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Bacterial pathogens isolated from blood cultures and their antibiotic susceptibility patterns in a tertiary care hospital

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Abstract

Background: Bloodstream infections are still a significant cause of morbidity and mortality in children. Adequate knowledge of bacterial pathogens, timely blood culture results, and suitable antibiotic therapy are essential to reduce adverse outcomes. Understanding the nature of bacterial profile and their antibiotic susceptibility patterns are necessary to guide rational antimicrobial therapy and improve overall clinical outcomes in paediatric patients.

Objectives: This study aimed to determine the spectrum of bacteria isolated from paediatric blood cultures and assess their antibiotic susceptibility profiles.

Methods: A retrospective study was conducted from 1st January 2024 to 30th October 2024 at Bangladesh Shishu Hospital and Institute to determine bacteriological profile of paediatric blood cultures and their antibiotic susceptibility patterns. Data were collected from hospital records of 406 blood culture and sensitivity reports of children admitted to Bangladesh Shishu Hospital and Institute with suspected bacterial infection between January to October 2024.Of the 406 reports 177 were positive and remaining were negative. Identification of bacteria and their antibiotic susceptibility pattern were done according to standard microbiological methods.

Results: Out of 406 blood samples submitted for culture and sensitivity, 177 (43.6%) yielded bacterial growth, of which 171 (96.6%) were Gram-negative bacilli, 5 (2.8%) were Gram-positive cocci, and 1 (0.6%) was Gram-negative coccobacillus. Among these positive cultures, *Klebsiella pneumoniae* (59.3%) was the predominant isolate followed by *Acinetobacter spp.* (19.8%) and *Pseudomonas aeruginosa* (13%). Double bacterial growth was detected in 4 samples (2.3%), all involving both *Acinetobacter spp.* and *Klebsiella pneumoniae*. Less frequently isolated organisms included *Haemophilus influenzae* (0.6%), *Streptococcus pneumoniae* (0.6%), *Staphylococcus aureus* (1.1%), *Enterococcus spp.* (1.1%), *Flavobacterium spp.* (1.1%), and *Escherichia coli* (1.1%). The antibiotic susceptibility profile showed that the isolated bacterial pathogens were most sensitive to Chloramphenicol (48.9%), followed by Cotrimoxazole (20.5%), Levofloxacin (20.2%), and Ciprofloxacin (12.8%). All Gram-positive cocci demonstrated complete (100%) susceptibility to Chloramphenicol, Vancomycin, and Linezolid, while 80% remained susceptible to Levofloxacin and 60% to Ampicillin/Amoxicillin and Penicillin.

Conclusion: The findings of our study revealed a high frequency of Gram-negative bacilli, among which *Klebsiella pneumoniae* was identified as the most common pathogen. Overall antibiotic susceptibility was low. However, Chloramphenicol showed the highest effectivity against the organisms. Gram-positive cocci presented outstanding susceptibility to Chloramphenicol, Vancomycin and Linezolid.

Keywords: Blood cultures, Antibiotic susceptibility

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Introduction

Blood culture is a critical diagnostic tool for identifying bloodstream infections (bacteraemia) in children, a population particularly vulnerable due to their immature immune systems and the rapid progression of sepsis. Early and accurate detection of causative bacterial pathogens through blood cultures enables timely initiation of appropriate antimicrobial therapy, which is essential for reducing morbidity and mortality.

Alongside culture, antibiotic susceptibility testing provides vital information on the sensitivity and resistance patterns of isolated organisms, guiding clinicians in selecting the most effective antibiotics. In an era of rising antimicrobial resistance, understanding local susceptibility trends is especially important for optimizing treatment and improving clinical outcomes in paediatric patients.[1, 2]

A 6-month prospective cross-sectional study in a tertiary care hospital assessed the bacteriological profile of blood cultures and antibiotic susceptibility patterns. Among 3,324 blood samples 345 (10.3%) showed bacterial growth, with *Staphylococcus aureus*, *Salmonella spp*. and *Acinetobacter spp*. being the most common isolates. Antibiotic susceptibility testing revealed that Gram-positive bacteria were sensitive to Vancomycin and Gentamicin, whereas Gram-negative isolates demonstrated poor sensitivity to commonly used antibiotics.[3]

