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Emerging antibiotic resistance in bacterial bloodstream infections: a clinical study at the Holy Family Hospital, Nkawkaw, Ghana

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Abstract

Background Bacteraemia, a critical bloodstream infection caused by various bacterial pathogens, poses significant health challenges, particularly when compounded by antibiotic resistance. This current study determined the prevalence of bloodstream bacterial isolates and their antibiotic-resistant patterns at the Holy Family Hospital, Nkawkaw, Ghana, spanning a six-year period.

Methodology A hospital-based retrospective study was carried out to review records of bacterial isolates of bloodstream infections and their antibiotic-resistant pattern among patients who visited the Holy Family Hospital between 2018 and 2023. The data was collected into an Excel sheet version 2021, cleaned, and exported to the appropriate statistical software, SPSS v26 for statistical analysis. A *P*-value less than 0.05 was considered statistically significant for all analyses.

Results Of 3,228 records in this study, the majority (66.0%) were found to be under 1 year of age, while 18.6% were aged 1–10 years. The prevalence of bacteraemia was 8.7% (95% CI: 7.8–9.7%). *Klebsiella species* was found to be the most prevalent at 30.2%, followed by *S. aureus* (26.0%). The highest levels of antibiotic resistance were detected against tetracycline (94.5%), penicillin (92.3%), and chloramphenicol (90.9%). Also, significant resistance was also found against vancomycin (88.3%), cefuroxime (86.5%), and cloxacillin (84.4%). Conversely, amikacin demonstrated the highest susceptibility rate (90.5%), followed by ciprofloxacin (75.0%).

Conclusion The study highlights the significant public health burden posed by bacteraemia and the growing challenge of antibiotic resistance. The prevalence of bacteraemia, particularly caused by Gram-negative organisms such as *Klebsiella species and E. coli* underscores the need for targeted interventions to improve infection control in healthcare settings.

Keywords Antibiotic resistance, Bacteria, Bloodstream infections, Holy Family Hospital, *Klebsiella* spp.

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Introduction

Bloodstream infections are characterized by the presence of microorganisms in the circulating blood, either continuously or intermittently, posing a serious threat to every organ in the body [1]. Bacteraemia is a term for the presence of bacteria in the bloodstream. According toTak, Kanne [2], approximately 200,000 cases of bacteraemia and fungemia occur annually in India with mortality rates ranging from 20 to 50%. *Staphylococcus aureus* is the most commonly isolated organism from bloodstream infections in Ethiopia and some other part of the world [3]. *Escherichia coli*, *Klebsiella*, *Enterobacter*, *Salmonella*, *Citrobacter*, *Pseudomonas*, *Acinetobacter*, etc. are some common causes of bacteraemia. It is important to note that bloodstream infections can have serious consequences such as shock, disseminated intravascular coagulation, multiple organ failure, and even death [4].

The prevalence of multidrug resistance (MDR) organisms is alarmingly high, particularly among Gram-negative bacteria. Reports indicate that resistant rates can reach up to 90% for certain pathogens in regions like Asia and Sub-Saharan Africa [5, 6]. The liberal use of broad-spectrum antibiotics without proper diagnostic support has led to increased resistance. In many healthcare settings, antibiotics are prescribed without adequate microbiological testing, resulting in unnecessary exposure of pathogens to these agents [7, 8]. This practice not only fosters resistance but also diminishes the effectiveness of existing antibiotics.

Inadequate surveillance systems hinder the understanding of local antibiotic resistance (ABR) patterns, preventing healthcare providers from making informed decisions about empirical therapy [9, 10]. A major global health concern is antibiotic resistance, especially in situations of bacteraemia, which can result in serious infections and high death rates. Antibiotic treatment outcomes in bacteraemia vary widely depending on pathogen type, host factors, and treatment regimens. A study on heterogeneous vancomycin-intermediate *S. aureus* (hVISA) bacteraemia reported a high vancomycin treatment failure rate of 78%, primarily linked to older age, infection severity, and higher comorbidity scores, whereas success was associated with solid organ transplantation and low vancomycin Minimum Inhibitory Concentration (MIC) values (≤ 1.0 mg/L) [11]. For *Pseudomonas aeruginosa* bacteraemia in intensive care units' patients, clinical failure correlated with severe burns and high Sequential Organ Failure Assessment (SOFA) scores, advocating for therapeutic drug monitoring to optimize antibiotic efficacy [12]. Meanwhile, a multicentre study on common infections with bacteraemia found no significant difference in overall failure rates between short (5–9 days) and long (10–15 days) antibiotic courses, though shorter treatments had higher relapse rate of *C. difficile* infection [13]. Additionally, a systematic review of ceftolozane/tazobactam in bacteraemia revealed favourable outcomes in both primary and secondary cases, though heterogeneity in study design limited definitive conclusions [14].

In the Kwahu West Municipality located in the Eastern Region of Ghana, there is no study on the prevalence of bloodstream infections and their antibiotic-resistant pattern, hence this current study determined the prevalence of bloodstream bacterial isolates and their antibiotic-resistant patterns at the Holy Family Hospital, Nkawkaw, spanning a six-year period. The urgent need to close this knowledge gap justifies this investigation on the trends of antibiotic resistance in bacteraemia at Holy Family Hospital. This work will yield important information to guide empiric antibiotic therapy and enhance clinical decision-making by identifying the bacterial species and their resistance profiles ultimately improving patient outcomes.

Methodology

Study design

This research was a hospital-based retrospective cross-sectional study conducted at the Microbiology unit of the Laboratory Department of the Holy Family Hospital. The study retrieved secondary data on bacteraemia and their antibiotic susceptibility testing from 2018 to 2023.

