which may reflect the predominance of inducible AmpC β -lactamase-mediated resistance mechanisms in *Enterobacter* spp.

When *A. baumannii* was compared with other isolates using univariate binary logistic regression analysis, *A. baumannii* isolation was found to be significantly associated with ICU admission, with approximately 5.4-fold higher odds of isolation in ICU patients (OR=5.441, 95% CI: 3.762–7.870; $p<0.001$). *P. aeruginosa* isolation was associated with male gender, with approximately 1.5-fold higher odds in males (OR=1.509, 95% CI: 1.229–1.852; $p<0.001$). *S. aureus* isolation was associated with female gender, with approximately 1.5-fold higher odds in females (OR=1.500, 95% CI: 1.250–1.799; $p<0.001$). For *S. aureus*, the odds of isolation in ICU patients were 72.4% lower compared with other clinical units (OR=0.276, 95% CI: 0.216–0.354; $p<0.001$). No significant association was found between *K. pneumoniae* isolation and age group, gender, or clinical unit ($p>0.05$). *Enterobacter* spp. isolation was associated with ICU admission, with approximately 3.9-fold higher

odds in ICU patients (OR=3.919, 95% CI: 2.502–6.141; $p<0.001$). *E. faecium* isolation was more frequent in patients aged ≥ 65 years, with approximately 1.6-fold higher odds compared with other age groups (OR=1.586, 95% CI: 1.009–2.492; $p=0.045$) (Table 6).

Discussion

In our study, the proportion of ESKAPE pathogens was found to be 29.6%. In Africa, the prevalence of ESKAPE pathogens is reported to be highest in West Africa (77.3%), followed by Central Africa (43.5%) and East Africa (25.1%) [17]. Considering that Somalia is located in East Africa, our findings appear broadly comparable to reports from this region; however, differences in study design, specimen selection, healthcare settings, and inclusion criteria should be considered when interpreting prevalence estimates. In the literature, these rates are known to vary widely depending on the center, specimen type, and patient population [18–21].

In this study, a clear predominance of Gram-negative bacteria (70.7%) was observed among ESKAPE pathogens (Fig. 1). This finding is consistent with studies emphasizing the increasing role of Gram-negative pathogens, particularly in hospital-associated infections [4, 18, 22, 23]. However, some studies have reported higher proportions of Gram-positive bacteria [24, 25], and these differences

Table 5 Antibiotic susceptibility, resistance numbers and percentages (%) of isolates

