

Antimicrobial Resistance Patterns among Bacterial Isolates Causing Bloodstream Infections in a Tertiary Care Hospital in Khartoum State, Sudan

Abdelhakam H. Ali ^{1,2}, Tibyan A. F. Abdallah ¹, Susan Ali Zroog^{3,4}, Fatima Elhag Ahmed^{3,4}, Wahaj M. Mohammed⁵, Balsem Hayder ⁶, Eltaib M Abd Elrhman², Khaled Abdelsamea⁷, Yassin Nor-Aldaiem², Sababil S. A. Ali ¹.

¹Department of Medical Microbiology, Faculty of Graduate Studies and Scientific Research, National University-Khartoum, Sudan

²Department of Medical Microbiology, Faculty of Medical Laboratory Science, University of Al-Butana, Rufaa, Sudan

³Department of Nursing, Faculty of Nursing, Ruffaa, Sudan

⁴Department of Nursing, Nursing college, Omar Al-Mukhtar University, Al-Bayda, Libya.

⁵Department of Parasitology, Faculty of Medical Laboratory Sciences, Shendi University, Shendi, Sudan

⁶Department of Hematology, Faculty of Medical Laboratory Sciences, University of Khartoum, Sudan

⁷Department of Medical Laboratory Sciences, Faculty of Medical Laboratory Sciences Jerash University, Jordan

DOI: <https://doi.org/10.51584/IJRIAS.2026.11080129>

Received: 22 August 2026; Accepted: 27 August 2026; Published: 17 September 2026

ABSTRACT

Background: Bloodstream infections (BSIs) are still a cause of sickness and death all over the world and are one of the most serious types of infections. The treatment of BSIs is getting harder because of the growing problem of resistance.

Objective: To detect the patterns of resistance among the bacteria that cause bloodstream infections in a tertiary care hospital in Soba locality, Sudan.

Methods: A descriptive cross-sectional study was done in a tertiary care hospital in Soba locality, from September to October 2021. A total of 51 blood samples were taken from patients who were thought to have BSIs. Bacterial identification was done using the Analytical Profile Index (API) system. Antimicrobial susceptibility testing was done with the Kirby–Bauer disk diffusion method and results were read based on Clinical and Laboratory Standards Institute (CLSI) guidelines. Data was analyzed using the Statistical Package for the Social Sciences (SPSS) version 23.

Results: Out of the 51 isolates Gram-negative bacteria were the most common (94.1%) while Gram-positive bacteria were 5.9%. *Acinetobacter baumannii* and *Enterobacter cloacae* were the often-found organisms each making up 19.6% followed by *Pseudomonas aeruginosa* (11.8%) *Klebsiella pneumoniae* (9.8%) and *Escherichia coli* (7.8%). In total 28 (54.9%) isolates were classified as multidrug- MDR) 6 (11.8%) were classified as extensively drug-resistant (XDR) and 4 (7.8%) were classified as pandrug-resistant (PDR) while 13 (25.5%) were sensitive to all antibiotics tested. The highest resistance among the agents tested was seen with amoxicillin–clavulanate (84.0%) followed by ceftazidime (57.6%) and ceftriaxone (55.6%). *Pseudomonas aeruginosa* had the number of MDR isolates within the species (83.3%) while *Acinetobacter baumannii* and *Enterobacter cloacae* were main causes of the overall resistant bacterial load.

Conclusion: A big problem with resistance was found among the bacteria that cause BSIs in the hospital studied. The high number of MDR plus the presence of XDR and PDR isolates and high resistance to antibiotics show the urgent need for ongoing surveillance of antimicrobial resistance, better use of antibiotics, and better ways to prevent and control infections to improve treatment and stop more resistant bacteria from spreading.

Keywords: Keywords: Bloodstream infections, antimicrobial resistance, multidrug-resistant, extensively drug-resistant, pandrug-resistant, antimicrobial susceptibility, *Acinetobacter baumannii*; *Enterobacter cloacae*, Sudan.

INTRODUCTION

Bloodstream infections (BSI) are infectious diseases defined by the presence of viable microorganisms in the bloodstream, it remains a major cause of mortality and morbidity worldwide and one of the most serious infectious condition. Its affect millions of individuals each year and associated with long period hospitalization, that is increased healthcare cost [1]. And mortality rate particularly in low- and middle-income countries [2,3]. In this sense, the definitions of BSI and that of sepsis are 2 sides of the same phenomenon, since sepsis is an infectious syndrome triggered by an infectious disease, while BSI is a sepsis triggered by viable microorganisms circulating in the bloodstream. Because the blood stream is normally sterile environment, any detection of bacteria in the blood through blood culture considered clinically significant and warrants immediate attention [4].

Bloodstream infections (BSIs) are serious infections characterized by the presence of viable microorganisms in the bloodstream. They remain a major cause of morbidity and mortality worldwide and represent one of the most severe infectious conditions encountered in clinical practice. BSIs affect millions of individuals annually and are associated with prolonged hospitalization, increased healthcare costs, and substantial mortality, particularly in low- and middle-income countries [1–3]. Although BSIs and sepsis are closely related, they are not synonymous. BSI refers specifically to the presence of microorganisms in the bloodstream, whereas sepsis is a life-threatening organ dysfunction caused by a dysregulated host response to infection. BSI may occur with or without sepsis, and bloodstream infection can be an important source of systemic infection and sepsis [4].

BSIs are caused by a wide range of Gram-positive and Gram-negative bacterial pathogens. The distribution of causative organisms varies according to geographical region, healthcare setting, patient population, and underlying clinical conditions. Common Gram-positive pathogens associated with BSIs include *Staphylococcus aureus*, coagulase-negative staphylococci, and *Enterococcus* species, while important Gram-negative pathogens include *Escherichia coli*, *Klebsiella* species, *Acinetobacter baumannii* complex, and *Pseudomonas aeruginosa* [5–7]. In tertiary healthcare settings, these infections are particularly important because patients frequently have severe underlying diseases, undergo invasive procedures, require intensive care, and are exposed to broad-spectrum antimicrobial agents. BSIs may originate from localized infections, including pneumonia, urinary tract infections, intra-abdominal infections, wound infections, and endovascular infections, and may progress to severe systemic disease, organ dysfunction, and death [7].