Study site

The study was carried out in the Microbiology Unit of the Laboratory Department of the Holy Family Hospital, Nkawkaw. The Holy Family Hospital, Nkawkaw has a bed capacity of two hundred and fourteen, (214), and a staff strength of about six hundred and fifty (650). The hospital has ten (10) wards and provides in-patient and outpatient services. The services of the hospital, are being patronized by patients from Kwahu West Municipality and neighbouring towns in the Eastern region of the country.

The hospital is located in the Nkawkaw Township of the Kwahu West Municipality in the Eastern Region of Ghana. Nkawkaw serves as the administrative capital of the municipality; and it is the second-largest urban town in the Eastern Region. It has 214 settlements within its jurisdiction. Nkawkaw is located about 241 kilometres northwest of Accra. According to the 2021 Population and Housing Census, the Municipality had a population of 145,429. The sex distribution of the population indicates that the male population constitutes 70,532 (48%) and the female population constitutes 74,897 (52%). 64.9% of the population resides in the urban localities whilst 35.1% in rural localities. The municipality lies between latitudes 6°30' North, and 7° North and longitudes 0°30' West and 1° West of the equator [15].

Inclusion and exclusion criteria

The study included culture and susceptibility records of suspected bacteraemic patients at the Holy Family Hospital from 2018 to 2023. Also, bacteraemia records with incomplete data (age, sex, and susceptibility testing results) were excluded in this study.

Data collection

Data for the study were collected using a structured data extraction sheet designed to systematically capture relevant information from bacteraemia records and their corresponding antibiotic susceptibility test results. The parameters collected included the year of sample collection, the source (ward) of each sample, such as the emergency ward, intensive care unit, or general wards, was recorded to evaluate the distribution of bloodstream infections across different hospital departments. Patient demographics, including age and sex, were noted to assess variations in infection prevalence and resistance patterns among different age groups and genders. Additionally, the culture and susceptibility results of bacterial isolates were documented to determine the specific bacterial species involved and their resistance profiles against tested antibiotics. The extracted data were then entered into Microsoft Excel 2021 for analysis.

Sample processing

Blood samples were collected using standard aseptic techniques to prevent contamination. Venous blood was drawn using a sterile syringe and immediately transferred into culture bottles containing enriched media. The samples were incubated at 37 °C for 7 days, with periodic sub-culturing on blood agar, chocolate agar, and MacConkey agar plates for isolation. Blood agar and MacConkey agar plates were incubated in ambient air, while chocolate agar plates were incubated in a CO_2-enriched environment [16, 17, 18].

Bacterial identification was performed based on colonial morphology, haemolysis patterns on blood agar, Gram staining and other biochemical tests including catalase, coagulase, oxidase, urease, citrate, indole, and triple sugar iron (TSI) fermentation tests and motility. Quality control was done using in-house generated quality control materials.

Antibiotic susceptibility testing

Antibiotic susceptibility testing was carried out using the Kirby-Bauer disc diffusion method, in line with the Clinical and Laboratory Standards Institute (CLSI) guidelines [19]. Sterile saline was used to prepare bacterial suspensions, which were adjusted to match the turbidity of the 0.5 McFarland standard via visual comparison. Mueller-Hinton agar plates were inoculated with the standardized suspension, and antibiotic-impregnated discs were placed on the surface. Plates were incubated at 37 °C for 18–24 h, and zone diameters were measured and interpreted according to CLSI breakpoints [19].

Data handling and analysis

Statistical analysis was performed using IBM SPSS version 26 (Armonk, NY: IBM Corp). Descriptive statistics were used to summarize key variables, including patient demographics (age and sex), ward distribution, bacterial isolates identified, and their corresponding susceptibility profiles. To assess trends in antibiotic resistance over time, the data were stratified by year, bacterial species, and antibiotic agents. Chi-square tests were employed to compare resistant rates across years, wards, and demographic groups, where applicable. Organisms were classified as Multidrug resistance (MDR), Extensively drug resistance (XDR) and Pandrug resistance (PDR) according to criteria used by Deku, Aninagyei [20]. Results were presented in the form of tables, charts, and graphs to ensure clarity and facilitate interpretation of findings. For all statistical tests, a p-value of less than 0.05 was considered statistically significant.

Results

Sociodemographic characteristics of study participants

A total of 3,228 participants were included in this study. The majority of participants (66.0%) were under 1 year of age, while 18.6% were aged 1–10 years. The remaining age groups were represented in smaller proportions. A higher percentage of females (62.3%) was observed compared to males (37.7%). With regard to hospital wards, the Neonatal Intensive Care Unit (NICU) was noted to have the highest representation at 58.2%, followed by the Paediatric Unit at 24.6%. Over the six-year period from 2018 to 2023, it was revealed that the highest number of participants (21.7%) was recorded in 2018. The distribution across the remaining years was observed to be relatively balanced, ranging from 14.0 to 17.4% of the total participants per year. (Table 1).

Prevalence of bacterial infection among study participants

The study revealed the majority of participants, 91.3% (95% confidence interval (CI): 90.3–92.3%), were found to have no bacterial bloodstream infection. In contrast, a much smaller proportion, 8.7% (95% CI: 7.8–9.7%), was identified as having a bloodstream infection.

Types of bacteria isolated

Klebsiella species was found to be the most prevalent at 30.2% (95% CI: 24.9–35.9%), followed by *S. aureus* at 26.0% (95% CI: 21.0-31.5%) and *E. coli* at 22.8% (95% CI:18.0-28.2). *Proteus mirabilis* was the list prevalent with 0.4% (95% CI: 0.0–2.0). (Fig. 1).