A 2-year study (2019-2020) analysed 1,367 suspected blood culture samples from Rajshahi Medical College, Bangladesh. The overall positivity rate was 35% with similar rates in 2019 (34%) and 2020 (37%). All positive culture showed single organism growth with *E.coli* being the predominant isolate (39.09%), followed by *Staphylococcus aureus*, *Candida albicans*, *Klebsiella pneumoniae*, *Staphylococcus epidermidis*, *Salmonella spp*. *Streptococcus viridians*, and *Pseudomonas aeruginosa*. Both Gram-positive and Gram-negative bacteria demonstrated high sensitivity to Cefepime and Meropenem. Alarmingly many isolates exhibited resistance to 4, 6 or more antibiotics, indicating a significant antimicrobial resistance problem.[4]

Bangladesh Shishu Hospital and Institute, as the largest referral paediatric center in the country, encounters a wide range of severe infections requiring evidence-based management. However, local data on the distribution of bacterial pathogens and their resistance patterns remain limited. As the blood culture is the most sensitive method in the detection of bacteraemia.[5] Therefore, this study aimed to determine the spectrum of bacteria isolated from blood cultures and assess their antibiotic susceptibility profiles, providing essential insights to support rational antimicrobial use and strengthen infection control strategies.

Materials and methods

A retrospective study was conducted from 1st January 2024 to 30th October 2024 at Bangladesh Shishu Hospital and Institute to determine bacteriological profile of blood cultures and their antibiotic susceptibility patterns. This study was done by analysing the hospital ward records of a total of 406 blood samples of children who were hospitalized during the study period and clinically suspected of having bacterial infection. One to three ml blood were collected from patients into BACTEC Peds Plus bottles (FAN method) for culture with proper aseptic precaution. Then the bottles were incubated at a controlled temperature (usually 35-37^0 C) in an automated system that monitors for bacterial growth. The system detects growth by changes in the medium (e.g., pH, CO_2) and flags positive bottles. Growth is usually identified after 12-24 hours, depending on the organism and the system used. If no growth is detected, the system will continue to monitor the bottles until the pre-set incubation period (typically up to 5 days). The automated system generates an alert by alarm and red light when microbial growth is detected. Once the system detects growth, the bottle is flagged as "positive" and then the sample is removed from the automated system. A subculture is done on solid media (e.g., blood agar, MacConkey agar, Chocolate agar) to further isolate organisms. The culture-positive samples were identified by colony morphology, microscopy, and conventional biochemical tests as per the standard protocol followed in the microbiology laboratory.[6] Then antimicrobial susceptibility test is done according to Clinical and Laboratory Standards Institute (CLSI) guidelines.[7] Finally, all the data were analysed with Microsoft Excel version 2024.

Results

A total of 406 blood samples were collected from suspected bacterial infections patients. Among them 177 were blood culture positive patients and the majority (73.4%) of them were male, while more than one-fourth (26.6%) were female (Figure 1).

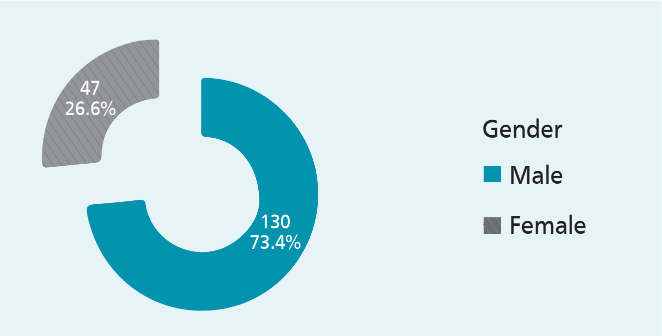

Figure 1: Gender distribution of positive paediatric blood culture isolates

Our study revealed that the majority of blood culture isolates were Gram-negative bacilli (96.6%), while Gram-positive cocci and Gram-negative coccobacilli accounted for only 2.8% and 0.6%, respectively. *Klebsiella pneumoniae* was the most prevalent pathogen (59.3%) followed by *Acinetobacter spp*. (19.8%) and *Pseudomonas aeruginosa* (13%). The remaining bacterial species collectively contributed only 7.9% of all positive blood culture isolates (Table I).

The antibiotic susceptibility profile demonstrated that most of the tested antibiotics showed high resistance among the isolated bacterial pathogens (Table II). The highest sensitivity was observed for Ofloxacin (100%), Vancomycin (100%), Clindamycin (100%), Linezolid (100%), and Nitrofurantoin (100%). Moderate sensitivity was noted for Penicillin (60%) and Chloramphenicol (48.9%) shown in (Table II).

