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Antibiotic resistance patterns among bacterial pathogens isolated from bloodstream infections at the Maternal and Child Health Hospital, Kumasi, Ghana

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Background: Bloodstream infections remain a major public health concern globally and are increasingly associated with multidrug-resistant bacterial pathogens. Limited data on antimicrobial resistance patterns among bloodstream isolates in Ghana hinder appropriate empirical therapy, particularly in maternal and child health settings. The study aimed to assess the prevalence, bacterial causes, and antibiotic resistance patterns of bloodstream infections, including multidrug resistance, extensively drug-resistance, pandrug-resistance, extended-spectrum β-Lactamase and carbapenemase-producing pathogens, and their association with patient demographics at the Maternal and Child Health Hospital, Kumasi, Ghana.

Methodology: A hospital-based cross-sectional study was conducted from July to September 2025 at the Maternal and Child Health Hospital. Blood samples were collected from 229 suspected bloodstream infection patients referred for culturing and susceptibility testing, and were cultured using the BD BACTEC automated system. Isolates were identified and tested for antibiotic susceptibility using the Phoenix BD BACTEC automated machine. Data were analysed using Stata version 15, applying descriptive and logistic regression analyses with significance set at $p<0.05$.

Results: Out of 229 participants, 61.6% had positive blood cultures. Among the Gram negatives, *Escherichia coli* (22.7%) and *Klebsiella* species (13.5%) were the predominant isolates. Coagulase-negative staphylococci (16.3%) and *Staphylococcus aureus* (14.9%) were the major Gram-positive causing bloodstream infections. The highest resistance was recorded against cefazolin (54.6%) and ceftriaxone (45.4%), while amikacin (3.5%) and daptomycin (4.3%) showed the greatest efficacy. ESBL and carbapenemase production among the Gram-negative isolates were observed in 27.2% and 12.0% of isolates,

respectively. Overall, 96.5% of isolates exhibited some form of resistance, with 81.6% classified as multidrug resistant, 8.5% as extensively drug-resistant, and 5.0% as pandrug-resistant. Longer hospital stays significantly increased infection risk (aPR=2.86; 95% CI: 1.92–4.27; p<0.001).

Conclusion: The high prevalence of multidrug resistant bloodstream pathogens at the Maternal and Child Health Hospital, particularly *Staphylococcus* and *Escherichia coli*, underscores the urgent need for enhanced infection prevention, antimicrobial stewardship, and periodic surveillance of resistance patterns to guide effective empirical therapy.

KEYWORDS

bloodstream infection, antibiotics resistance, multidrug resistance, extended-spectrum b-Lactamase, carbapenemase

Introduction

Bloodstream infections (BSIs) are usually confirmed by a positive blood culture in individuals exhibiting systemic signs of infection (Timsit et al., 2020; Deku et al., 2025). BSIs can be categorised as secondary when linked to a known infection site or as primary when no clear source is identified (Timsit et al., 2020). BSIs are frequently encountered in hospital environments, pose significant life-threatening risks, and are becoming increasingly prevalent (Holmes et al., 2025). With regard to bacterial agents causing BSIs, a 2024 review by a 2014 renew by Homes et al. (2025) highlighted the leading causes, which include bacteria such as *Escherichia coli, Staphylococcus aureus*, Coagulase-Negative Staphylococci (CoNs) and *Klebsiella pneumoniae*. These microorganisms have unique mechanisms that enable colonisation, survival, and dissemination in the bloodstream (Holmes et al., 2025). Also, a study analysing bloodstream infection records from 2019 to 2021 in a specialised hospital found bacterial BSIs prevalence at 14.8%, with Gram-negative bacteria making up about 63.5% of cases. *K. pneumoniae, S. aureus*, and *E. coli* were common isolates (Deress et al., 2025).

Antibiotic resistance (ABR) among bacterial pathogens isolated from BSIs presents a formidable challenge to global health, complicating effective treatment and leading to increased morbidity and mortality (Allel et al., 2023). The primary bacterial agents involved in BSIs include Gram-negative bacteria as well as Gram-positive bacteria. These pathogens frequently exhibit multidrug resistance, showing resistance to key antibiotic classes such as carbapenems, cephalosporins, and fluoroquinolones (Zhang et al., 2022; Bitew et al., 2023; Donkor et al., 2023). Alarmingly, around 60.9% of blood pathogens isolated in a study at University of Gondar Comprehensive Specialised Hospital, Ethiopia by Deress et al (Deress et al., 2025). showed multidrug resistance, particularly *Klebsiella* and *E. coli* species, underscoring the challenges in treatment in resource-limited settings. Another multicentre study in France by Pilmis and Dortet (2025) in a retrospective study confirmed the high burden and prevalence of drug-resistant pathogens in BSIs.

Approximately 9.3% to 11.2% of hospitalised patients in Ghana are estimated to have a BSI, which is an extremely high prevalence (Deku et al., 2019). In addition, Boakye-Yiadom et al (2023) reported limited local data on antibiotic susceptibility patterns in a tertiary hospital which hinders clinicians' decision-making regarding empirical therapy for BSIs. Also, most clinical facilities in Ghana and other Low- and Middle-Income Countries (LMICs) do not have clinical microbiology laboratories for testing prior to administration of antibiotics, hence rely on empirical treatment with broad-spectrum antibiotics. As a deeply rooted problem in the healthcare delivery system in such LMICs, the clinical decision making can only be improved if guided by relevant local data. Hence, there is a need for periodic research to describe common patterns of resistance and predominant microbes.