Antibiotics	R S	<i>A. baumannii</i> N=138	<i>Enterobacter spp.</i> N=84	<i>E. faecium</i> N=102	<i>K. pneumoniae</i> N=1033	<i>P. aeruginosa</i> N=500	<i>S. aureus</i> N=629
Amikacin	R S	85 (61.6) 53 (38.4)	45 (53.6) 39 (46.4)	- -	251 (24.3) 782 (75.7)	71 (14.2) 429 (85.8)	0 (0.0) 629 (100)
Penicillin	R S	- -	- -	- -	- -	- -	580 (92.2) 49 (7.8)
Amoxicillin-Clavulanic Acid	R S	- -	79 (94.0) 5 (6.0)	- -	729 (70.6) 304 (29.4)	- -	- -
Ampicillin	R S	- -	- -	65 (63.7) 37 (36.3)	- -	- -	- -
Ampicillin-sulbactam	R S	107 (77.5) 31 (22.5)	- -	- -	635 (61.5) 398 (38.5)	- -	- -
Daptomycin	R S	- -	- -	- -	- -	- -	9 (1.4) 620 (98.6)
Erythromycin	R S	- -	- -	- -	- -	- -	360 (57.2) 269 (42.8)
Fusidic acid	R S	- -	- -	- -	- -	- -	130 (20.7) 499 (79.3)
Gentamicin	R S	101 (73.2) 37 (26.8)	49 (58.3) 35 (41.7)	- -	381 (36.9) 652 (63.1)	126 (25.2) 374 (74.8)	204 (32.4) 425 (67.6)
Gentamicin (High-Level)	R S	- -	- -	61 (59.8) 41 (40.2)	- -	- -	- -
Clindamycin	R S	- -	- -	- -	- -	- -	85 (13.5) 544 (86.5)
Levofloxacin	R S	- -	- -	35 (34.3) 67 (65.7)	- -	- -	- -
Linezolid	R S	- -	- -	0 (0.0) 102 (100)	- -	- -	7 (1.1) 622 (98.9)
Meropenem	R S	99 (71.7) 39 (28.3)	50 (59.5) 34 (40.5)	- -	254 (24.6) 779 (75.4)	82 (16.4) 418 (83.6)	- -
Piperacillin-Tazobactam	R S	- -	59 (70.2) 25 (29.8)	- -	- -	120 (24) 380 (76)	- -
Cefepime	R S	116 (84.1) 22 (15.9)	65 (77.4) 19 (22.6)	- -	570 (55.2) 463 (44.8)	315 (63) 185 (37)	- -
Cefoxitin	R S	- -	- -	- -	- -	- -	266 (42.3) 363 (57.7)
Ceftazidime	R S	128 (92.8) 10 (7.2)	69 (82.1) 15 (17.9)	- -	700 (67.8) 333 (32.2)	263 (52.6) 237 (47.4)	- -
Ceftriaxone	R S	- -	67 (79.8) 17 (20.2)	- -	659 (63.8) 374 (36.2)	- -	- -
Ciprofloxacin	R S	115 (83.3) 23 (16.7)	54 (64.3) 30 (35.7)	74 (72.5) 28 (27.5)	464 (44.9) 569 (55.1)	139 (27.8) 361 (72.2)	122 (19.4) 507 (80.6)
Teicoplanin	R S	- -	- -	- -	- -	- -	22 (3.5) 607 (96.5)
Tetracycline	R S	- -	- -	- -	- -	- -	402 (63.9) 227 (36.1)
Trimethoprim-sulfamethoxazole	R S	121 (87.7) 17 (12.3)	56 (66.7) 28 (33.3)	53 (52) 49 (48)	672 (65.1) 361 (34.9)	- -	184 (29.3) 445 (70.7)
Vancomycin	R S	- -	- -	5 (4.9) 97 (95.1)	- -	- -	6 (1.0) 623 (99.0)

R: Resistance, S: Sensitive, -: Not applicable

are likely related to variations in patient profiles, clinical settings, and specimen types.

In our study, the most frequently isolated pathogen was *K. pneumoniae* (41.6%) (Fig. 1). This finding is in agreement with studies conducted in different countries [22, 26–30]. In contrast, a meta-analysis reported

that *S. aureus* was the predominant pathogen in countries such as Ethiopia (21.5%), Nigeria (45.7), and Cameroon (42.2) [17], as well as in India (34.4%) [1] and Iran (30%) [25], highlighting the variability in pathogen distribution across different settings. The marked predominance of *K. pneumoniae* could be associated with

Table 6 Univariate binary logistic regression analysis of demographic and clinical factors associated with isolates

Variables		B	OR (Exp(B))	%95 GA	p
<i>A. baumannii</i> vs. Other isolates	ICUs vs. Others	1.694	5.441	3.762–7.870	< 0.001
<i>P. aeruginosa</i> vs. Other isolates	Gender	-0.412	0.663	0.540–0.813	< 0.001
<i>S. aureus</i> vs. Other isolates	Gender	-0.405	0.667	0.556–0.800	< 0.001
<i>S. aureus</i> vs. Other isolates	ICUs vs. Others	-1.287	0.276	0.216–0.354	< 0.001
<i>Enterobacter</i> spp. vs. Other isolates	ICUs vs. Others	1.366	3.919	2.502–6.141	< 0.001
<i>E. faecium</i> vs. Other isolates	Age ≥ 65 years vs. Others	0.461	1.586	1.009–2.492	0.045

OR (Exp(B)): Odds Ratio (Exponentiated Beta coefficient); B: Regression coefficient; ICUs: Intensive Care Units

its high colonization capacity, transmission related to invasive procedures, and selective pressure resulting from broad-spectrum antibiotic use. In Somalia, limited antimicrobial stewardship practices, widespread empirical antibiotic use, and restricted access to susceptibility-guided therapy may also contribute to the persistence and dissemination of resistant *K. pneumoniae* strains.