Table I: Bacteriological profile of blood culture isolates (n=177)

Organism	No	%
Gram-negative coccobacillus		
Haemophilus Influenzae	1	0.6
Gram-positive cocci		
Streptococcus pneumoniae	1	0.6
Staphylococcus aureus	2	1.1
Enterococcus spp.	2	1.1
Gram-negative bacilli		
Flavobacterium spp.	2	1.1
Escherichia coli	2	1.1
Acinetobacter spp.+ *klebsiella pneumoniae*	4	2.3
Pseudomonas aeruginosa	23	13
Acinetobacter spp.	35	19.8
Klebsiella pneumoniae	105	59.3

Table II: Antibiotic susceptibility pattern of bacterial pathogens isolated from blood cultures

Antibiotic name	Susceptible n (%)	Intermediate n (%)	Resistant n (%)
Ampicillin/Amoxicillin (n = 141)	3 (2.1)	0 (0)	138 (97.9)
Ceftazidime (n = 178)	15 (8.4)	6 (3.4)	157 (88.2)
Cefuroxime (n = 1)	0 (0)	0 (0)	1 (100)
Imipenem (n = 179)	11 (6.1)	1 (0.6)	167 (93.3)
Tetracycline (n = 4)	2 (50)	0 (0)	2 (50)
Levofloxacin (n = 179)	36 (20.2)	16 (8.9)	127 (70.9)
Ofloxacin (n = 2)	2 (100)	0 (0)	0 (0)
Chloramphenicol (n =141)	69 (48.9)	5 (3.6)	67 (47.5)
Ceftriaxone (n = 161)	7 (4.4)	5 (3.1)	149 (92.5)
Cefepime (n = 178)	13 (7.3)	1 (0.6)	164 (92.1)
Meropenem (n = 178)	17 (9.6)	8 (4.5)	153 (85.9)
Ciprofloxacin (n = 180)	23 (12.8)	5 (2.8)	152 (84.4)
Moxifloxacin (n = 9)	3 (33.3)	0 (0)	6 (66.7)
Cotrimoxazole (n = 161)	33 (20.5)	7 (4.4)	121 (75.1)
Cefixime (n = 138)	2 (1.4)	1 (0.7)	135 (97.9)
Azithromycin (n = 111)	3 (2.7)	4 (3.6)	104 (93.7)
Penicillin (n = 5)	3 (60)	0 (0)	2 (40)
Doxycycline (n = 3)	1 (33.3)	0 (0)	2 (66.7)
Vancomycin (n = 5)	5 (100)	0 (0)	0 (0)
Clindamycin (n = 1)	1 (100)	0 (0)	0 (0)
Erythromycin (n = 5)	1 (20)	1 (20)	3 (60)
Linezolid (n = 5)	5 (100)	0 (0)	0 (0)
Gentamicin (n = 157)	10 (6.4)	0 (0)	147 (93.6)
Netilmicin (n = 155)	7 (4.6)	3 (1.9)	145 (93.5)
Amikacin (n = 177)	12 (6.7)	1 (0.6)	164 (92.7)
Piperacillin-tazobactam (n = 103)	11 (10.7)	3 (2.9)	89 (86.4)
Nitrofurantoin (n = 2)	2 (100)	0 (0)	0 (0)
Amoxycillin+Clavulanic acid (n = 27)	1 (3.7)	0 (0)	26 (96.3)

Almost all tested antibiotics were resistant to *Klebsiella pneumoniae*, except Chloramphenicol, which showed the highest sensitivity (57.1%) against this pathogen (Table III).

Table III: Antibiotic susceptibility pattern of *Klebsiella pneumoniae* (n=105)