Antimicrobial resistance (AMR) among bacterial pathogens has become a major global public health challenge, contributing to increased morbidity, mortality, prolonged hospitalization, and healthcare expenditure. The emergence and spread of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacteria have substantially reduced the effectiveness of commonly used antimicrobial agents, making some infections increasingly difficult to treat [8]. The inappropriate prescribing and excessive use of antimicrobials, inadequate infection prevention and control practices, and limited availability of effective antimicrobial agents have contributed to the selection and dissemination of resistant organisms [9,10].

BSIs caused by antimicrobial-resistant bacteria are of particular concern in tertiary hospitals. Studies conducted in different healthcare settings have reported high and variable proportions of MDR organisms among BSI isolates, highlighting the challenges faced in infection prevention, antimicrobial selection, and patient management [11,12]. Intensive care units (ICUs) are especially vulnerable to healthcare-associated infections caused by resistant pathogens because of prolonged hospitalization, invasive procedures, use of indwelling

medical devices, and frequent exposure to broad-spectrum antimicrobial agents [13]. The transmission of resistant organisms within healthcare facilities can further increase the burden of AMR and compromise the effectiveness of empirical antimicrobial therapy.

Early identification of the causative pathogen and determination of its antimicrobial susceptibility are essential for the appropriate management of bloodstream infections. However, in many healthcare settings, delays in microbiological diagnosis and limited availability of antimicrobial susceptibility data may result in the empirical and sometimes unnecessary use of broad-spectrum antibiotics. Such practices can further promote the emergence and dissemination of antimicrobial-resistant organisms. Effective infection prevention and control measures, rational antimicrobial use, microbiological diagnosis, and continuous AMR surveillance are therefore essential components of efforts to control the spread of resistant pathogens [7,13].

Continuous surveillance of bacterial pathogens causing BSIs and their antimicrobial susceptibility patterns can provide valuable information for developing hospital-specific antibiograms and optimizing empirical antimicrobial therapy [5]. Local surveillance data are particularly important because the distribution of bacterial pathogens and resistance patterns can vary considerably between hospitals and geographical regions. Furthermore, antimicrobial stewardship programs that incorporate local and regularly updated susceptibility data can support evidence-based antimicrobial prescribing, improve clinical outcomes, and reduce unnecessary antimicrobial exposure [14].

In Sudan, where healthcare facilities face considerable challenges in diagnostic capacity, antimicrobial availability, infection prevention, and antimicrobial stewardship, data on the bacterial causes of BSIs and their antimicrobial resistance patterns are important for guiding clinical management and infection control policies. Therefore, this study was conducted to determine the antimicrobial resistance patterns among bacterial isolates causing bloodstream infections in a tertiary hospital in Khartoum, Sudan.

MATERIALS AND METHODS

Study design:

A descriptive cross-sectional study was conducted among patients attending tertiary hospitals in the Soba locality, Khartoum State, Sudan. The study was conducted from September to October 2021. Patients from whom blood samples were collected for blood culture during the study period were included. Bacterial isolates recovered from blood cultures and identified as causative agents of bloodstream infections were included in the study. A convenience sampling technique was used to select the eligible bacterial isolates.

Data Collection

Data were collected using a structured data collection form. Information obtained included patients' sociodemographic characteristics and hospitalization status, as well as laboratory findings. Laboratory data included the results of bacterial identification, including genus and species, and antimicrobial susceptibility testing for each bacterial isolate. Preserved bacterial isolates recovered from blood cultures were also used for laboratory investigation.

Data Analysis

Data were entered, coded, and analyzed using the Statistical Package for the Social Sciences (SPSS), version 23. Descriptive statistics were used to summarize the data and included frequencies, percentages, means, and standard deviations, where appropriate. Results were presented using tables, graphs, and numerical summaries.

The Chi-square test was used to assess associations between categorical variables. Analysis of variance (ANOVA) was used to compare means between appropriate groups when the assumptions for the test were met. Statistical significance was considered at a *P*-value of <0.05 .

Ethical Considerations

Ethical approval for the study was obtained from the University of Al-Butana. Administrative permission was obtained from the participating hospitals before commencement of the study. Patient information was treated confidentially and used solely for the purposes of the study. All laboratory procedures were performed using appropriate aseptic and biosafety practices.

Laboratory Investigation

Blood Sample Collection and Processing

Using aseptic techniques, two blood specimens were collected from peripheral venous or arterial sites when clinically indicated and, whenever possible, before initiation of antimicrobial therapy to increase the likelihood of recovering the causative pathogen [10]. The blood samples were inoculated into appropriate aerobic and anaerobic blood culture media and transported and processed according to standard microbiological procedures.

Culture Media and Incubation

Blood specimens were inoculated into Brain Heart Infusion (BHI) broth for aerobic culture and thioglycolate broth for anaerobic culture. The inoculated culture bottles were incubated at 35–37°C and examined periodically for evidence of microbial growth.

Evidence of growth included floccular deposits, uniform or subsurface turbidity, hemolysis, coagulation of the broth, surface pellicle formation, gas production, and the appearance of white colonies or granules within the blood-broth mixture [10].

Subculture

When visible evidence of microbial growth was observed, the culture bottles were opened using aseptic techniques, and a small volume of broth was withdrawn using a sterile syringe.

For aerobic cultures, specimens were subcultured onto blood agar, chocolate agar, and MacConkey agar. Blood agar and MacConkey agar plates were incubated aerobically at 35–37°C for approximately 18–24 hours. Chocolate agar plates were incubated at 35–37°C in a CO₂-enriched atmosphere for 18–24 hours.

For anaerobic cultures, specimens were subcultured onto blood agar and incubated under anaerobic conditions at 35–37°C for 18–24 hours.

Identification of Bacterial Isolates

Bacterial isolates were identified using conventional microbiological methods, including colony morphology, Gram staining, and biochemical testing. Where required, species-level identification was confirmed using the Analytical Profile Index (API) system.

Analytical Profile Index (API 20E)

The API 20E system (bioMérieux, France) was used for the identification of Gram-negative bacteria, particularly members of the family Enterobacterales. The system consists of 20 miniature biochemical tests containing dehydrated substrates for the identification of bacterial species.