In our study, a higher proportion of ESKAPE-positive isolates was observed among male patients, and the gender-based distribution difference was statistically significant ($\chi^2=28.21$, $p < 0.001$) (Table 1). In addition, the association between age group and gender distribution was also significant ($\chi^2=12.26$, $p = 0.0066$), with male predominance being particularly evident in the 18–40 years age group (Table 2). However, univariate logistic regression analysis demonstrated that gender-related associations differed according to pathogen type, with male gender associated with *P. aeruginosa* and female gender associated with *S. aureus* isolation (Table 6). These findings suggest that the higher isolation rates observed among males may be partially influenced by the age composition and clinical characteristics of the study population. This finding is broadly consistent with the literature reporting a higher incidence of bacteremia in males [29, 31, 32]. However, it should be considered that this association may vary depending on the study population and clinical characteristics. In the subgroup analysis, *K. pneumoniae* and *P. aeruginosa* were found to be more prevalent in both genders, whereas *S. aureus* exhibited a more balanced distribution (Table 3). The literature also indicates that pathogen distribution may vary according to gender [30, 33, 34]. This variability could be associated with differences in immunological status, comorbidities, and the frequency of invasive procedures.

When evaluated by age groups, the predominance of the 18–64 age group (Tables 1 and 2) is consistent with the literature [20, 33], although some studies have reported higher rates in the ≥ 65 age group [29]. These findings may be associated with the widespread use of urinary catheters, the high prevalence of urinary tract and skin-soft tissue infections, frequent invasive procedures, and increased healthcare exposure. These differences could be related to age-related immune changes, chronic disease burden, and differences in healthcare

exposure. In addition, differences in healthcare utilization patterns and delayed access to healthcare services in Somalia may also influence the demographic distribution of resistant pathogens.

In our study, ESKAPE pathogens were most frequently isolated from wound (32.6%) and urine samples (22.0%) (Table 1). This distribution is consistent with studies conducted in different countries, where ESKAPE isolates are commonly reported to originate primarily from urine and wound/pus samples [3, 19, 20, 35, 36]. This distribution may reflect the widespread use of urinary catheters, the frequency of urinary tract and wound infections, invasive procedures, and increased contamination risk in hospital settings. These findings may also reflect infection prevention and control challenges frequently encountered in resource-limited healthcare settings such as Somalia.

When pathogen distribution was analyzed according to specimen type, *K. pneumoniae* was most frequently isolated from urine, wound, and tracheal aspirate samples, whereas *S. aureus* was more commonly detected in wound and blood samples (Table 3). Similarly, previous studies have reported that *K. pneumoniae* is more frequently isolated from respiratory tract and urine samples, while *S. aureus* is more commonly identified in wound/pus samples and in some blood culture series [3, 24, 26, 31, 35–37]. This distribution may be associated with differences in infection source, frequency of invasive procedures, colonization patterns, and healthcare exposure in hospital environments.

In the analysis by clinical units, ESKAPE pathogens were most frequently isolated from inpatient wards (36.5%) (Table 1). This finding is consistent with the study by Pipitò et al. (2025) [32]. In our study, *K. pneumoniae* was the most commonly detected pathogen in both inpatient wards and ICUs (Table 3). This observation is in line with studies reporting that ICUs represent important reservoirs for multidrug-resistant Gram-negative bacteria [26, 38]. Consistent with these findings, univariate logistic regression analysis demonstrated significant associations between ICU admission and the isolation of *A. baumannii* and *Enterobacter* spp. (Table 6). This distribution may reflect the high frequency of invasive procedures, extensive broad-spectrum antibiotic use, and increased colonization pressure in hospital settings.