In light of these, this current research focused on the prevalence of BSIs and the antibiotics susceptibility testing of pathogens causing these infections at the Maternal and Child Health Hospital (MCHH) in Kumasi. The findings from this study will have significant implications for public health policies aimed at combating antimicrobial resistance. By identifying the prevalence of ESBL and carbapenemase-producing organisms in Kumasi, this research can inform infection prevention and control measures within healthcare facilities.

Methodology

Study design

A hospital-based cross-sectional study was conducted from July through to September 2025 at the MCHH in the Kumasi Metropolis among patients referred for blood culture and susceptibility testing upon suspicion.

Study site and population

The study was carried out in MCHH in the Kumasi Metropolis among patients referred for blood culture and susceptibility testing coming to the laboratory unit of the hospital. The MCHH is centrally located in the Subin Sub-Metro within the Kumasi Metropolis, established in 1910. The facility provides a wide range of services, including Outpatient Department (OPD) care, admissions, antenatal care (ANC), deliveries, postnatal care (PNC), and laboratory services. Emergency services are also available, along with specialised clinics such as mental health, eye, and ear, nose, and throat (ENT). Additional diagnostic and treatment services include ultrasound scanning, management of sexually transmitted infections (STIs), prevention of mother-to-child transmission (PMTCT), antiretroviral therapy (ART), and physiotherapy. Public health services, family planning, cervical and breast cancer screening, as well as comprehensive theatre services are also offered. The hospital also serves as a referral centre for patients who need culture and susceptibility testing due to its well-resourced microbiology laboratory. According to the 2021 Population and Housing Census, the Kumasi Metropolis has a total population of 443, 981, representing 8.2% of the regional population. Of this figure, males account for 213, 662 (48.1%), while females number 230, 319 (51.9%) (Ghana Statistical Service, 2021).

Inclusion criteria

Patients referred to the laboratory upon suspicion of blood stream infection were recruited for this study after informed consent and assent were obtained.

Exclusion criteria

Patients with suspected bloodstream infections who were already receiving any form of antibiotic treatment were excluded from the study. In addition, suspected patients who declined to provide consent or assent were also excluded.

Sample size determination

On average, about 150 patients visit the hospital each month for culture and susceptibility testing. Since sample collection took place over a three-month period, the total population of suspected patients was estimated to be 450. Using the Raosoft online calculator (Rapsoft, 2004), with 5% margin of error, 95% confidence interval, and 50% response distribution, the minimum sample size calculated was 208. However, 229 samples were collected at the end of study.

Sampling technique

In this study, a convenience sampling technique was used to recruit participants. Patients who met the inclusion criteria were selected based on their availability and willingness to participate. This method was chosen because it allowed for easy access to participants within the study facility and was practical given the time and resource constraints of the study.

Data collection and laboratory procedures

After written informed consent, and parental consent and the child's assent (for those below 18 years) were obtained, 1.5mL and 8-10mL of blood samples were aseptically collected from paediatric and adult patients, respectively, into paediatric and adult blood culture bottles. The inoculated blood culture bottles were incubated in the BD BACTEC automated blood processor (Model: Fx40) for the initial twenty-four hours. After 24 hours, culture bottles that showed no indication of growth were incubated further for six days. For culture bottles that indicated growth after 24 hours, the samples were sub-cultured on Blood agar, MacConkey agar, and Chocolate agar and incubated for 24–48 hours. Blood agar and MacConkey agar plates were incubated aerobically at 37°C, while the inoculated Chocolate agar plates were incubated in a microaerophilic environment at 37°C.

Gram staining was performed on plates with visible growth to determine the appropriate blood culture vial for identification and antibiotic panels for susceptibility testing. For isolation and susceptibility testing Phoenix BD BACTEC Machine (Model: M50) was used. Quality control was done using in-house generated quality control organisms. Data were collected using a data collection sheet that included demographic characteristics such as age, sex, and ward. Results of bacterial identification and antimicrobial susceptibility testing were also documented.

Extended-spectrum β-lactamase, carbapenemase and antimicrobial susceptibility testing interpretation

Extended-spectrum β-lactamase (ESBL) and carbapenemase production among Gram-negative isolates were determined using the BD Phoenix M50 automated system, which applies Clinical and Laboratory Standards Institute (CLSI)-defined algorithms that compare antimicrobial Minimum Inhibitory Concentrations (MIC) patterns in the presence and absence of β-lactamase inhibitors (BD Phoenix). For ESBL detection, the Phoenix system evaluates reductions in MICs of cefotaxime, ceftriaxone, ceftazidime, and aztreonam when combined with clavulanic acid, and isolates flagged as ESBL-positive were reported in accordance with CLSI 2024 criteria (Lewis II et al., 2024). Carbapenemase production was similarly analysed using Phoenix-based confirmatory reactions that detect characteristic MIC elevations to ertapenem, imipenem, and meropenem indicative of serine carbapenemases or metallo-β-lactamases. For isolates showing carbapenem non-susceptibility, results were interpreted using CLSI 2024 breakpoints; no modified Hodge test or Carba NP test was required due to the platform's validated detection algorithms.

AST interpretive criteria strictly followed CLSI 2024 guidelines (Lewis II et al., 2024).

Justification of antibiotic selection and interpretation

A comprehensive panel of antibiotics was selected based on CLSI guidelines (2024) and the routine therapeutic agents used for managing bloodstream infections in Ghanaian hospitals. The panel included β-lactams, carbapenems, aminoglycosides, fluoroquinolones, glycopeptides, lipopeptides, oxazolidinones, and other clinically relevant classes. Antibiotic choices were tailored to the Gram reaction and expected resistance mechanisms of the isolates. For Gram-negative bacteria, agents such as cephalosporins, β-lactam/β-lactamase inhibitor combinations, carbapenems, aminoglycosides, and fluoroquinolones were tested. For Gram-positive isolates, β-lactams, macrolides, lincosamides, glycopeptides, and oxazolidinones were included.