Table 1 Sociodemographic characteristics of study participants

Variables	Frequency	Percentage (%)
Total	3228	100.0
Age		
< 1	2130	66.0
1–10	600	18.6
11–20	121	3.7
21–30	87	2.7
31–40	66	2.0
> 40	224	6.9
Sex		
Female	2012	62.3
Male	1216	37.7
Ward		
NICU	1879	58.2
Paediatric Unit	794	24.6
OPD	226	7.0
Female/Maternity/Antenatal Care Unit	163	5.0
Male Ward	110	3.4
Emergency Ward	56	1.7
Year		
2018	701	21.7
2019	561	17.4
2020	505	15.6
2021	453	14.0
2022	535	16.6
2023	473	14.7

NICU-Neonatal Intensive Care Unit, OPD- Out Patient Department

Distribution of bacterial infection over the period of 6 years stratified by sex

The prevalence of bloodstream infection among females was consistently higher than males throughout the period, peaking at 68.4% in 2021 before declining to 46.3% in 2023 ($p < 0.001$). Male infection rates showed more variability, reaching their lowest point of 32.0% in 2021 before rising to 54.0% in 2023 ($p < 0.001$). The overall infection rate demonstrated an increase from 4.9% in 2018 to a peak of 19.6% in 2022, followed by a sharp decline to 8.7% in 2023 ($p < 0.001$). Interestingly, a convergence of male and female rates was observed towards the end of the study period, with male rates surpassing female rates in 2023 (Fig. 2).

Bivariate logistic regression of bacterial infection among study participants

In the bivariate logistic regression analysis, significant associations were observed between bloodstream infection and age ($p < 0.001$), sex ($p < 0.001$), ward ($p < 0.001$), and year ($p = 0.014$). Males were found to have 33.0% higher odds of bacterial infection compared to females (aOR: 1.33, 95% CI: 1.02–1.73, $p = 0.038$). Regarding the year of study, significantly higher odds of bacterial infection were detected in 2021 (aOR: 1.65, 95% CI: 1.02–2.67, $p = 0.042$), 2022 (aOR: 4.04, 95% CI: 2.71–6.10, $p < 0.001$), and 2023 (aOR: 1.63, 95% CI: 1.01–2.63, $p = 0.044$) compared to 2018. The highest prevalence of the infection was observed in 2022 (19.6%), while the lowest was seen in 2018 (4.9%) Table 2.

Antibiotic resistant pattern

A high prevalence of antibiotic resistance was observed, with 62.4% of the samples showing resistance to at least one antibiotic. The highest levels of resistance were detected against tetracycline (94.5%), penicillin (92.3%), and chloramphenicol (90.9%). Also, significant resistance was also found against vancomycin (88.3%), cefuroxime (86.5%), and cloxacillin (84.4%). Conversely, most of the organisms were susceptible to amikacin (90.5%), followed by ciprofloxacin (75.0%). Intermediate resistance was rarely observed, accounting for only 0.2% of the total isolates (Table 3).