A well-isolated colony from a pure culture was selected and suspended in sterile distilled water to prepare the bacterial suspension according to the manufacturer's instructions. The suspension was then inoculated into the appropriate compartments of the API 20E strip using a sterile Pasteur pipette.

The ADH, LDC, ODC, H₂S, and URE compartments were overlaid with sterile mineral oil where required to create anaerobic conditions. The strip was placed in the incubation tray, and the tray was supplemented with sterile water to maintain humidity. The tray was covered and incubated at 37°C for 18–24 hours.

Interpretation of API Results

After incubation, the biochemical reactions were examined according to the manufacturer's interpretation guide. Some reactions were interpreted directly based on the observed color changes, whereas appropriate reagents were added to the designated compartments before reading the final reactions.

Each biochemical reaction was recorded as positive or negative according to the API interpretation chart. The resulting biochemical profile was converted into an identification code and compared with the API database/catalogue to determine the identity of the bacterial isolate [10].



Photo-1: API confirming *Staphylococcus aureus* isolate

Antimicrobial Susceptibility Testing

Disk Diffusion Method (Kirby–Bauer Method)

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method. Briefly, three to five well-isolated colonies from a fresh 18–24-hour culture were suspended in 0.9% sterile normal saline. The bacterial suspension was adjusted to a turbidity equivalent to a 0.5 McFarland standard.

A sterile cotton swab was immersed in the standardized bacterial suspension, excess fluid was removed by pressing the swab against the inner wall of the tube, and the suspension was uniformly inoculated over the entire surface of Mueller–Hinton agar. The appropriate antimicrobial discs were then placed aseptically on the inoculated agar surface. The discs were positioned approximately 10 mm from the edge of the plate and sufficiently separated from one another, with an inter-disc distance of approximately 20–25 mm, to prevent overlapping of inhibition zones.

The inoculated plates were incubated aerobically at 35–37°C for 18–24 hours. Following incubation, the diameters of the zones of inhibition around each antimicrobial disc were measured in millimeters. The results were categorized as **susceptible, intermediate, or resistant** according to the applicable zone-diameter interpretive standards [10].

Antimicrobial Discs Tested

The antimicrobial agents tested varied according to the Gram-stain characteristics of the bacterial isolates.

For Gram-positive organisms: Erythromycin, Clindamycin, Ciprofloxacin, Trimethoprim–sulfamethoxazole, Chloramphenicol, Gentamicin, Rifampicin and Vancomycin

For Gram-negative organisms: Amoxicillin–clavulanic acid, Ceftriaxone, Ceftazidime, Piperacillin–tazobactam, Meropenem, Amikacin, Gentamicin, Trimethoprim–sulfamethoxazole, Chloramphenicol and Colistin

The antimicrobial susceptibility results were recorded for each isolate and subsequently analyzed to determine the antimicrobial resistance patterns among bacterial pathogens causing bloodstream infections.



Photo-1: Antimicrobial susceptibility test before incubation.

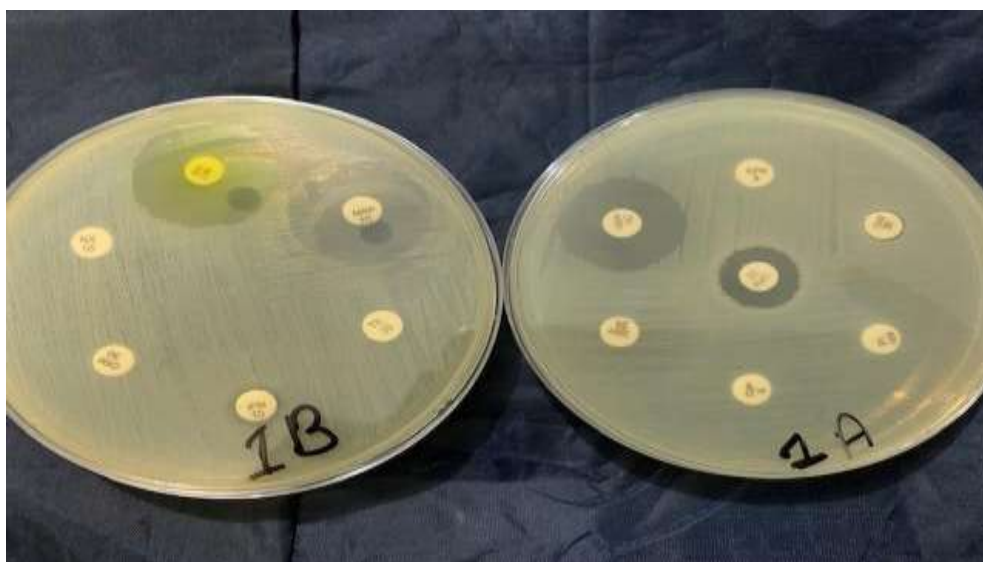


Photo-2: Antimicrobial susceptibility test after incubation at 37° for 24 hours.

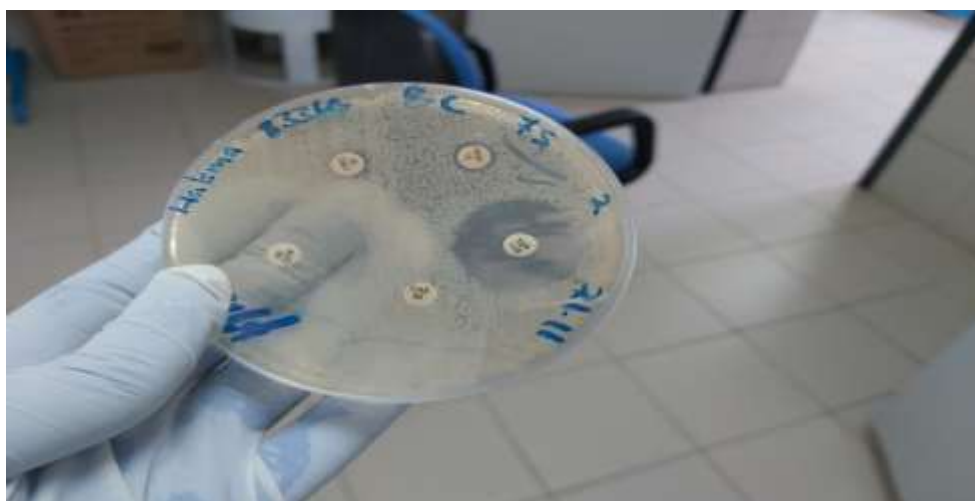


Photo-3: Zone of Inhibition

Screening for Multidrug-Resistant (MDR) Bacterial Isolates

Multidrug-resistant (MDR) bacterial isolates were identified based on their antimicrobial susceptibility profiles obtained from the disk diffusion method. An isolate was considered multidrug-resistant when it showed acquired non-susceptibility to at least one antimicrobial agent in three or more antimicrobial categories, according to the standardized definition proposed by Magiorakos et al. [11].