Intrinsic resistance was taken into account when interpreting results. For instance, *Pseudomonas aeruginosa* and *Acinetobacter baumannii* are intrinsically resistant to agents such as amoxicillin–clavulanate, cefazolin, and cefuroxime, and these were interpreted accordingly. The inclusion of mupirocin for *Staphylococcus aureus* was intended to assess resistance patterns relevant to MRSA surveillance rather than systemic therapy. Similarly, ertapenem was included to assess carbapenem susceptibility among Enterobacterales, with interpretation for non-fermenters limited to descriptive reporting.

Quality control was performed using in-house reference isolates with known susceptibility profiles, validated periodically against ATCC standard strains to ensure assay reliability.

Data handling and analysis

Data were cleaned, coded, and validated for completeness using Microsoft Excel 365 before being exported into Stata version 15.0 (StataCorp, College Station, TX, USA) for statistical analysis. Descriptive statistics were computed to summarise the prevalence of bacterial isolates, with proportions and 95% confidence intervals presented. For calculating the overall percentages of ESBL- and carbapenemase-producing isolates, the total number of Gram-negative organisms identified during the study period was used as the denominator. Associations between sociodemographic/clinical characteristics and bacterial infection were analysed using a modified Poisson regression with robust variance to derive adjusted Prevalence Ratios (aPR) and 95% confidence intervals. This method was selected over standard logistic regression to provide a direct measure of risk association, as the high prevalence outcome (>60%) makes odds ratios less interpretable. Predictors of multidrug resistance (MDR), extensively drug-resistance (XDR), pan drug-resistance (PDR), and overall antibiotic resistance (ABR) were assessed using Firth's penalised-likelihood logistic regression, reporting adjusted Odds Ratios (aOR) with 95% confidence intervals. This approach was implemented to address potential small-sample bias, particularly for the rarer XDR and PDR outcomes. The assumption of independence was upheld as only one isolate per patient was analysed. The discriminative performance of each resistance model was evaluated using Receiver Operating Characteristic (ROC) curves. Statistical significance was set at $p < 0.05$.

Ethical consideration

Ethical clearance was obtained from the Research Ethics Committee of the University of Health and Allied Sciences (REC-UHAS) with reference number UHAS-REC A.8[64] 24-25. An administrative approval was also obtained from the study facility to conduct the study. Written informed consent was also obtained from all participants aged 18 years and above who agreed to take part in the study. For participants below the legal age of 18 years, both informed parental consent and the child's assent were obtained. All data were kept anonymous, and no personal or identifiable details were collected as part of the study. No third parties had access to any of the information provided. Confidentiality of all participants' information and study data was strictly maintained in accordance with REC-UHAS guidelines.

Results

Prevalence of bacterial infection stratified by sociodemographic characteristics

The study analysed samples from 229 participants to determine the prevalence of bacterial infections across sociodemographic and clinical factors. Overall, 61.6% had bacterial infections, with the highest prevalence observed among children aged 6–10 years (67.4%) and those over 10 years (65.0%), though age differences were not statistically significant (p>0.05). Infection rates were similar between males (62.4%) and females (60.7%), showing no significant sex association (p=0.795). Notably, duration of hospital stay strongly predicted infection: children admitted for 5–7 days had almost three times higher risk of infection compared to those admitted for 2–4 days (cPR=2.94, 95% CI: 1.98–4.37; aPR=2.86, 95% CI: 1.92–4.27; p<0.001). Although infections were slightly more common in the paediatric ward (63.2%) than in the emergency ward (48.0%), this difference was not statistically significant (p=0.201). (Table 1).

Prevalence of specific bacteria isolated among study participants

Figure 1 shows that *E. coli* was the most frequently isolated organism, accounting for 22.7% of all isolates (95% CI: 16.1–30.5).

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TABLE 1 Prevalence of bacterial infection stratified by sociodemographic characteristics.

Variables	Total	Bacterial infection				
	n (%)	n (%)	cPR [95% CI]	p-value	aPR [95% CI]	p-value
Total	229 (100.0)	141 (61.6)				
Age groups						
<1	48 (21.0)	29 (60.4)	1			
1-5	98 (42.8)	57 (58.2)	0.96 [0.72-1.28]	0.793		
6-10	43 (18.8)	29 (67.4)	1.11 [0.82-1.52]	0.486		
>10	40 (17.5)	26 (65.0)	1.08 [0.78-1.47]	0.658		
Sex						
Female	122 (48.9)	68 (60.7)	1			
Male	117 (51.1)	73 (62.4)	1.03 [0.84-1.26]	0.795		
Duration of hospital stay						
2-4	72 (31.4)	19 (26.4)	1		1	
5-7	157 (68.6)	122 (77.7)	2.94 [1.98-4.37]	**0.000**	2.86 [1.92-4.27]	**0.000**
Ward						
Emergency	25 (10.9)	12 (48.0)	1			
Paediatric	204 (89.1)	129 (63.2)	1.32 [0.86-2.01]	0.201		

aPR, Adjusted prevalence ratio; cPR, Crude prevalence ratio; CI, Confidence interval; P<0.05 is statistically significant. Bold, statistically significant.