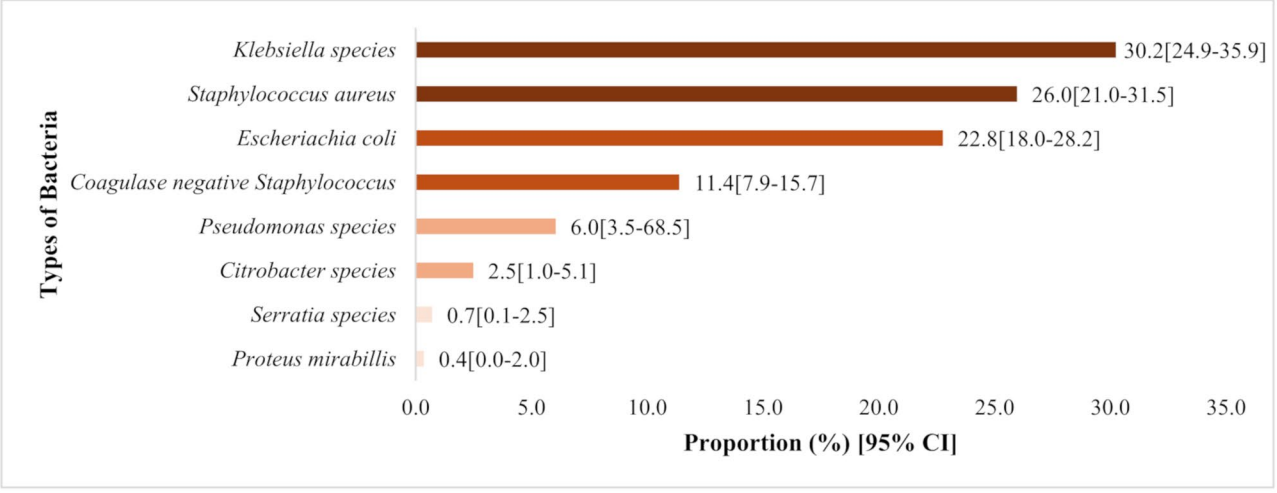

Fig. 1 Types of bacteria isolated

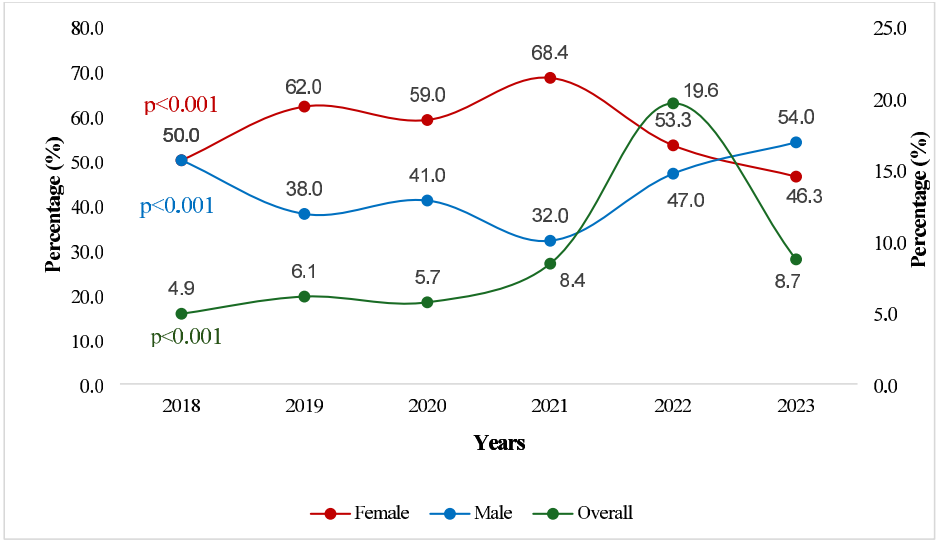

Fig. 2 Distribution of bacterial infection over the period of 6 years stratified by sex

Table 2 Bivariate logistic regression of bacterial infection among study participants

Variables	Total *n* (%)	Bacterial infection *n* (%)	*P*-value	aOR [95% CI]	*P*-value
Total	3228 (100.0)	281 (8.7)			
Age					
< 1	2130 (66.0)	222 (10.4)		1	
1–10	600 (18.6)	43 (7.2)		0.87 [0.53–1.44]	**0.593**
11–20	121(3.7)	3 (2.5)		0.33 [0.09–1.28]	**0.109**
21–30	87 (2.7)	5 (5.7)	**< 0.001**	0.85 [0.24–3.05]	0.798
31–40	66 (2.0)	1 (1.5)		0.23 [0.03–2.08]	0.191
> 40	224 (6.9)	7 (3.1)		0.50 [0.14–1.72]	**0.27**
Sex					
Female	2012 (62.3)	156 (7.8)	**< 0.001**	1	
Male	1216 (37.7)	125 (10.3)		1.33 [1.02–1.73]	**0.038**
Ward					
NICU	1879 (58.2)	199 (1.1)		2.96 [0.38–23.28]	0.302
OPD	226 (7.0)	11 (4.9)		1.97 [0.25–15.83]	0.523
Female/ Maternity/ ANC	163 (5.0)	3 (1.8)	**< 0.001**	1.42 [0.13–15.13]	0.77
Male Ward	110 (3.4)	6 (5.5)		2.93 [0.32-27]	0.343
Emergency	56 (1.7)	1 (1.8)		1	
Year					
2018	701 (21.7)	34 (4.9)		1	
2019	561 (17.4)	34 (6.1)		1.26 [0.75-2.00]	0.420
2020	505 (15.6)	29 (5.7)	**0.014**	1.18 [0.71–1.97]	0.533
2021	453 (14.0)	38 (8.4)		1.65 [1.02–2.67]	**0.042**
2022	535 (16.6)	105 (19.6)		4.04 [2.71–6.10]	**< 0.001**
2023	473 (14.7)	41 (8.7)		1.63 [1.01–2.63]	**0.044**

aOR; Adjusted Odds ratio, *P* value is significant at $P < 0.05$ and $P < 0.001$

Distribution of antibiotics resistance

A comparison was made between the resistance patterns of isolated bacteria and their ABR profiles, with a *p*-value of 0.091 indicated for this comparison. The resistance levels were observed to vary considerably across different bacterial species. *Citrobacter species*, *Escherichia coli*, and *Klebsiella species* were found to exhibit relatively high levels of antimicrobial resistance. *Proteus mirabilis* and *Serratia species* displayed lower levels of resistance. *Staphylococcus aureus*, *Pseudomonas species*, and *coagulase-negative Staphylococcus* showed moderate resistance levels. Figure 3.

Table 3 Characteristics of antibiotics

Variables	Resistant *n* (%)	Intermediate *n* (%)	Susceptible *n* (%)	Total
Total	1010 (62.4)	4 (0.2)	605 (37.4)	1618 (100.0)
PEN	84 (92.3)	0 (0.0)	7 (7.7)	91
COX	38 (84.4)	0 (0.0)	7 (15.6)	45
TET	172 (94.5)	0 (0.0)	10 (5.5)	182
COT	61 (74.4)	1 (1.2)	20 (24.4)	82
GEM	131 (53.5)	3 (1.2)	111 (45.3)	245
CIP	56 (24.6)	1(0.4)	171 (75.0)	228
AMK	19 (9.5)	0 (0.0)	180 (90.5)	199
VAN	68 (88.3)	0 (0.0)	9 (11.7)	77
AUG	50 (75.8)	0 (0.0)	16 (24.2)	66
CHL	42 (90.9)	0 (0.0)	4 (9.1)	44
CTR	55 (69.6)	0 (0.0)	24 (30.4)	79
CRX	141 (86.5)	0 (0.0)	22 (13.5)	163
MEM	93 (79.5)	0 (0.0)	24 (20.5)	117

PEN; Penicillin, COX; Cloxacillin, TET; Tetracycline, COT; GEM; Gentamicin, CIP; Ciprofloxacin, AMK; Amikacin, VAN; Vancomycin, AUG; Augmentin, CHL; Chloramphenicol, CTR; Ceftriaxone, CRX; cefuroxime, MEM; Meropenem