For selected bacterial isolates, the minimum inhibitory concentration (MIC) of the relevant antimicrobial agent was determined using the ETEST method. ETEST (bioMérieux, France) is a quantitative antimicrobial susceptibility testing method consisting of a plastic strip impregnated with a predefined continuous gradient of antimicrobial concentrations. The strip was applied to the surface of a Mueller–Hinton agar plate previously inoculated with a standardized bacterial suspension equivalent to 0.5 McFarland.

Following incubation under the appropriate conditions, the MIC was read at the point where the elliptical zone of inhibition intersected the antimicrobial gradient on the ETEST strip. The MIC value was recorded as the antimicrobial concentration at the intersection point and interpreted according to the applicable antimicrobial susceptibility breakpoints [10].

RESULTS

Sociodemographic Characteristics of the Study Population

A total of 51 bacterial isolates were recovered from blood culture samples collected from patients attending different hospitals in Khartoum State. The mean age of the patients was 26.3 ± 14.3 years, with an age range of 8–55 years. Males constituted slightly more than half of the study population, accounting for 51.0% (26/51), while females accounted for 49.0% (25/51).

The patients were from several states and regions of Sudan and South Sudan. The highest proportion was from Khartoum State (19.6%), followed by North Kordofan (15.7%), South Kordofan (13.7%), and Blue Nile (9.8%). North Darfur, South Darfur, and South Sudan each accounted for 5.9% of the study population. West Darfur, Al Qadarif, Al Jazirah, and East Darfur each represented 3.9%, while Eastern Sudan, Kassala, Northern State, and White Nile each accounted for 2.0%. The demographic characteristics of the study population are presented in Table 3.1.

Table 3.1: Demographic Characteristics of study Participants (n=51)

Characteristic	Frequency	Percentage (%)
Age (Years)		
Mean $\pm$ SD	26.3 $\pm$ 14.3 year	-
Range (min – max)	8 – 55 year	-
Gender		
Female	25	49.0
male	26	51.0
Place of Residence / State		
Algadarif	2	3.9
Aljazirah	2	3.9

Blue Nile	5	9.8
East Darfur	2	3.9
Eastern	1	2.0
Kassala	1	2.0
Khartoum	10	19.6
North Darfur	3	5.9
North Kurdufan	8	15.7
Northern	1	2.0
South Darfur	3	5.9
South Kurdufan	7	13.7
South Sudan	3	5.9
West Darfur	2	3.9
White Nile	1	2.0
Total	51	100

Distribution of Bacterial Isolates

A total of 51 bacterial isolates were recovered from blood culture samples. Gram-negative bacteria predominated, accounting for 48 (94.1%) of the isolates, whereas Gram-positive bacteria accounted for 3 (5.9%) isolates.

Among the Gram-negative bacteria, *Acinetobacter baumannii* and *Enterobacter cloacae* were the most frequently isolated organisms, each accounting for 19.6% (10/51) of the isolates. These were followed by *Pseudomonas aeruginosa* (11.8%, 6/51), *Klebsiella pneumoniae* (9.8%, 5/51), *Escherichia coli* (7.8%, 4/51), and *Raoultella terrigena* (5.9%, 3/51). *Acinetobacter* spp. and *Pseudomonas fluorescens* each accounted for 3.9% (2/51). *Aeromonas hydrophila*, *Burkholderia cepacia*, and *Enterobacter aerogenes* each represented 2.0% (1/51) of the isolates.

Among the Gram-positive bacteria, *Staphylococcus aureus* was the most frequently isolated organism, accounting for 7.8% (4/51) of all isolates, followed by *Staphylococcus epidermidis* and *Staphylococcus hominis*, each accounting for 2.0% (1/51). The distribution of the bacterial isolates is presented in Table 3.2.

Table 3.2: Pathogenic Bacteria species Isolated:

Type of Bacteria	Frequency (n)	Percentage (%)
<i>Acinetobacter baumanii</i>	10	19.6
<i>Acinetobacter spp</i>	2	3.9
<i>Aeromonas hydrophila</i>	1	2.0

<i>Burkholderia cepacia</i>	1	2.0
<i>Enterobacter aerogenes</i>	1	2.0
<i>Enterobacter cloacae</i>	10	19.6
<i>Escherichia coli</i>	4	7.8
<i>Klebsiella pneumoniae</i>	5	9.8
<i>Peudomonas fluorescens</i>	2	3.9
<i>pseudomonas aeruginosa</i>	6	11.8
<i>Raoultella terigena</i>	3	5.9
<i>Staphylococcus aureus</i>	4	7.8
<i>Staphylococcus epidermidis</i>	1	2.0
<i>Staphylococcus hominis</i>	1	2.0
Total	51	100.0

Antimicrobial Susceptibility Patterns

The antimicrobial susceptibility patterns of the bacterial isolates are presented in Table 3.3. Among the Gram-negative isolates, the highest resistance rate was observed against amoxicillin–clavulanate, with 21 of 25 tested isolates (84.0%) showing resistance. This was followed by ceftazidime, with 19 of 33 isolates (57.6%), and ceftriaxone, with 15 of 27 isolates (55.6%). Resistance to piperacillin–tazobactam was observed in 10 of 33 isolates (30.3%), while 13 of 45 isolates (28.9%) were resistant to trimethoprim–sulfamethoxazole. Ciprofloxacin resistance was observed in 14 of 50 isolates (28.0%), followed by gentamicin (12/50; 24.0%), chloramphenicol (6/26; 23.1%), and amikacin (10/46; 21.7%). Colistin showed the lowest resistance rate among the tested Gram-negative isolates, with 6 of 51 isolates (11.8%) resistant.