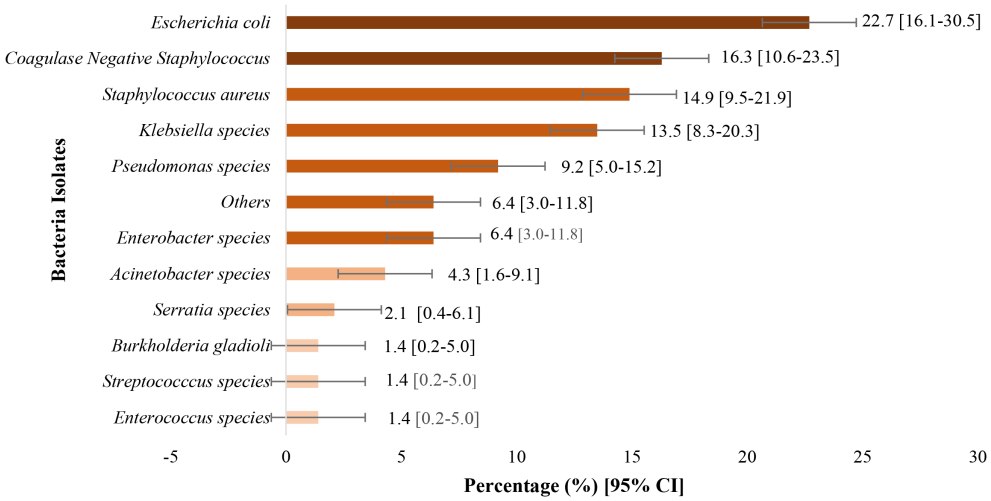

FIGURE 1
Prevalence of bacteria isolated among study participants. CI, Confidence interval, "Others", Micrococcus luteus, Citrobacter koseri, Yersinia intermedia, Morganella morganii, Cupriavidus pauculus, Aeromonas hydrophila, Raoultella ornithinolytica, Cedecia davisae, Pantoea agglomerans. Coagulase-Negative staphylococcus: S. hominis, S. epidermidis, S. saprophyticus, S. carnosus, S. kloosii, S. haemolyticus, S. sciuri, S. intermedius.

This was followed by CoNS at 16.3% (95% CI: 10.6–23.5) and *S. aureus* at 14.9% (95% CI: 9.5–21.9). *Klebsiella* species were also common, representing 13.5% of isolates (95% CI: 8.3–20.3), while *Pseudomonas* species comprised 9.2% (95% CI: 5.0–15.2). Less frequent isolates included *Enterobacter* species and organisms grouped as "others, " each contributing 6.4% (95% CI: 3.0–11.8), followed by *Acinetobacter* species (4.3%, 95% CI: 1.6–9.1). Rare isolates such as *Serratia* species (2.1%), *Burkholderia gladioli*, *Streptococcus* species, and *Enterococcus* species (each 1.4%) were also isolated.

TABLE 2 Antibiotics resistance pattern across bacterial species.

Bacterial species	Antibiotics resistance pattern									
	Amikacin	Ertapenem	Imipenem	Meropenem	Cefazolin	Cefuroxime	Ceftazidime	Ceftriaxone	Cefepime	Levofloxacin
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
Total resistance	5 (3.5)	30 (21.3)	25 (17.7)	11 (7.8)	77 (54.6)	1 (0.7)	54 (38.3)	64 (45.4)	50 (35.5)	48 (34.0)
Gram-negative bacteria										
E. coli	0 (0.0)	3 (10.0)	9 (36.0)	2 (18.2)	29 (37.7)	1 (100.0)	23 (42.6)	29 (45.3)	26 (52.0)	26 (54.2)
Acinetobacter spp	0 (0.0)	4 (13.3)	1 (4.0)	1 (9.1)	4 (5.2)	0 (0.0)	2 (3.7)	3 (4.7)	3 (6.0)	4 (66.7)
Enterobacter spp	1 (20.0)	4 (13.3)	4 (16.0)	1 (11.1)	9 (11.7)	0 (0.0)	5 (9.3)	5 (7.8)	4 (8.0)	5 (10.4)
Pseudomonas spp	2 (40.0)	10 (33.3)	3 (12.0)	2 (15.4)	12 (15.6)	0 (0.0)	3 (5.6)	11 (17.2)	2 (4.0)	2 (4.2)
Serratia spp	0 (0.0)	1 (3.3)	2 (66.7)	0 (0.0)	3 (3.9)	0 (0.0)	2 (3.7)	0 (0.0)	0 (0.0)	1 (2.1)
Klebsiella spp	1 (20.0)	5 (16.7)	4 (16.0)	3 (27.3)	14 (18.2)	0 (0.0)	13 (24.1)	12 (18.8)	12 (24.0)	10 (20.8)
Burkholderia gladioli	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.9)	0 (0.0)	0 (0.0)	0 (0.0)
Others	1 (20.0)	3 (10.0)	2 (8.0)	2 (18.2)	6 (7.8)	0 (0.0)	5 (9.3)	4 (6.3)	3 (6.0)	0 (0.0)
	Antibiotics resistance pattern									
	Gentamicin	Cefoxitin	Cefotaxime	Ampicilin	Penicillin	Oxacilin	Daptomycin	Vancomycin	Clindamycin	
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	
Total resistance	11 (7.8)	33 (23.4)	29 (20.6)	37 (26.2)	42 (29.8)	33 (23.4)	6 (4.3)	13 (9.2)	24 (17.0)	
Gram-Positive bacteria										
Staphylococcus aureus	5 (45.5)	10 (30.3)	7 (24.1)	17 (46.0)	18 (42.8)	12 (36.4))	0 (0.0)	8 (61.5)	7(29.2)	
CONS	4 (36.3)	20 (60.6)	20 (70.0)	17 (46.0)	21 (50.0)	20 (60.6)	0 (0.0)	3 (23.1)	13 (54.2)	
Enterococcus spp	2 (18.2)	2 (6.1)	2 (6.9)	2 (5.4)	2 (4.8)	1 (3.0)	0 (0.0)	2 (15.4)	2 (8.3)	
Streptococcus spp	0 (0.0)	1 (3.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	6 (100.0)	0 (0.0)	1 (4.2)	
Others	0 (0.0)	0 (0.0)	0 (0.0)	1 (2.6)	1 (2.4)	0 (0.0)	0 (0.0)	0 (0.0)	1 (4.2)	