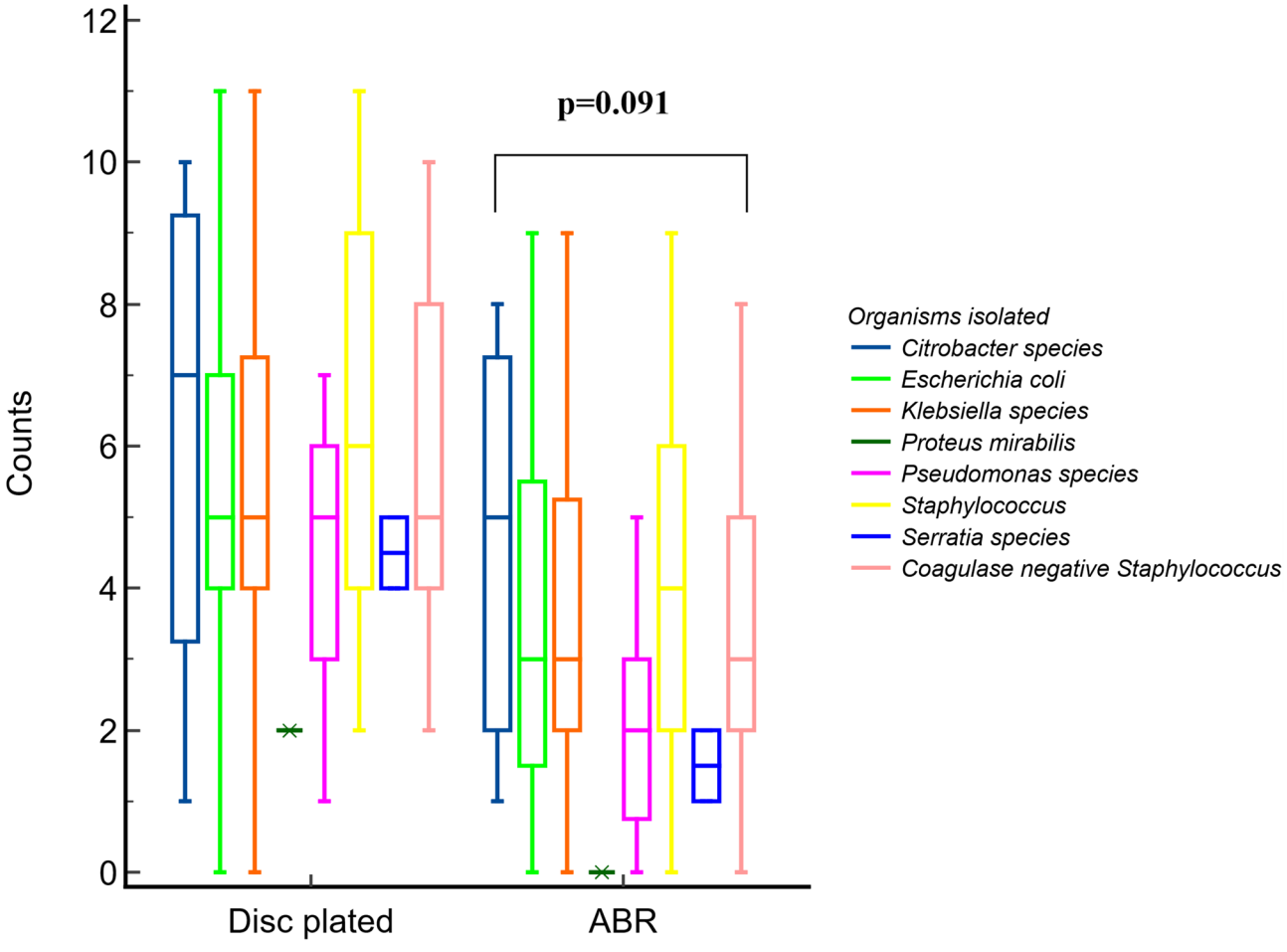

Fig. 3 Antibiotic resistance stratified by bacteria isolated

Bivariate logistic regression of ABR among study participants

The bivariate logistic regression analysis of antibiotic among isolates was conducted and presented in Table 4. No statistically significant differences in resistant rates were observed between age groups or sexes, although males showed a slightly higher adjusted odds ratio (aOR) of 1.97 (95% CI: 0.83–4.69) compared to females. The ward of admission was not found to be significantly associated with resistant rates. However, a significant variation in resistance was noted across the study years ($p < 0.001$). Compared to 2018, significantly lower odds of ABR were observed in 2019 (aOR: 0.08, 95% CI: 0.01–0.47, $p = 0.005$) and 2020 (aOR: 0.09, 95% CI: 0.01–0.53, $p = 0.008$). The years 2021, 2022, and 2023 did not show statistically significant differences in resistance compared to 2018 (Table 4).

Antibiotic resistance stratified by bacteria isolated

Klebsiella species and *S. aureus* emerged as predominant resistant organisms against multiple antibiotics. High resistant rates were observed against tetracycline (165/175, 94.3%), cefuroxime (140/162, 86.4%), and penicillin (84/91, 92.3%). *S. aureus* demonstrated substantial resistance to multiple antibiotics, particularly penicillin (50%), Augmentin (44%), and cloxacillin (44.7%). Among Gram-negative organisms, *Klebsiella* species showed concerning resistance patterns, especially to gentamicin (42%), meropenem (37%), and cefuroxime (32.1%). *E. coli* exhibited varying resistance patterns, with higher resistance to chloramphenicol (47.3%) and cotrimoxazole (33.3%). Table 5.

Table 6 below shows the categorisation of various antibiotic resistance by the bacterial isolates according to multidrug resistance (MDR), extensively-drug resistance (XDR), and pandrug resistance (PDR). For Gram-negative isolates, the highest multidrug resistance was observed for *Klebsiella species* (22.4%), followed by *Pseudomonas species* (11.8%). The only Gram-negative isolates that was pandrug resistance was *Klebsiella* species at 1.2%. Gram positive *S. aureus* isolates were extensively drug resistant and pandrug resistant at 43.8% and 2.7% respectively.