Among the Gram-positive isolates, vancomycin showed the highest resistance rate, with 2 of 6 isolates (33.3%) classified as resistant, followed by clindamycin (1/6; 16.7%) and erythromycin (1/7; 14.3%). All four isolates tested against rifampicin were susceptible (100%). Overall, the antimicrobial susceptibility patterns demonstrated substantial resistance to several commonly used antimicrobial agents, particularly among the Gram-negative bacterial isolates.

Table 3.3 : Antimicrobial susceptibility patterns of bacterial isolates:

Antimicrobial agent	Susceptible, n (%)	Intermediate n (%)	Resistant n (%)	Total tested n (%)
Amikacin	31 (67.4)	5 (10.9)	10 (21.7)	46 (100)
Gentamicin	36 (72.0)	2 (4.0)	12 (24.0)	50 (100)
Vancomycin	4 (66.7)	—	2 (33.3)	6 (100)
Clindamycin	5 (83.3)	—	1 (16.7)	6 (100)
Ceftazidime	12 (36.4)	2 (6.1)	19 (57.6)	33 (100)

Ceftriaxone	10 (37.0)	2 (7.4)	15 (55.6)	27 (100)
Amoxicillin–clavulanate	4 (16.0)	—	21 (84.0)	25 (100)
Piperacillin–tazobactam	20 (60.6)	3 (9.1)	10 (30.3)	33 (100)
Ciprofloxacin	35 (70.0)	1 (2.0)	14 (28.0)	50 (100)
Erythromycin	6 (85.7)	—	1 (14.3)	7 (100)
Trimethoprim–sulfamethoxazole	30 (66.7)	2 (4.4)	13 (28.9)	45 (100)
Chloramphenicol	20 (76.9)	—	6 (23.1)	26 (100)
Rifampicin	4 (100.0)	—	—	4 (100)
Colistin	44 (86.3)	1 (2.0)	6 (11.8)	51 (100)

E TEST results

The ETEST method was used to determine the minimum inhibitory concentration (MIC) of selected antimicrobial agents. Among the isolates tested for vancomycin susceptibility, 2 isolates (100%) were resistant. For colistin, 2 isolates (33.3%) were resistant, while 4 isolates were susceptible, as shown in Table 3.4.

Table 3.4 Colistin and vancomycin Susceptibility by E-test :

E. test	Average (mean $\pm$ standard deviation)	Range (min – max)	Resistant	Sensitive
vancomycin (n=2)	28 $\pm$ 5.6	24 - 32	2 (100%)	0 (0%)
colistin (n = 6)	1.36 $\pm$ 1.69	0.09 - 4	2 (33%)	4 (66%)

Distribution of Antimicrobial Resistance Categories

The distribution of bacterial isolates according to antimicrobial resistance category is presented in Table 3.5. Of the 51 bacterial isolates, 28 (54.9%) were classified as multidrug-resistant (MDR), representing the largest resistance category. Six isolates (11.8%) were classified as extensively drug-resistant (XDR), while four (7.8%) were classified as pandrug-resistant (PDR). In contrast, 13 isolates (25.5%) were susceptible to all tested antimicrobial agents.

Overall, 38 (74.5%) of the bacterial isolates demonstrated some degree of antimicrobial resistance, including MDR, XDR, or PDR phenotypes.

Table 3.5 : Distribution of bacterial isolates according to antimicrobial resistance category

Antimicrobial resistance category	Frequency (n)	Percentage (%)
Susceptible to all tested antibiotics	13	25.5
Multidrug resistant (MDR)	28	54.9

Extensively drug resistant (XDR)	6	11.8
Pandrug resistant (PDR)	4	7.8
Total	51	100.0

Distribution of Resistance Patterns According to Bacterial Species

The distribution of antimicrobial resistance patterns among the bacterial species is presented in Table 3.6. Among the 28 MDR isolates, *Pseudomonas aeruginosa* showed the highest contribution, accounting for 5 (17.9%) of the MDR isolates, followed by *Enterobacter cloacae* with 4 (14.3%). *Escherichia coli*, *Staphylococcus aureus*, and *Acinetobacter baumannii* each contributed 3 (10.7%) of the MDR isolates. *Acinetobacter* spp. and *Klebsiella pneumoniae* each accounted for 2 (7.1%), while *Enterobacter aerogenes*, *Pseudomonas fluorescens*, *Raoultella terrigena*, *Staphylococcus epidermidis*, and *Staphylococcus hominis* each contributed 1 (3.6%).

Among the six XDR isolates, *Enterobacter cloacae* and *Klebsiella pneumoniae* each accounted for 2 (33.3%), while *Aeromonas hydrophila* and *Burkholderia cepacia* each accounted for 1 (16.7%). Of the four PDR isolates, *Enterobacter cloacae* accounted for 2 (50.0%), while *Klebsiella pneumoniae* and *Raoultella terrigena* each accounted for 1 (25.0%).

Among the 13 isolates that were susceptible to all tested antibiotics, *Acinetobacter baumannii* was the predominant organism, accounting for 7 (53.8%), followed by *Enterobacter cloacae* with 2 (15.4%). *Escherichia coli*, *Pseudomonas aeruginosa*, *Raoultella terrigena*, and *Staphylococcus aureus* each accounted for 1 (7.7%) of these susceptible isolates.