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TABLE 2 Continued

	Antibiotics resistance pattern							
	Erythromycin	Linezolid	Mupirocin	Ciprofloxacin	Moxifloxacin	Rifampin	Tetracycline	Tigecycline
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
Gram-Positive bacteria								
Total resistance	28 (19.9)	9 (6.4)	7 (5.0)	57 (40.4)	7 (5.0)	11 (7.8)	27 (19.1)	67 (47.5)
Gram-negative bacteria								
E. coli	NT	NT	NT	27 (47.4)	NT	NT	NT	27 (40.3)
Acinetobacter spp	NT	NT	NT	4 (7.0)	NT	NT	NT	0 (0.0)
Enterobacter spp	NT	NT	NT	5 (8.8)	NT	NT	NT	9 (13.4)
Pseudomonas spp	NT	NT	NT	3 (5.3)	NT	NT	NT	12 (92.3)
Serratia spp	NT	NT	NT	1 (1.8)	NT	NT	NT	2 (3.0)
Klebsiella spp	NT	NT	NT	13 (22.8)	NT	NT	NT	14 (20.9)
Burkholderia gladioli	NT	NT	NT	0 (0.0)	NT	NT	NT	0 (0.0)
Gram-positive bacteria								
Staphylococcus aureus	7 (25.0)	7 (77.8)	0 (0.0)	0 (0.0)	3 (42.9)	4 (36.4)	12 (44.4))	0 (0.0)
CONS	18 (64.3)	2 (22.2)	0 (0.0)	2 (3.5)	2 (28.6)	5 (45.5)	11 (40.7)	1 (1.5)
Streptococcus spp	1 (3.6)	0 (0.0)	4 (57.1)	1 (1.8)	1 (14.3)	1 (9.1)	2 (7.4)	0 (0.0)
Enterococcus spp	2 (7.1)	0 (0.0)	1 (14.3)	1 (1.8)	1 (14.3)	1 (9.1)	2 (7.4)	0 (0.0)
Others	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	2 (3.0)

Species	Antibiotics resistance pattern				
	Piperacillin-Tazobactam	Amoxicillin-Clavulanate	Ceftolozane-Tazobactam	Trimethoprim-Sulfamethoxazole	Colistin
	n (%)	n (%)	n (%)	n (%)	n (%)
Total resistance	23 (16.3)	65 (46.1)	17 (12.1)	62 (44.0)	15 (10.6)
Gram-negative bacteria					
E. coli	8 (25.0)	17 (26.2)	5 (29.4)	27 (43.5)	4 (26.7)
Acinetobacter spp	2 (8.7)	6 (9.2)	0 (0.0)	2 (3.2)	0 (0.0)

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TABLE 2 Continued

Species	Antibiotics resistance pattern							
	Piperacillin-Tazobactam		Amoxicillin-Clavulanate		Ceftolozane-Tazobactam		Trimethoprim-Sulfamethoxazole	Colistin
	n (%)		n (%)		n (%)		n (%)	n (%)
Gram-negative bacteria								
Enterobacter spp	2 (8.7)		9 (13.8)		4 (23.5)		5 (8.1)	0 (0.0))
Pseudomonas spp	1 (4.3)		13 (20.0)		1 (5.9)		11 (17.7)	3 (20.0)
Serratia spp	0 (0.0)		3 (4.6)		0 (0.0)		1 (1.6)	2 (13.3)
Klebsiella spp	10 (43.5)		11 (16.9)		6 (31.6)		0 (0.0)	0 (0.0)
Burkholderia gladioli	0 (0.0)		2 (3.1)		0 (0.0)		0 (0.0)	0 (0.0)
Others	0 (0.0)		4 (6.2)		1 (5.9)		1 (1.6)	6 (40.0)

NT, Not tested.

Antibiotic resistance pattern across bacterial species

Gram-negative isolates exhibited substantial resistance to cephalosporins, with *E. coli* showing 45.3% and 52.0% resistance to ceftriaxone and cefepime, respectively, and 54.2% resistance to levofloxacin. In contrast, amikacin demonstrated excellent activity, with only 3.5% of the organisms showing resistance to it. Among Gram-positive bacteria, staphylococcal isolates were particularly problematic, with CoNS showing high resistance to cefoxitin (60.6%), penicillin (50.0%), and oxacillin (60.6%), indicative of methicillin resistance. Notably, resistance to last-resort agents like vancomycin and daptomycin remained low at 9.2% and 4.3%, respectively. The β-lactam/β-lactamase inhibitor combination, piperacillin-tazobactam, retained good efficacy against most Gram-negative pathogens (16.3% overall resistance), whereas resistance to amoxicillin-clavulanate was considerably higher (46.1%). Table 2.

Antibiotics resistance stratified by bacterial species

Table 3 shows analysis of antimicrobial resistance among the 141 bacterial isolates, with 81.6% classified as MDR, 8.5% as XDR, and 5.0% as PDR. Gram-negative pathogens demonstrated significant production of ESBL and carbapenemase, particularly in *E. coli* (56.3% ESBL) and *Klebsiella* species (36.8% ESBL, 21.1% carbapenemase). Notable pan-drug resistance was observed in *Pseudomonas* species (23.1%) and Enterobacter species (22.2%). Among Gram-positive isolates, both *S. aureus* (81.0% MDR) and CoNS (91.3% MDR) exhibited high rates of multidrug resistance, while nearly all isolates (96.5%) demonstrated resistance to at least one antibiotic.