Discussion

Bacteraemia are a significant cause of morbidity and mortality worldwide [21], because untreated and clinically significant bacteraemia progresses to systemic inflammatory response syndrome (SIRS), sepsis, septic shock, and multiple organ dysfunction syndrome (MODS). The study revealed an 8.7% prevalence of bacteraemia among participants, with *Klebsiella species* (30.2%) and *S. aureus* (26.0%) being the most commonly isolated bacteria, followed by *E. coli* (22.8%). This indicates that while the overall prevalence of bacteraemia is relatively low, certain bacteria, particularly Gram-negative pathogens, are more frequently implicated in bloodstream infections. This is supported by finding from other studies conducted in Thailand [22], United states [23], Iran [24], Peru [25], and South Korea by Yun, Chang [11]. The dominance of *Escherichia coli* and *Klebsiella spp*, may suggest hospital-acquired infections, potentially linked to compromised hygiene or invasive medical procedures, which are common sources of such infections in healthcare settings. Additionally, these bacteria are known for causing

Table 4 Bivariate logistic regression of ABR among study participants

Variable	Total *n* (%)	ABR *n* (%)	*P*-value	aOR [95% CI]	*P*-value
Age					
< 1	222 (79.0)	199 (89.6)	0.162	1	
≥ 1	59 (21.0)	49 (83.1)		0.49 [0.08–2.80]	0.420
Sex					
Female	156 (55.5)	133 (85.3)	0.081	1	
Male	125 (44.5)	115 (92.0)		1.97 [0.83–4.69]	0.127
Ward					
Male/Female/Emergency/OPD	21 (7.5)	17 (81.0)		1	
Paediatric unit	61 (21.7)	54 (88.5)		0.96 [0.21–4.34]	0.956
NICU	199 (70.8)	177 (88.9)	0.555	0.61 [0.8–4.9]	0.639
Year					
2018	34 (12.1)	33 (97.1)		1	
2019	34 (12.1)	21 (61.8)		0.08 [0.01–0.47]	**0.005**
2020	29 (10.3)	19 (65.5)		0.09 [0.01–0.53]	**0.008**
2021	38 (13.5)	38 (100.0)	**< 0.001**	3.83 [0.14-100.39]	0.420
2022	105 (37.4)	100 (95.2)		0.77 [0.12–5.16]	0.791
2023	41 (14.6)	37 (90.2)		0.34 [0.05–2.48]	0.288

ABR; Antibiotic resistance. *P* value is significant at $P < 0.05$ and $P < 0.001$

Table 5 Antibiotic resistance stratified by bacteria isolated

Bacteria isolated									
Antibiotics	**Citrobacter species *n* (%)**	**E. coli *n* (%)**	**Klebsiella species *n* (%)**	**Proteus mirabilis *n* (%)**	**Pseudomonas species *n* (%)**	**Staphylococcus aureus *n* (%)**	**Serratia species *n* (%)**	**Coagulase-negative Staphylococcus *n* (%)**	**Total *n* (%)**
PEN									
R	0(0.0)	10(11.9)	13(15.5)	0(0.0)	1(1.2)	42(50.0)	1(1.2)	17(20.2)	84(100.0)
S	0(0.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	3(42.9)	0(0.0)	4(57.1)	7(100.0)
COX									
R	0(0.0)	3(7.9)	8(21.1)	0(0.0)	0(0.0)	17(44.7)	0(0.0)	10(26.3)	38(100.0)
S	0(0.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	5(71.4)	0(0.0)	2(28.6)	7(100.0)
CIP									
I	0(0.0)	0(0.0)	1(100.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	1(100.0)
R	0(0.0)	15(27.3)	15(27.3)	0(0.0)	2(3.6)	11(20)	0(0.0)	12(21.8)	55(100.0)
S	5(2.9)	31(18.1)	58(33.9)	0(0.0)	11(6.4)	46(26.9)	2(1.2)	18(10.5)	171(100.0)
AUG									
R	0(0.0)	6(12.0)	9(18.0)	0(0.0)	3(6.0)	22(44.0)	0(0.0)	10(20.0)	50(100.0)
S	0(0.0)	1(6.3)	0(0.0)	0(0.0)	0(0.0)	11(68.8)	0(0.0)	4(25.0)	16(100.0)
MEM									
R	6(6.5)	21(22.8)	34(37)	0(0.0)	7(7.6)	18(19.6)	1(1.1)	5(5.4)	92(100.0)
S	0(0.0)	4(16.7)	4(16.7)	0(0.0)	1(4.2)	13(54.2)	0(0.0)	2(8.3)	24(100.0)
GEM									
I	0(0.0)	3(100.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	3(100.0)
R	7(5.3)	26(19.8)	55(42.0)	0(0.0)	6(4.6)	26(19.8)	0(0.0)	11(8.3)	131(100.0)
S	0(0.0)	25(22.7)	18(16.4)	1(0.9)	9(8.2)	38(34.5)	2(1.8)	17(15.5)	110(100.0)
TET					-				
R	4(2.4)	39(23.6)	43(26.1)	0(0.0)	-	53(32.1)	1(0.6)	25(15.2)	165(100.0)
S	0(0.0)	1(10.0)	3(30.0)	0(0.0)	-	2(20.0)	0(0.0)	4(40.0)	10(100.0)
COT					-				
I	0(0.0)	1(100.0)	0(0.0)	0(0.0)	-	0(0.0)	0(0.0)	0(0.0)	1(100.0)
R	2(3.5)	19(33.3)	16(28.1)	0(0.0)	-	19(33.3)	0(0.0)	1(1.8)	57(100.0)
S	0(0.0)	3(15.8)	5(26.3)	0(0.0)	-	8(42.1)	0(0.0)	3(15.8)	19(100.0)
AMK					-				
R	0(0.0)	1(5.2)	5(26.3)	0(0.0)	-	10(52.6)	0(0.0)	3(15.8)	19(100.0)
S	6(3.3)	51(28.5)	71(39.7)	0(0.0)	-	23(12.8)	2(1.1)	11(6.1)	179(100.0)
CHL					-				
R	2(5.2)	18(47.3)	15(39.5)	0(0.0)	-	2(5.3)	0(0.0)	1(2.6)	38(100.0)
S	0(0.0)	2(66.7)	1(33.3)	0(0.0)	-	0(0.0)	0(0.0)	0(0.0)	3(100.0)
CTR					-				
R	4(7.4)	17(31.5)	20(37.0)	0(0.0)	-	6(11.1)	0(0.0)	1(1.9)	54(100.0)
S	0(0.0)	10(41.7)	3(12.5)	1(0.2)	-	3(12.5)	0(0.0)	1(1.2)	24(100.0)
CRX					-				
R	4(2.9)	29(20.7)	45(32.1)	0(0.0)	-	38(27.1)	0(0.0)	15(10.7)	140(100.0)
S	0(0.0)	3(13.6)	3(13.6)	0(0.0)	-	11(50.0)	0(0.0)	5(22.7)	22(100.0)
VAN					-				
R	2(3.3)	17(27.9)	21(34.4)	0(0.0)	-	17(27.9)	0(0.0)	4(6.6)	61(100.0)
S	0(0.0)	0(0.0)	2(22.2)	0(0.0)	-	3(33.3)	0(0.0)	4(44.4)	9(100.0)