Table 3.6: Cross-tabulation of bacterial isolates according to antimicrobial resistance pattern

Bacterial species	Susceptible to all tested antibiotics n (%)	MDR n (%)	XDR n (%)	PDR n (%)	Total n (%)
<i>Acinetobacter baumannii</i>	7 (53.8)	3 (10.7)	0 (0.0)	0 (0.0)	10 (19.6)
<i>Acinetobacter</i> spp.	0 (0.0)	2 (7.1)	0 (0.0)	0 (0.0)	2 (3.9)
<i>Aeromonas hydrophila</i>	0 (0.0)	0 (0.0)	1 (16.7)	0 (0.0)	1 (2.0)
<i>Burkholderia cepacia</i>	0 (0.0)	0 (0.0)	1 (16.7)	0 (0.0)	1 (2.0)
<i>Enterobacter aerogenes</i>	0 (0.0)	1 (3.6)	0 (0.0)	0 (0.0)	1 (2.0)
<i>Enterobacter cloacae</i>	2 (15.4)	4 (14.3)	2 (33.3)	2 (50.0)	10 (19.6)
<i>Escherichia coli</i>	1 (7.7)	3 (10.7)	0 (0.0)	0 (0.0)	4 (7.8)
<i>Klebsiella pneumoniae</i>	0 (0.0)	2 (7.1)	2 (33.3)	1 (25.0)	5 (9.8)
<i>Pseudomonas fluorescens</i>	0 (0.0)	2 (7.1)	0 (0.0)	0 (0.0)	2 (3.9)
<i>Pseudomonas aeruginosa</i>	1 (7.7)	5 (17.9)	0 (0.0)	0 (0.0)	6 (11.8)
<i>Raoultella terrigena</i>	1 (7.7)	1 (3.6)	0 (0.0)	1 (25.0)	3 (5.9)
<i>Staphylococcus aureus</i>	1 (7.7)	3 (10.7)	0 (0.0)	0 (0.0)	4 (7.8)

<i>Staphylococcus epidermidis</i>	0 (0.0)	1 (3.6)	0 (0.0)	0 (0.0)	1 (2.0)
<i>Staphylococcus hominis</i>	0 (0.0)	1 (3.6)	0 (0.0)	0 (0.0)	1 (2.0)
Total	13 (100.0)	28 (100.0)	6 (100.0)	4 (100.0)	51 (100.0)

DISCUSSION

Bloodstream infections (BSIs) remain a major cause of morbidity and mortality worldwide and represent one of the most serious infectious conditions, particularly in tertiary healthcare settings. In the present study, 51 bacterial isolates were recovered from blood culture samples collected from patients attending tertiary hospitals in Khartoum State. The study population showed a nearly equal distribution by sex, with males accounting for 51.0% of culture-positive cases and females for 49.0%.

Gram-negative bacteria predominated among the recovered isolates. *Acinetobacter baumannii* and *Enterobacter cloacae* were the most frequently isolated organisms, each accounting for 19.6% of all isolates, followed by *Pseudomonas aeruginosa* (11.8%), *Klebsiella pneumoniae* (9.8%), and *Escherichia coli* (7.8%). Other Gram-negative organisms included *Raoultella terrigena* (5.9%), *Acinetobacter* spp. (3.9%), and *Pseudomonas fluorescens* (3.9%). *Aeromonas hydrophila*, *Burkholderia cepacia*, and *Enterobacter aerogenes* each represented 2.0% of the isolates. Among Gram-positive bacteria, *Staphylococcus aureus* was the predominant organism (7.8%), followed by *Staphylococcus epidermidis* and *Staphylococcus hominis*, each accounting for 2.0%.

The predominance of *A. baumannii* and *E. cloacae* in the present study suggests that these organisms may represent important bloodstream pathogens in the studied tertiary healthcare setting. This finding is consistent with reports from South Africa, where *A. baumannii* has been identified as an important cause of bloodstream infections [15]. However, the frequency of individual pathogens varies considerably between studies. A South African study reported *A. baumannii* in 44% of bloodstream infections, whereas *E. cloacae* accounted for approximately 5% [16]. The differences between these findings and the present study may be related to differences in patient populations, hospital settings, infection-control practices, antimicrobial use, and local epidemiological characteristics.

In the present study, the isolates were categorized according to their antimicrobial resistance profiles. Of the 51 isolates, 13 (25.5%) were susceptible to all tested antibiotics, whereas 28 (54.9%) were classified as multidrug-resistant (MDR), 6 (11.8%) as extensively drug-resistant (XDR), and 4 (7.8%) as pandrug-resistant (PDR). Thus, 74.5% of the isolates demonstrated at least one of these major antimicrobial resistance phenotypes. The prevalence of MDR in the present study was comparable to that reported in Bangladesh, where MDR was observed in 53.7% of bloodstream isolates, while the prevalence of XDR was 15.5% [13]. Similarly, a study conducted in a tertiary-care ICU in India reported MDR, XDR, and PDR rates of 58%, 16%, and 1.2%, respectively [17]. The MDR prevalence in the present study was higher than that reported in Saudi Arabia (47.6%) but lower than the 62.9% reported in Ethiopia [18]. These variations may reflect differences in antimicrobial prescribing practices, infection-control measures, patient characteristics, healthcare infrastructure, and local patterns of antimicrobial resistance.

Analysis of resistance patterns according to bacterial species demonstrated considerable variation. Although *Acinetobacter baumannii* contributed substantially to the MDR group, *Pseudomonas aeruginosa* had the highest proportion of MDR isolates within its species, with 5 of 6 isolates (83.3%) classified as MDR. *Escherichia coli* and *Staphylococcus aureus* each had 3 of 4 isolates (75.0%) classified as MDR. *Acinetobacter baumannii* had 3 of 10 isolates (30.0%) classified as MDR, while *Enterobacter cloacae* had 4 of 10 isolates (40.0%) classified as MDR. These findings highlight the substantial resistance burden among several clinically important bloodstream pathogens.

The relatively high contribution of *A. baumannii* to the resistant isolates is consistent with studies identifying this organism as an important hospital-associated bloodstream pathogen with a strong propensity for multidrug

resistance [19]. A study from Botswana identified closely related *A. baumannii* isolates in environmental sites, including bed rails and sink drains, as well as on the hands of healthcare workers, supporting the potential role of persistent environmental and healthcare-associated reservoirs in transmission [20]. The ability of *A. baumannii* to survive in hospital environments and acquire multiple resistance mechanisms may contribute to its persistence and its importance as a healthcare-associated pathogen [21].

Enterobacter cloacae also demonstrated considerable heterogeneity in antimicrobial resistance in the present study, with isolates distributed across the susceptible, MDR, XDR, and PDR categories. This pattern indicates substantial variation in the resistance profiles of isolates belonging to the same species and emphasizes the importance of species-level identification and antimicrobial susceptibility testing in guiding treatment decisions [22].