When resistance profiles were evaluated, *A. baumannii* was found to be at the center of the resistance burden, with MDR (97.8%) and XDR (70.3%) rates (Fig. 2). This finding is consistent with studies identifying this pathogen as one of the most problematic members of the ESKAPE group globally [4, 23, 30, 39, 40]. In particular, carbapenem resistance and the presence of multiple resistance genes severely limit treatment options [41, 42]. This high level of resistance could be associated with resistance mechanisms previously reported for *A. baumannii*, including carbapenemase production and dissemination of high-risk clones [41–43]. Additionally, prolonged hospitalization in ICUs, invasive procedures, widespread use of broad-spectrum antibiotics, and increased colonization pressure may contribute to this situation. In Somalia, over-the-counter accessibility of antibiotics and inconsistent regulation of antimicrobial use may contribute to selective pressure and the emergence of multidrug-resistant organisms. The high resistance burden observed in *A. baumannii* may considerably complicate empirical treatment decisions, particularly in critically ill patients. Furthermore, limited access to reserve antibiotics in Somalia may contribute to prolonged hospitalization, increased healthcare costs, and adverse clinical outcomes.

Temporal analysis revealed a significant decrease in MDR prevalence between 2024 and 2025, while XDR prevalence remained relatively stable (Table 4). Although this finding may reflect changes in antimicrobial use or infection control practices over time, the persistently high resistance rates continue to represent a major clinical concern. Ongoing surveillance is needed to better understand longitudinal resistance dynamics among ESKAPE pathogens.

The high MDR rates observed for *Enterobacter* spp. (84.5%) and *K. pneumoniae* (74.0%) (Fig. 2) are consistent with studies demonstrating that these pathogens can rapidly develop multidrug resistance due to their diverse resistance mechanisms [44]. In our study, *Enterobacter* spp. isolates exhibited high resistance rates to third-generation cephalosporins and cefepime (Table 5), which is associated with the production of inducible AmpC β -lactamases. Indeed, it is well established that AmpC-producing Enterobacteriaceae commonly develop resistance to broad-spectrum β -lactams [45], and recent studies have shown that this resistance is largely associated with chromosomal AmpC enzymes [46]. Furthermore, studies focusing on ESKAPE pathogens have highlighted the increasing resistance of *Enterobacter* spp. to multiple antibiotic classes [19–21].

High resistance rates were observed in *K. pneumoniae* isolates against third-generation cephalosporins, trimethoprim-sulfamethoxazole, and certain β -lactam/ β -lactamase inhibitor combinations (Table 5). This finding

may reflect β -lactamase-mediated resistance mechanisms, particularly extended-spectrum β -lactamases (ESBLs) [47]. Similarly, Benkő et al. (2020) [35] reported low susceptibility to β -lactam antibiotics, supporting our results. In the literature, studies by Jawade et al. (2024) [48] and Kharat et al. (2024) [49] have also emphasized high resistance rates to various antibiotic groups, especially β -lactams, and their association with β -lactamase genes. Data reported from Türkiye likewise demonstrate high resistance to cephalosporins and an increasing trend of carbapenem resistance in *K. pneumoniae* over time [27]. In contrast, some studies have reported lower resistance rates [50], which may be explained by geographical and clinical variations. Although susceptibility to carbapenems remained relatively preserved in our study [51, 52], the high resistance rates to third-generation cephalosporins and trimethoprim-sulfamethoxazole may reduce the effectiveness of commonly used empirical regimens and increase reliance on carbapenems or other reserve agents. However, increasing reliance on carbapenems may accelerate the emergence of carbapenem-resistant strains in the future, highlighting the importance of antimicrobial stewardship programs to preserve the effectiveness of these agents. This apparent discrepancy between high MDR prevalence and retained susceptibility to certain agents may be explained by the predominance of resistance mechanisms targeting β -lactams and fluoroquinolones, while carbapenem resistance mechanisms may not yet be fully established in all isolates. Overall, our findings suggest that *K. pneumoniae* remains a significant therapeutic challenge, particularly in relation to β -lactams and trimethoprim-sulfamethoxazole.

The relatively lower MDR (31.6%) and XDR (10.0%) rates observed in *P. aeruginosa* (Fig. 2) compared to other Gram-negative pathogens are consistent with studies reporting relatively preserved susceptibility patterns in this organism [53]. However, the ability of *P. aeruginosa* to rapidly develop resistance to newly introduced antibiotics represents a significant clinical concern [54]. In our study, *P. aeruginosa* isolates showed relatively preserved susceptibility to carbapenems, aminoglycosides, and piperacillin-tazobactam, whereas moderate resistance was observed against cephalosporins and fluoroquinolones (Table 5). This resistance pattern may reflect intrinsic resistance mechanisms, β -lactamase production, and efflux pump systems, and is further supported by reports of ESBL and MBL production by Pandey et al. (2021) [55].