PEN; Penicillin, COX; Cloxacillin, TET; Tetracycline, COT; GEM; Gentamycin, CIP; Ciprofloxacin, AMK; Amikacin, VAN; Vancomycin, AUG; Augmentin, CHL; Chloramphenicol, CTR; Ceftriaxone, CRX; cefuroxime, MEM; Meropenem

infections in vulnerable populations, including neonates, the elderly, and immunocompromised individuals. This distribution of bacterial species may highlight potential lapses in infection prevention and control practices, and it suggests that targeted interventions could help reduce the incidence of bacteraemia. In comparison, the prevalence of bacteraemia among febrile neonates in a study by Biondi, Lee [26] was 2.9%. Another study in Kenya found a low prevalence of bacteraemia (3.3%) among febrile

Table 6 Classification of bacterial isolates according to antibiotic resistance

Bacterial isolates	Category of antibiotic resistance		
	MDR *n* (%)	XDR *n* (%)	PDR *n* (%)
Gram negatives			
Klebsiella species (*n* = 85)	19 (22.4)	28 (32.9)	1 (1.2)
E. coli (*n* = 64)	5 (7.8)	27 (42.2)	0 (0.0)
Pseudomonas species (*n* = 17)	2 (11.8)	8 (47.1)	0 (0.0)
Citrobacter species (*n* = 7)	0 (0.0)	4 (57.1)	0 (0.0)
Serratia species (*n* = 2)	0 (0.0)	0 (0.0)	0 (0.0)
Proteus mirabilis (*n* = 1)	0 (0.0)	0 (0.0)	0 (0.0)
Gram positives			
S. aureus (*n* = 73)	13 (17.8)	32 (43.8)	2 (2.7)
Coagulase Negative staphylococci (*n* = 32)	9 (28.1)	12 (37.5)	0 (0.0)
Total (***n*** = **281**)	**48 (17.1)**	**111 (39.5)**	**3 (1.1)**

MDR non-susceptible to ≥ 1 agent in ≥ 3 antimicrobial categories, XDR non-susceptible to ≥ 1 agent in all but ≤ 2 categories, PDR non-susceptible to all antimicrobial agents listed

children, with *Salmonella spp*. being the most pathogens isolated [27].

Nielsen, Sarpong [28] also reported a 19.9% of bacteraemia in their study, with nontyphoidal salmonellae, *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Salmonella* Typhi as the most frequently isolated organisms. This finding contrasts our current study findings. Also, in a study by Verway, Brown [29] where *Escherichia coli*, *Staphylococcus aureus*, coagulase-negative staphylococci, *Klebsiella species*, and *Enterococcus species* were identified as the predominant bacterial isolates, the findings from this study shares some similarities and differences. Both studies highlighted *Escherichia coli* and *Klebsiella species* as significant contributors to bacteraemia. However, in the Holy Family Hospital where this current study was carried out, *P. Mirabilis* had a lowest prevalence (0.4%). The absence of *Enterococcus spp* in the latter study suggests differences in the patient population, hospital environment, or regional variations in bacterial pathogens. These differences could also reflect the specific clinical practices or infection control measures in place at each facility. In a systematic review by Hindy, Quintero-Martinez [30], the incidence of *Staphylococcus aureus* bacteraemia ranged from 9.3 to 65 cases per 100,000 people per year across various countries. In China, Wang, Zhao [31] identified that, 73.7% of bacteraemia cases were caused by Gram-negative bacilli, with *Escherichia coli* being the most common pathogen. The causative organisms of bloodstream infections are influenced by factors such as the geographic region, patient population, drug resistance, and infection prevention practices at each institution [32].

In this study, the prevalence of bacteraemia increased over the study period, peaking in 2022 at 19.6% before declining in 2023. The increase in bacteraemia cases over time, particularly in 2022, could be influenced by factors such as outbreaks, changes in hospital admission rates, or shifts in patient demographics. Further investigation into these dynamics may reveal underlying causes, such as variations in healthcare delivery or external environmental factors affecting hospital infection rates. Previous studies by Deku, Dakorah [33] and Mortensen, Søgaard [34] reported an increase in bloodstream infection overtime.