Antibiotic name	Susceptible n (%)	Intermediate n (%)	Resistant n (%)
Ampicillin /Amoxacillin	0 (0)	0 (0)	105 (100)
Ceftazidime	1 (0.9)	0 (0)	104 (99.1)
Cefixime	1 (0.9)	0 (0)	104 (99.1)
Meropenem	3 (2.8)	0 (0)	102 (97.2)
Amikacin	1 (0.9)	1 (0.9)	103 (98.2)
Ciprofloxacin	1 (0.9)	0 (0)	104 (99.1)
Moxifloxacin (n=3)	0 (0)	0 (0)	3 (100)
Chloramphenicol	60 (57.1)	4 (3.8)	41 (39.1)
Ceftriaxone	1 (0.9)	0 (0)	104 (99.1)
Cefepime	1 (0.9)	0 (0)	104 (99.1)
Imipenem	3 (2.8)	1 (0.9)	101 (96.3)
Gentamicin (n=104)	2 (1.9)	0 (0)	102 (98.1)
Netilmicin (n=103)	1 (1)	1 (1)	101 (98)
Levofloxacin	9 (8.6)	8 (7.6)	88 (83.8)
Cotrimoxazole	9 (8.6)	0 (0)	96 (91.4)
Azythromicin (n=79)	2 (2.5)	1 (1.3)	76 (96.2)
Piperacillin-tazobactam (n=47)	1 (2.1)	0 (0)	46 (97.9)
Amoxicillin+ Clavulanic acid (n=25)	1 (4)	0 (0)	24 (96)

Ciprofloxacin (60.9%) and Levofloxacin (60.9%) showed the highest sensitivity against *Pseudomonas aeruginosa*, followed by Cotrimoxazole (50%). In contrast, Piperacillin-Tazobactum (26.3%), Ceftazidime (26.1%), Chloramphenicol (25%), Ceftriaxone (25%), and Gentamicin (25%) exhibited only mild sensitivity (Table V).

The majority of the antibiotics showed resistance to *Acinetobacter spp* (Table IV). The highest sensitivity was observed for Cotrimoxazole (37.1%), followed by Levofloxacin (20%) and Ceftazidime (20%) (Table IV).

Table IV: Antibiotic susceptibility pattern of *Acinetobacter spp*. (n = 35)

Antibiotic name	Susceptible n (%)	Intermediate n (%)	Resistant n (%)
Ceftriaxone	0 (0)	5 (14.3)	30 (85.7)
Cefepime	6 (17.1)	0 (0)	29 (82.9)
Meropenem	6 (17.1)	0 (0)	29 (82.9)
Amikacin	4 (11.4)	0 (0)	31 (88.6)
Levofloxacin	7 (20)	2 (5.7)	26 (74.3)
Piperacillin-tazobactam (n=28)	4 (14.3)	1 (3.6)	23 (82.1)
Ceftazidime	7 (20)	0 (0)	28 (80)
Imipenem	0 (0)	0 (0)	35 (100)
Gentamicin	5 (14.3)	0 (0)	30 (85.7)
Ciprofloxacin	5 (14.3)	2 (5.7)	28 (80)
Cotrimoxazole	13 (37.1)	7 (20)	15 (42.9)
Ampicillin/ Amoxacillin (n=20)	0 (0)	0 (0)	20 (100)
Cefixime (n=20)	0 (0)	1 (5)	19 (95)
Azythromycin (n=20)	0 (0)	2 (10)	18 (90)
Netilmicin (n=21)	2 (9.5)	1 (4.8)	18 (85.7)
Chloramphenicol (n=20)	1 (5)	1 (5)	18 (90)

Table V: Antibiotic susceptibility pattern of *Pseudomonas aeruginosa* (n = 23)

Antibiotic name	Susceptible, n (%)	Intermediate, n (%)	Resistant, n (%)
Ampicillin/Amoxacillin (n = 4)	0 (0)	0 (0)	4 (100)
Ceftazidime	6 (26.1)	5 (21.7)	12 (52.2)
Cefixime (n = 4)	0 (0)	0 (0)	4 (100)
Meropenem	4 (17.4)	8 (34.8)	11 (47.8)
Amikacin	5 (21.7)	0 (0)	18 (78.3)
Ciprofloxacin	14 (60.9)	3 (13)	6 (26.1)
Moxifloxacin (n = 2)	0 (0)	0 (0)	2 (100)
Chloramphenicol (n = 4)	1 (25)	0 (0)	3 (75)
Ceftriaxone (n = 4)	1 (25)	0 (0)	3 (75)
Cefepime	3 (13)	1 (4.4)	19 (82.6)
Imipenem	4 (17.4)	0 (0)	19 (82.6)
Gentamicin (n = 4)	1 (25)	0 (0)	3 (75)
Netilmicin	2 (8.7)	1 (4.4)	20 (86.9)
Levofloxacin	14 (60.9)	5 (21.7)	4 (17.4)
Cotrimoxazole (n = 4)	2 (50)	0 (0)	2 (50)
Azythromycin (n = 4)	0 (0)	0 (0)	4 (100)
Piperacillin-tazobactam (n = 19)	5 (26.3)	2 (10.5)	12 (63.2)

*Susceptible or Resistant to multiple drugs

Gram-positive cocci showed complete susceptibility to Vancomycin, Linezolid, and Chloramphenicol. Gentamicin, Netilmicin, and Amikacin were susceptible to *Staphylococcus aureus* but resistant to *Flavobacterium spp.* and *Escherichia coli*. Levofloxacin was susceptible to all except *Escherichia coli* (Table VI).