Categories of resistance and their associated predictors among study participants

The majority of isolates exhibited MDR (81.6%) and acquired resistance to at least one antibiotic class (ABR, 96.5%), while XDR and PDR categories were less common, occurring in 8.5% and 5.0% of cases, respectively. MDR was consistently high across all age groups, although those >10 years had a lower prevalence (65.4%) compared to infants and younger children (>80%). In contrast, XDR was significantly more frequent among participants >10 years (19.2%; aOR = 7.16, 95% CI: 1.02–15.07, $p = 0.047$). Table 4. Model performance of predictors associated with various categories of resistance.

Figure 2 shows the predictive performance of models for different resistance categories using ROC curves. The MDR and XDR models demonstrated comparable discriminative ability, each with an AUC of 0.7452, indicating moderate predictive accuracy. The PDR model performed best, achieving an AUC of 0.8513,

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TABLE 3 Antibacterial resistance stratified by bacterial species.

Species	MDR	XDR	PDR	ABR	ESBL	Carbapenemase
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
Overall (n=141)	115 (81.6)	12 (8.5)	7 (5.0)	136 (96.5)	25 (27.2)	11 (12.0)
Gram-negative bacteria						
Escherichia coli (n=32)	28 (87.5)	2 (6.3)	1 (3.1)	31 (96.8)	18 (56.3)	1 (3.1)
Klebsiella species *(n=19)*	13 (68.4)	4 (21.1)	0 (0.0)	17 (89.5)	7 (36.8)	4 (21.1)
Pseudomonas species *(n=13)*	8 (61.5)	2 (15.4)	3 (23.1)	13 (100.0)	0 (0.0)	3 (23.1)
Enterobacter species *(n=9)*	7 (77.8)	0 (0.0)	2 (22.2)	9 (100.0)	0 (0.0)	2 (22.2)
Acinetobacter species *(n=6)*	4 (66.7)	1 (16.7)	1 (16.7)	6 (100.0)	0 (0.0)	1 (16.7)
Serratia species *(n=3)*	3 (100.0)	0 (0.0)	0 (0.0)	3 (100.0)	0 (0.0)	0 (0.0)
Burkholderia gladioli (n=2)	2 (100.0)	0 (0.0)	0 (0.0)	2 (100.0)	0 (0.0)	0 (0.0)
Others (n=9)*	9 (100.0)	0 (0.0)	0 (0.0)	9 (100.0)		
Gram-positive bacteria						
Staphylococcus aureus (n=21)	17 (81.0)	1 (4.8)	0 (0.0)	20 (95.2)	–	–
Coagulase-Negative staphylococcus (n=23)	21 (91.3)	1 (4.3)	0 (0.0)	22 (95.7)	–	–
Streptococcus species *(n=2)*	2 (100.0)	0 (0.0)	0 (0.0)	2 (100.0)	–	–
Enterococcus species *(n=2)*	1 (50.0)	1 (50.0)	0 (0.0)	2 (100.0)	–	–

*, 8 out of the 9 other organisms are Gram-negative.

reflecting strong discriminatory power. In contrast, the ABR model showed the lowest predictive performance with an AUC of 0.7250, suggesting only fair accuracy.

Discussion

Globally, BSIs are estimated to affect around 30 million individuals each year, resulting in about 6 million deaths, including 3 million newborns and 1.2 million children (Fleischmann et al., 2016; Fleischmann-Struzek et al., 2018). This current study found BSIs were highly prevalent at the Maternal and Child Health Hospital, affecting 61.6% of patients recruited for this study. This prevalence is much higher than the prevalence reported in a tertiary hospital in Ghana (9.3–11.2%) by Obeng-Nkrumah et al (Obeng-Nkrumah et al., 2026). and 11–28% range reported in Queen Elizabeth Central Hospital, Malawi by Musicha et al (Musicha et al., 2017). The very high prevalence observed in this study may reflect hospital-acquired infections, especially since children with longer hospital stays had nearly three times the risk of infection. This finding agrees with a study in Moscow by Ershova et al (Ershova et al., 2018). who highlighted prolonged admission and gaps in infection prevention as major drivers of BSIs. Additionally, unlike general tertiary hospitals, the Maternal and Child Health Hospital receives a disproportionate number of referrals for severe or complicated infections, possibly leading to a higher detection rate. Although other studies had functional microbiology laboratories, the current study site's laboratory serves as a referral hub for suspected BSI cases from surrounding health facilities, likely enriching the sample with high-risk patients. Therefore, the positivity rate reported in this study reflects a facility-specific, high-risk clinical population, and does not represent the epidemiological prevalence of bloodstream infections at the population level. The high prevalence observed may also reflect the increased risk of hospital-acquired infections among children with prolonged hospital stays, consistent with Ershova et al (Ershova et al., 2018), who linked extended admissions and lapses in infection prevention to elevated BSI rates.

With regards to bacterial agents accounting for this prevalence, the leading bacterial species isolated were *E. coli* and coagulase negative staphylococci, followed by *S. aureus*. *Klebsiella* and *Pseudomonas* species. Other studies by Kang et al (Kang et al., 2012). and Lee et al (Lee et al., 2018). also identified *E. coli*, *S. aureus*, and *K. pneumoniae* as the main pathogens causing BSIs. This shows strong agreement between the findings. However, the relatively high proportion of *Staphylococcus* species (*S. aureus* and coagulase negative staphylococci) in this study suggests that Gram-positive bacteria may play a larger role locally compared to some regions where Gram-negative pathogens dominate. Wilson et al (Wilson et al., 2011). noted that the epidemiological pattern of causative agents is dynamic and can change over time, which supports the importance of regular local surveillance.