The present study demonstrated the highest resistance among the tested Gram-negative isolates to amoxicillin–clavulanate (84.0%), followed by ceftazidime (57.6%) and ceftriaxone (55.6%). The high level of resistance to β -lactam antimicrobial agents observed in this study may reflect the widespread dissemination of β -lactam resistance mechanisms among Gram-negative bloodstream pathogens. However, resistance rates vary considerably between geographical regions and healthcare settings because of differences in antimicrobial consumption, prescribing practices, infection-control measures, and circulating bacterial clones [23].

The 84.0% resistance to amoxicillin–clavulanate observed in the present study indicates a substantial reduction in the effectiveness of this agent against the tested isolates. This finding is consistent with reports of high resistance to commonly used β -lactam/ β -lactamase inhibitor combinations in some healthcare settings, although considerable geographical variation has been reported [24].

The finding of 57.6% resistance to Ceftazidime relative to study conducted in a tertiary hospital in Palestine found that 47.2% of isolates were resistance to Ceftazidime[25]. While study done in Bangladesh the bloodstream isolates Ceftazidime resistance reaches 94.1%[13]. Also Iranian study showed 76.5% resistance to Ceftazidime [26].

Ceftazidime resistance was observed in 57.6% of the tested isolates in the present study. This was higher than the 47.2% resistance reported in a tertiary hospital in Palestine [25], but lower than the 94.1% reported among bloodstream isolates in Bangladesh [13] and the 76.5% reported in Iran [26]. Such differences may be associated with variations in antimicrobial utilization, prevalence of extended-spectrum β -lactamase-producing organisms, infection-control practices, and the distribution of resistant bacterial clones in different settings.

The high prevalence of resistance to third-generation cephalosporins observed in the present study is of particular clinical concern because these agents are commonly used for empirical treatment of serious Gram-negative infections. The findings emphasize the need for continuous antimicrobial susceptibility surveillance and development of local hospital antibiograms to support appropriate empirical therapy. In addition, strengthening antimicrobial stewardship and infection-prevention and control measures is essential to limit further emergence and transmission of resistant bloodstream pathogens.

CONCLUSION

This study demonstrated that antimicrobial resistance is a significant public health concern among bacterial isolates causing bloodstream infections in tertiary healthcare settings in Khartoum State. Gram-negative bacteria predominated, with *Acinetobacter baumannii* and *Enterobacter cloacae* being the most frequently isolated pathogens. A substantial proportion of the isolates exhibited antimicrobial resistance, with MDR (54.9%) being more prevalent than XDR (11.8%) and PDR (7.8%). *Pseudomonas aeruginosa* showed the highest proportion of MDR isolates within its species, while *Acinetobacter baumannii* and *Enterobacter cloacae* contributed substantially to the overall resistant bacterial burden. The highest resistance rates were observed against amoxicillin–clavulanate (84.0%), ceftazidime (57.6%), and ceftriaxone (55.6%). These findings highlight the importance of continuous surveillance of antimicrobial resistance patterns, development of hospital-specific antibiograms, appropriate antimicrobial stewardship, and strengthened infection-prevention and control

measures. These interventions are essential for optimizing empirical antimicrobial therapy and limiting the emergence and transmission of multidrug-resistant bloodstream pathogens.

Conflicts of interest: None

RECOMMENDATION

- Antibiotics should be prescribed rationally and guided by culture and antimicrobial susceptibility testing whenever possible.
- Continuous surveillance of antimicrobial resistance and regular hospital antibiograms should be established to guide empirical therapy.
- Strict infection-prevention and control measures should be strengthened to reduce the transmission of MDR, XDR, and PDR pathogens.
- Laboratory diagnostic capacity should be improved by incorporating advanced identification and molecular techniques, particularly PCR, where available.
- Further multicentre studies are recommended to investigate the epidemiology, risk factors, and molecular mechanisms of antimicrobial resistance in bloodstream infections.

REFERENCES

1. Sharew B, Tilahun M. Bacterial profile and antimicrobial resistance patterns among pediatric patients with suspected bloodstream infections in Ethiopia: a systematic review and meta-analysis. *BMC Infect Dis.* 2025;25(1):1008. doi:10.1186/s12879-025-11427-y.
2. Mahmud RB, Fuad MN, Nispu SS, Hafiz HB, Nahid IH, Akter M, et al. Microbiological spectrum and antimicrobial resistance patterns of bloodstream infection isolates in a tertiary care hospital. *World J Biol Pharm Health Sci.* 2026;25(1):370-8. doi:10.30574/wjbphs.2026.25.1.0072
3. Munyemana JB, Uwizeyimana G, Ndayisaba MC, Dusabe A, Mutsaka-Makuvaza MJ, Sinumvayo JP, et al. Five-year surveillance of antimicrobial resistance patterns among blood culture isolates at the University Teaching Hospital, Kigali, Rwanda. *Ann Clin Microbiol Antimicrob.* 2026;25(1):2. doi:10.1186/s12941-025-00837-0.
4. Akter A, Rahman A, Rahman MZ, Tabassum N. Bloodstream infections and antimicrobial susceptibility patterns: a study in a tertiary care hospital in Bangladesh. *Merit Res J Med Med Sci.* 2021;9(7):290-297.
5. Datta S, Kumar A, Chatterjee B. Microbiological profile and antimicrobial resistance patterns of bloodstream infections in a tertiary care hospital in eastern India. *Curr Med Res Pract.* 2025;15(4):145-150. doi:10.4103/cmrip.cmrip_162_24.
6. Abbas DA, Alsaedi AA, Hadi BA, Al-Safi MH. Antimicrobial resistance patterns in bacterial isolates from hospital-acquired infections. *SAR J Pathol Microbiol.* 2025;6(6):248-254. doi:10.36346/sarjpm.2025.v06i06.003.
7. Bavafa N, Jamasbi S, Yaghubi Kalurazi T, Hasannejad-Bibalan M. Bacterial pathogens and antibiotic resistance in bloodstream infections: a three-year retrospective analysis from a tertiary hospital in Northern Iran. *J Current Biomed Rep.* 2025;6(4):118-122. doi:10.66224/jcbior.6.4.333.
8. Murray CJL, Ikuta KS, Sharara F, Swetschinski L, Robles Aguilar G, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet.* 2022;399(10325):629-655. doi:10.1016/S0140-6736(21)02724-0.
9. Banin E, Hughes D, Kuipers OP. Editorial: bacterial pathogens, antibiotics and antibiotic resistance. *FEMS Microbiol Rev.* 2017;41(3):450-452. doi:10.1093/femsre/fux016.
10. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect.* 2012;18(3):268-81. doi:10.1111/j.1469-0691.2011.03570.x.