The literature also indicates an increasing trend of resistance to β -lactams and fluoroquinolones, with high resistance rates reported particularly for cephalosporins and ciprofloxacin [27, 50]. Moreover, an overall increase in resistance to multiple antibiotic classes among ESKAPE pathogens has been emphasized [48, 49]. In contrast, the

relatively preserved susceptibility to carbapenems and aminoglycosides [55] suggests that these agents may still remain effective treatment options. Nevertheless, considering that MDR/XDR strains constitute a significant proportion in intensive care settings [26] and that notable XDR rates have been reported in Türkiye (10.1%) [30], *P. aeruginosa* continues to pose a substantial risk in terms of resistance development.

Overall, these findings highlight the clinical importance of emerging resistance to β -lactams and fluoroquinolones in *P. aeruginosa*, while the relatively preserved susceptibility to carbapenems and aminoglycosides provides a therapeutic advantage. However, the presence of MDR/XDR strains limits empirical treatment options and underscores the need for continuous surveillance.

In contrast to Gram-negative pathogens, lower XDR rates were observed among Gram-positive isolates, including *E. faecium* (9.8%) and *S. aureus* (20.0%) (Fig. 2). These findings are consistent with the literature indicating that resistance levels in this group are generally lower than those observed in Gram-negative bacteria [55]. In our study, *S. aureus* isolates showed high resistance to penicillin (92.2%), while relatively preserved susceptibility was observed for agents such as clindamycin (86.3%), ciprofloxacin (80.1%), and trimethoprim-sulfamethoxazole (70.7%). In addition, advanced therapeutic options, including linezolid (98.9%), vancomycin (99%), and teicoplanin (96.5%), demonstrated high effectiveness (Table 5). These findings indicate that β -lactam resistance is widespread in *S. aureus*, whereas glycopeptides and oxazolidinones largely retain their activity.

Similarly, the literature reports high β -lactam resistance and the increasing prevalence of multiple resistance mechanisms in *S. aureus* [27, 48, 49]. In a study conducted in India by Emamie et al. (2023) [25], high rates of Methicillin-resistant *Staphylococcus aureus* (MRSA) (71%) and MDR (79%) were reported, while the effectiveness of linezolid and vancomycin was preserved. In our study, the MRSA rate was found to be 42.3% (Table 5). A meta-analysis conducted in 2022 reported that MRSA prevalence varies by region, with rates of 49.6% (95% CI: 37.4–61.7) in Africa, 56.6% in the Eastern Mediterranean region, and 63.2% in the Western Pacific region, whereas a relatively lower rate of 41.0% was observed in South-east Asia [18]. These differences could be associated with regional variations in healthcare infrastructure, antibiotic usage practices, and infection control measures.

In *E. faecium* isolates, marked resistance to ampicillin (63.7%) and high-level gentamicin resistance (59.8%) were observed, while susceptibility to linezolid (100%) and vancomycin (95.1%) remained largely preserved (Table 5). These findings indicate that *E. faecium* offers limited treatment options against β -lactams and aminoglycosides, whereas advanced agents remain effective.

Similarly, the literature reports high resistance to ampicillin and aminoglycosides, with largely preserved activity of linezolid and vancomycin [30, 48, 49]. In addition, a study from India reporting a vancomycin-resistant enterococci (VRE) rate of 19% highlights the clinical significance of increasing glycopeptide resistance among enterococci [25].

Although overall PDR rates were low and consistent with the literature, the higher rate observed in *A. baumannii* (Fig. 2) further emphasizes the remarkable capacity of this pathogen to develop advanced levels of resistance [44].