The findings also showed sex-based variations, with males exhibiting a higher prevalence than females. The male preponderance of bloodstream infection is consistent with previous findings [35, 36]. Contrary to the finding in this current study that showed male bacteraemia preponderance, a previous study reported increased bacteraemia cases in females compared to their male counterpart in Iraq [37] and in Nigeria [38]. The variation in these findings could be influenced by demographic, geographical, or healthcare-related factors, such as differences in healthcare access, immune response, or exposure to risk factors among males and females across different settings. In general, females have stronger innate and adaptive immune responses than males [39].

The study revealed a high rate of antibiotic resistance, with 62.4% of bacterial isolates resistant to at least one antibiotic. Particularly concerning is the resistance to commonly used antibiotics like tetracycline (94.5%) and penicillin (92.3%), as well as last-resort antibiotics such as vancomycin (88.3%). This widespread resistance indicates the growing challenge of treating bacterial infections effectively, particularly in settings where antibiotic stewardship may be suboptimal. The resistance observed suggests overuse or misuse of antibiotics, both within and outside healthcare facilities, which can promote the development of resistant strains. These findings underscore the need for stricter antibiotic prescription guidelines, improved infection control measures, and enhanced efforts in monitoring antibiotic resistance patterns.

The findings from this study reflect a growing concern regarding the high levels of antibiotic resistance

among bacterial isolates. For instance, this study found that bacterial isolates exhibited high resistant to tetracycline (94.5%), penicillin (92.3%), and chloramphenicol (90.9%). This aligns with the findings by Deku, Dakorah [33], which demonstrated similarly high resistant rates to tetracyclines (73.4%) and penicillin (76.8%), as well as sulphonamides (90.2%). Likewise, Donkor, Muhsen [40] reported substantial resistance against amoxicillin (89.3%), tetracycline (76.1%), and chloramphenicol (59.7%). Further supporting these patterns, Labi, Obeng-Nkrumah [41] reported very high resistance to ampicillin/gentamicin and ampicillin/cefotaxime combinations, though cloxacillin/gentamicin exhibited relatively higher susceptibility. In Ghana's Northern Region, Gnimatin, Weyori [42] found similarly high resistance rates for penicillin V (95.2%) and amoxicillin (77.4%), along with several other antibiotics such as cefoxitin (74.4%) and trimethoprim/sulfamethoxazole (68.2%). This parallels the findings of this study, where a broad spectrum of bacterial resistance was observed. Additionally, in the Upper East Region of Ghana, Wuni, Kukeba [43] highlighted high resistance to flucloxacillin, penicillin, ampicillin, and tetracycline, while bacterial isolates showed greater susceptibility to amikacin and ciprofloxacin, which corresponds with the susceptibility observed to amikacin (90.5%) in this study. These comparisons highlight that antibiotic resistance is a widespread issue across various regions of Ghana, with a notable resistance to commonly used antibiotics, which poses a significant public health challenge. Such findings emphasize the urgent need for improved antibiotic stewardship and stricter regulations on antibiotic use to curb the rise of resistant strains.

Although no significant associations were found between age, sex, or ward and antibiotic resistance, a significant variation in resistance patterns was noted over the study period. The decrease in antibiotic resistance observed in 2019 and 2020, compared to 2018, may reflect temporary improvements in antibiotic stewardship or changes in the hospital's prescribing practices during that time. However, the high prevalence of resistance in subsequent years suggests that such gains were not sustained. These temporal trends could be influenced by changes in patient populations, antibiotic usage patterns, or the emergence of resistant bacterial strains. Addressing these variations will require continuous monitoring and adaptation of infection control and antibiotic policies to minimize the development and spread of resistant infections.

This study was limited by its retrospective design, which relied on secondary data from laboratory records. As a result, important clinical details such as patients' comorbidities, duration of hospital stay, prior antibiotic use, and clinical outcomes could not be assessed. Additionally, the inability to distinguish between community-acquired and hospital-acquired infections constrained the interpretation of resistance patterns. The study was conducted at a single hospital, which may limit the generalizability of the findings to other healthcare settings in Ghana.

Conclusion

The study highlights 8.7% prevalence of bacteraemia in Holy Family Hospital Nkawkaw, over a six-year period. Bacterial agents like *Klebsiella* species, *S. aureus* and *E. coli* were key bacterial agents that contributed to bacteraemia. The highest levels of antibiotic resistance were detected against tetracycline, penicillin, and chloramphenicol. In contrast, amikacin demonstrated the highest susceptibility rate. Continuous surveillance and adaptive infection control measures are essential to address these challenges, in line with broader efforts in Ghana and globally to combat antibiotic resistance.

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Author contributions
JGD, PKA and LKA conceptualised the study, JGD, ATL, PKA and LKA wrote the proposal for the acquisition of ethical clearance, JGD, KOD, EA, ATL, IB and IA provided resources, PKA, LKA, MA, AES and RA carried out the investigation, JGD supervised the study, PKA, LKA, MA, AES and RA curated the data. KA, KOD and IB analysed the data, JGD, KA, IB and IA wrote the original draft of the manuscript, JGD, EA and KOD critically reviewed and edited the manuscript. All authors read and approved the final version of the manuscript.

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Data availability
The data used for the study are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate
Ethical approval was obtained from the Research Ethics Committee of the University of Health and Allied Sciences (UHAS-REC) with reference number UHAS-REC A.1 [35] 24–25. The study was performed in compliance with the Helsinki declaration, and according to the guidelines laid out by the Research Ethics Committee of the university of Health and Allied Sciences. Written permission was received from the Management of the hospital for the use of their data. Confidentiality of the participants' information and data resulted was assured. Informed consent was waived by the Research Ethics Committee of the University of Health and Allied Sciences, Ghana.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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