Resistance to commonly used antibiotics was widespread in this study. *E. coli* showed high resistance to third- and fourth-generation cephalosporins (>45%) and fluoroquinolones (>50%), while *S. aureus and* coagulase negative staphylococci also showed high

TABLE 4 Categories of resistance and their associated predictors among study participants.

Variables	MDR		XDR		PDR		ABR	
	n (%)	aOR [95% CI] p-value	n (%)	aOR [95% CI] p-value	n (%)	aOR [95% CI] p-value	n (%)	aOR [95% CI] p-value
Total	115 (81.6)		12 (8.5)		7 (5.0)		136 (96.5)	
Age groups								
<1	25 (86.2)	1	2 (6.9)	1	1 (3.4)	1	28 (96.6)	1
1-5	48 (84.2)	0.88 [0.24-3.22] 0.851	3 (5.3)	0.67 [0.10-4.39] 0.678	2 (3.5)	0.91 [0.10-8.23] 0.936	55 (96.5)	1.20 [0.15-9.59] 0.861
6-10	25 (86.2)	1.04 [0.23-4.79] 0.955	2 (6.9)	0.99 [0.13-7.95] 0.988	1 (3.4)	0.78 [0.07-8.79] 0.842	28 (96.6)	0.74 [0.07-8.17] 0.809
>10	17 (65.4)	0.24 [0.05-1.14] 0.073	5 (19.2)	7.16 [1.02-15.07] **0.047**	3 (11.5)	0.86 [0.03-28.18] 0.935	25 (96.6)	0.54 [0.05-5.87] 0.616
Sex								
Female	57 (83.8)	1	4 (5.9)	1	4 (5.9)	1	67 (98.5)	1
Male	58 (79.5)	0.78 [0.32-1.93] 0.591	8 (11.0)	2.41 [0.62-9.31] 0.204	3 (4.1)	0.54 [0.12-2.51] 0.430	69 (94.5)	0.32 [0.05-2.14] 0.242
Duration on admission								
2-4	14 (73.7)	1	2 (10.5)	1	2 (10.5)	1	19 (100.0)	1
5-7	101 (82.8)	2.19 [0.67-7.14] 0.192	10 (8.2)	0.49 [0.09-2.72] 0.204	5 (4.1)	0.18 [0.03-1.11] 0.064	117 (95.6)	0.56 [0.03-10.40] 0.700
Ward								
Emergency	8 (66.7)	1	1 (8.3)	1	3 (25.0)	1	12 (100.0)	1
Paediatric	107 (82.9)	0.68 [0.13-3.61] 0.655	11 (8.5)	6.93 [0.61-23.45] 0.120	4 (3.1)	0.10 [0.00-2.31] 0.148	124 (96.1)	0.38 [0.01-11.17] 0.578
Gram status								
Negative	73 (79.3)	1	9 (9.8)	1	7 (7.6)	1	89 (96.7)	1
Positive	42 (85.7)	1.77 [0.65-4.82] 0.261	3 (6.1)	0.43 [0.10-1.89] 0.264	0 (100.0)	0.07 [0.03-1.85] 0.113	47 (95.9)	0.83 [0.16-4.45] 0.831

aOR, Adjusted odds ratio; P<0.05, is statistically significant. Bold, Statistically significant.

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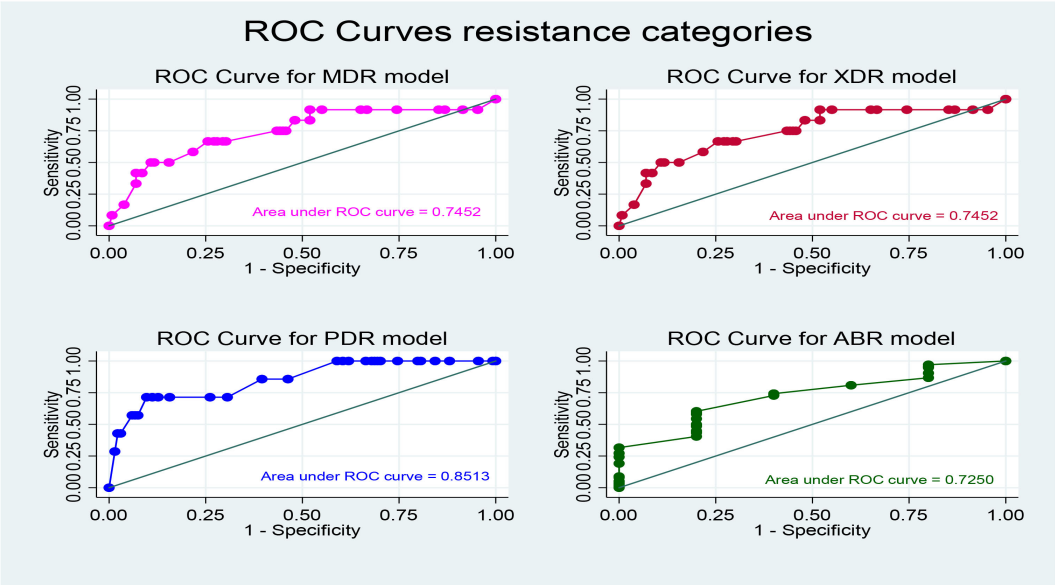

FIGURE 2
Model performance of predictors associated with various categories of resistance.