This study has several limitations. First, the retrospective and single-center laboratory-based design may limit the generalizability of the findings to other healthcare settings in Somalia. Second, only culture-positive ESKAPE isolates were included, and detailed clinical data such as patient outcomes, comorbidities, prior antibiotic exposure, duration of hospitalization, and mortality were not available. In addition, although duplicate isolates from the same patient were excluded whenever possible, the retrospective laboratory-based design may still carry a risk of residual duplicate inclusion or contamination. Another limitation is the lack of differentiation between community-acquired and hospital-acquired infections. Furthermore, molecular characterization of resistance genes and clonal relationships was not performed; therefore, the underlying resistance mechanisms and dissemination of resistant clones could not be fully evaluated. Finally, antimicrobial susceptibility testing was performed using conventional phenotypic methods, and automated identification or molecular confirmation methods were not routinely available during the study period.

Conclusion

In this study, the distribution and antimicrobial resistance profiles of ESKAPE pathogens isolated in a tertiary healthcare center in Somalia were comprehensively evaluated. The findings indicate a high burden of resistance, particularly among Gram-negative bacteria. While *K. pneumoniae* and *S. aureus* were the most frequently isolated pathogens, the resistance burden was primarily concentrated in *A. baumannii*. The high MDR and XDR rates observed in this pathogen pose a significant threat to clinical management. In contrast, the largely preserved susceptibility of Gram-positive pathogens to glycopeptides and linezolid represents an important therapeutic advantage. Furthermore, pathogen distribution was found to be more strongly associated with specimen type and clinical unit than with demographic factors, supporting the determining role of the anatomical site of infection and clinical context.

In conclusion, these findings highlight the need to revise empirical treatment strategies based on local surveillance data. Strengthening infection control measures, particularly in high-risk clinical units, and effectively implementing antimicrobial stewardship programs are of critical importance.

Abbreviations

AMR	Antimicrobial resistance
<i>E. coli</i>	<i>Escherichia coli</i>
<i>S. aureus</i>	<i>Staphylococcus aureus</i>
<i>K. pneumoniae</i>	<i>Klebsiella pneumoniae</i>
<i>S. pneumoniae</i>	<i>Streptococcus pneumoniae</i>
<i>A. baumannii</i>	<i>A. baumannii</i>
<i>P. aeruginosa</i>	<i>Pseudomonas aeruginosa</i>
MDR	Multidrug resistance
<i>E. faecium</i>	<i>E. faecium</i>
ESKAPE	<i>E. faecium</i> , <i>S. aureus</i> , <i>K. pneumoniae</i> , <i>A. baumannii</i> , <i>P. aeruginosa</i> , and <i>Enterobacter spp.</i>
GLASS	Antimicrobial Resistance and Use Surveillance System
WHO	World Health Organization
CSF	Cerebrospinal Fluid
EMB	Eosin Methylene Blue
CLSI	Clinical and Laboratory Standards Institute
ATCC	American Type Culture Collection
XDR	Extensively drug-resistant
PDR	Pan-drug-resistant
ESBLs	Extended-spectrum β -lactamases
MRSA	Methicillin-resistant <i>Staphylococcus aureus</i>
VRE	Vancomycin-resistant enterococci
CI	Confidence Interval
ICUs	Intensive Care Units

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Author contributions

SD, SMM, IMO, RYHM, LAN, and AK contributed to the conceptualization and design of the study. Data acquisition was performed by SD, RYHM, LAN, and SMM. Statistical analysis and interpretation were carried out by AD, ZO, and SD. The original manuscript draft was prepared by ZO and SD, while AD and AK critically reviewed and revised the manuscript for important intellectual content. AD, AK, LAN, IMO, and SMM also contributed to the statistical analysis, methodology, study design, and literature review. All authors read and approved the final version of the manuscript and agree to be accountable for all aspects of the work.

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Data availability

All data generated or analyzed during this study are included in this published article.

Declarations

Ethics approval and consent to participate

The research protocols were approved by the Ethics Committee of Mogadishu Somali Türkiye Recep Tayyip Erdoğan Training and Research Hospital (Date: 06.09.2025; Decision No: 1282; Reference No: MSH/23020). Due to the retrospective nature of the study and the use of anonymized patient records, the requirement for informed consent to participate was waived by the Ethics Committee. The study was conducted in accordance with the Declaration of Helsinki.

Consent for publication

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Competing interests

The authors declare no competing interests.

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