11. Chakraborty M, Sardar S, De R, Biswas M, Mascellino MT, Miele MC, et al. Current trends in antimicrobial resistance patterns in bacterial pathogens among adult and pediatric patients in the intensive care unit in a tertiary care hospital in Kolkata, India. *Antibiotics (Basel)*. 2023;12(3):459. doi:10.3390/antibiotics12030459.
12. Yanchumba E, Deku JG, Bedzina I, Mensah LK, Ablordey K, Banahene KK, et al. Antibiotic resistance patterns among bacterial pathogens isolated from bloodstream infections at the Maternal and Child Health Hospital, Kumasi, Ghana. *Front Bacteriol*. 2026;5:1735345. doi:10.3389/fbri.2026.1735345.
13. Tanni NN, Nesa M, Kabir RB, Habib FB, Asaduzzaman M, Sarker A, et al. Distribution, epidemiology, and antimicrobial resistance pattern of gram-negative bacteria isolated from blood: a retrospective study in a tertiary care hospital, Dhaka, Bangladesh. *PLOS Glob Public Health*. 2025;5(10):e0004915. doi:10.1371/journal.pgph.0004915.
14. Deihim B, Assarian AA, Shoja M. Prevalence, etiology, and antimicrobial resistance pattern of bacterial isolates from bloodstream infections in Ganjavian Hospital, Dezful, Iran. *Avicenna J Clin Microbiol Infect*. 2025;12(3):115-20. doi:10.34172/ajcmi.3647.
15. Ismail H, Lowman W, Govind CN, Swe-Han KS, Maloba MRB, Bamford C, et al. Surveillance and comparison of antimicrobial susceptibility patterns of ESKAPE organisms isolated from patients with bacteraemia in South Africa, 2016-2017. *S Afr Med J*. 2019;109(12):934-40. doi:10.7196/SAMJ.2019.v109i12.14079
16. Thomas R, Ondongo-Ezhet C, Motsoaledi N, Sharland M, Clements M, Velaphi S. Incidence, pathogens and antimicrobial resistance of blood and cerebrospinal fluid isolates from a tertiary neonatal unit in South Africa: a 10-year retrospective review. *PLoS One*. 2024;19(1):e0297371. doi:10.1371/journal.pone.0297371.
17. Acharya A, Vamsi Krishna M, Sri Hari Rayalu Veena, Nageswara Rao T. Prevalence of MDR, XDR and PAN drug-resistant organisms isolated from various clinical specimens from the medicine intensive care unit. *Acta Med Int*. 2025;12(3):723-6. doi:10.21276/amit.2025.v12.i3.165.
18. Bandy A, Almaeen AH. Pathogenic spectrum of bloodstream infections and resistance pattern in gram-negative bacteria from Aljouf region of Saudi Arabia. *PLoS One*. 2020;15(6):e0233704. doi:10.1371/journal.pone.0233704.
19. Mashau R, Meiring S, Dramowski A, Magobo R, Quan V, Perovic O, et al. Culture-confirmed neonatal bloodstream infections and meningitis in South Africa, 2014-19: a cross-sectional study. *Lancet Glob Health*. 2022;10(8):e1170-e1178. doi:10.1016/S2214-109X(22)00246-7.
20. Stryko J, Thela T, Thubuka J, et al. Hyperendemic carbapenem-resistant *Acinetobacter baumannii* at a hospital in Botswana: insights from whole-genome sequencing. *Antimicrob Steward Healthc Epidemiol*. 2023;3(Suppl 2):S115-S116. doi:10.1017/ash.2023.395.
21. Gedefie A, Alemayehu E, Mohammed O, Bambo GM, Kebede SS, Kebede B. Prevalence of biofilm producing *Acinetobacter baumannii* clinical isolates: a systematic review and meta-analysis. *PLoS One*. 2023;18(11):e0287211. doi:10.1371/journal.pone.0287211.
22. Elbehiry A, Shoaibi MA, Alzahrani H, Ibrahim M, Moussa I, Alzaben FA, et al. *Enterobacter cloacae* from urinary tract infections: frequency, protein analysis, and antimicrobial resistance. *AMB Express*. 2024;14:101. doi:10.1186/s13568-024-01675-7.
23. Jain N, Jansone I, Obidenova T, Simanis R, Meisters J, Straupmane D, et al. Antimicrobial resistance in nosocomial isolates of gram-negative bacteria: public health implications in the Latvian context. *Antibiotics (Basel)*. 2021;10(7):791. doi:10.3390/antibiotics10070791.
24. Yang Q, Kamat S, Mohamed N, Valdez R, Lin S, Su M, et al. Antimicrobial susceptibility among gram-negative isolates in pediatric patients in Latin America, Africa-Middle East, and Asia from 2016-2020 compared to 2011-2015: results from the ATLAS surveillance study. *J Pediatric Infect Dis Soc*. 2023;12:459-470. doi:10.1093/jpids/piad055.
25. Aiesh BM, Amoudi S, Bassalat L, Yousef A, Abuhailima D, Abutaha A, et al. Ceftazidime prescription and antibiotic resistance patterns in a tertiary care hospital. *Sci Rep*. 2025;15:39804. doi:10.1038/s41598-025-27433-8.
26. Mostafavi Esfahani SN, Rostami S, Rahimi Z. Causative agents and antibiotic resistance in nosocomial sepsis: a cross-sectional multicenter study from Isfahan Province, Iran. *Zahedan J Res Med Sci*. 2024;26(4):e151705. doi:10.5812/zjrms-151705.