resistance to oxacillin, penicillin, and ampicillin. These findings are consistent with Lee et al (Lee et al., 2018). who reported that resistance among Gram-negative bacilli has become a major global concern, surpassing resistance among Gram-positive cocci. Similar to this study, global reports highlight *E. coli*, *Klebsiella* species, *Pseudomonas* species., and *Acinetobacter* species as key resistant organisms (Rice, 2010; Nirmal et al., 2023). The high resistance levels observed here also reflect concerns raised by World Health Organisation who described antimicrobial resistance as a global health threat driven by overuse, poor stewardship, and weak regulation (WHO, 2023). With relation to categorisation of resistance, most isolates in this study were MDR (81.6%), while 8.5% were XDR and 5.0% were PDR. This aligns with the similar studies describing MDR as one of the most pressing global health challenges. In particular, Rice (2010) highlighted the "ESKAPE" pathogens as the most problematic MDR organisms. Azerefegne et al (Azerefegne et al., 2025). also reported a total MDR rate in blood culture isolates to be 81% which is almost equal to the rate recorded in this current study. Additionally, Golli et al (Golli et al., 2022). revealed an alarming prevalence of MDR strains isolated in blood samples of the patients admitted to the ICU, indicating the necessity of consistent application of the measures to control. The very high MDR rates in this study compared with global averages suggest that the local resistance situation is especially severe.

This study found 27.2% of the Gram-negative isolates produced ESBL and 12.0% produced carbapenemase. These findings are in line with reports of widespread ESBL production, especially among *E. coli* and *Klebsiella* species (Paterson and Bonomo, 2005; Ghafourian et al., 2015; Deku et al., 2021). Also, a tertiary care hospital study by Beshah et al (Beshah et al., 2023). found 54.0% and 25.7% of the Gram-negative bacteria in bacteraemia to be ESBL and carbapenemase-producing, respectively. These rates are slightly higher than recorded in this current study. In a similar study, Alebel et al (Alebel et al., 2021). reported 19.8% and 1.98% of Gram-negative bacteria were producing EBSL and carbapenemase which are lower than what has been reported in the current study. Additionally, Deku et al (Deku et al., 2022). reported no carbapenemase production in their study on *E. coli* isolates from the Ho Teaching Hospital in Ghana. Previous studies explain that carbapenem resistance often arises from carbapenemase production, sometimes carried on plasmids, which allows rapid spread across bacteria (Potter et al., 2016; Smith et al., 2024). While a global study often focuses on these resistant organisms in immunocompromised patients (Zhang et al., 2018), this study detected them even among general paediatric patients, suggesting that carbapenem resistance is already established in the hospital environment.

This study found no significant association between demographic factors such as sex, age, and ward of admission with antibiotics resistance, except for higher XDR rates in older children. Instead, the most important predictor of infection was length of hospital stay, with longer admission linked to higher infection risk. This is consistent with a study by Ershova et al (Ershova et al., 2018), who identified prolonged hospitalisation, invasive procedures, and poor infection prevention as key drivers of BSIs. The finding that demographic factors were not strong predictors reflects the widespread nature of antibiotics resistance, which can affect all patient groups. The findings from this study have direct practical value for guiding empirical therapy in the study setting. With high resistance observed against commonly used agents such as ceftriaxone and ciprofloxacin, the continued effectiveness of amikacin, piperacillin–tazobactam, and daptomycin offers more reliable options for initial treatment while awaiting culture results. These results also align with Ghana's antimicrobial stewardship

priorities, which emphasize the use of local resistance data to refine treatment guidelines, optimise antibiotic selection, and strengthen infection-prevention practices. By providing updated susceptibility patterns from a major maternal and child health facility, this study supports more informed clinical decision-making and reinforces national efforts to curb the spread of multidrug-resistant pathogens.

Limitation of the study

Even though sample collection and processing were performed under aseptic conditions, the high proportion of CoNS raises the possibility of contamination. This is particularly important because only a single blood culture was taken from each patient, limiting the ability to confirm whether the CoNS isolates represented true bacteraemia or skin flora contaminants. This may have led to an overestimation of CoNS as bloodstream pathogens. Additionally, molecular confirmation of isolates was not performed, and the three-month study duration does not account for seasonal variations in bloodstream infection epidemiology or antimicrobial resistance trends.

Conclusion

The study revealed a 61.6% prevalence of BSIs at the MCHH, with *E. coli* isolates emerging as the predominant pathogens. Multidrug resistance, ESBL and carbapenemase production were detected in 81.6%, 27.2% and 12.0% of isolates respectively, highlighting significant antimicrobial resistance challenges. The study also found that prolonged hospital stay increased the likelihood of infection, although demographic factors such as age and sex showed no strong association with resistance patterns. These findings underscore the urgent need for strengthened infection prevention, routine antimicrobial surveillance, and rational antibiotic use to curb the growing threat of drug-resistant bloodstream infections.

Data availability statement

The original contributions presented in the study are included in the article/supplementary material. Further inquiries can be directed to the corresponding authors.

Ethics statement

The studies involving humans were approved by University of Health and Allied Sciences Research Ethics Committee. The studies were conducted in accordance with the local legislation and institutional requirements. Written informed consent for participation in this study was provided by the participants' legal guardians/next of kin.

Author contributions

EY: Investigation, Writing – review & editing, Methodology, Data curation, Conceptualization. JGD: Conceptualization, Writing – original draft, Resources, Writing – review & editing, Methodology, Project administration, Supervision. IB: Data curation, Writing – original draft, Writing – review & editing, Formal analysis. LM: Supervision, Writing – review & editing, Methodology, Investigation, Data curation. KA: Writing – review & editing, Formal analysis, Writing – original draft, Data curation. KB: Data curation, Writing – review & editing, Investigation. CS: Investigation, Data curation, Writing – review & editing. KK: Investigation, Data curation, Writing – review & editing. PM: Data curation, Writing – review & editing, Investigation. IA: Writing – review & editing, Methodology. KD: Writing – review & editing, Conceptualization.

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Conflict of interest

Author IB was employed by Fly Zipline Ghana Limited.

The remaining authors declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declared that generative AI was not used in the creation of this manuscript.

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