Table VI: Antibiotic susceptibility pattern of *Haemophilus influenza* (n=1), *Streptococcus pneumonie* (n=1), *Staphylococcus aureus* (n=2) *Enterococcus spp*. (n=2), *Flavobacterium spp*. (n=2), and *Escherichia coli* (n=2)

Antibiotic name	Susceptible, n (%)	Intermediate, n (%)	Resistant, n (%)
Ampicillin/Amoxacillin (n = 10)	*Sp* +**2** *Ec* (30)	0 (0)	*Hi* +**2** *Sa* +**2** *Fb* +**2** *Esc* (70)
Ceftazidime (n = 7)	*Fb* (14.3)	*Sa* (14.3)	*Hi* + *Ec* + *Fb* +**2** *Esc* (71.4)
Cefuroxime (n = 1)	0 (0)	0 (0)	*Hi* (100)
Imipenem (n = 8)	**2** *Sa* + *Ec* + *Fb* (50)	0 (0)	*Hi* + *Fb* +**2** *Esc* (50)
Tetracycline (n = 4)	**2** *Ec* (50)	0 (0)	*Hi* + *Sp* (50)
Levofloxacin (n = 9)	*Hi* + *Sp* + *Sa* +**2** *Ec* + *Fb* (66.7)	*Esc* (11.1)	*Sa* + *Esc* (22.2)
Ofloxacin (n = 2)	*Hi* + *Sp* (100)	0 (0)	0 (0)
Chloramphenicol (n = 10)	*Sp* +**2** *Sa* +**2** *Ec* +**2** *Esc* (70)	0 (0)	*Hi Fb* (30)
Ceftriaxone (n = 9)	*Hi* + *Sp* +**2** *Sa* + *Ec* + *Fb* (66.7)	0 (0)	*Fb* +**2** *Esc* (33.3)
Cefepime (n = 7)	**2** *Sa* + *Fb* (42.9)	0 (0)	*Hi* + *Fb* +**2** *Esc* (57.1)
Cefixime (n = 7)	*Fb* (14.3)	0 (0)	*Hi* +**2** *Sa* + *Fb* +**2** *Esc* (85.7)
Meropenem (n = 7)	*Hi* +**2** *Sa* + *Fb* (57.1)	0 (0)	*Fb* +**2** *Esc* (42.9)
Ciprofloxacin (n = 9)	*Hi* +**2** *Ec* (33.3)	0 (0)	**2** *Sa* + *Fb* +**2** *Esc* (66.7)
Moxifloxacin (n = 4)	*Hi* + *Sp* + *Sa* (75)	0 (0)	*Sa* (25)
Cotrimoxazole (n = 9)	*Sp* +**2** *Sa* + *Ec* + *Fb* (55.6)	0 (0)	*Hi* + *Fb* +**2** *Esc* (44.4)
Azythromycin (n = 8)	*Sa* (12.5)	*Esc* (12.5)	*Hi* + *Sp* + *Sa* + *Ec* + *Fb* + *Esc* (75)
Penicillin (n = 5)	*Sp* +**2** *Ec* (60)	0 (0)	**2** *Sa* (40)
Doxycycline (n = 3)	*Ec* (33.3)	0 (0)	*Sp* + *Ec* (66.7)
Vancomycin (n = 5)	*Sp* +**2** *Sa* +**2** *Ec* (100)	0 (0)	0 (0)
Clindamycin (n = 1)	*Sp* (100)	0 (0)	0 (0)
Erythromicin (n = 5)	*Sa* (20)	*Ec* (20)	*Sp* + *Sa* + *Ec* (60)
Linezolid (n = 5)	*Sp* +**2** *Sa* +**2** *Ec* (100)	0 (0)	0 (0)
Gentamicin (n = 6)	**2** *Sa* (33.3)	0 (0)	**2** *Fb* +**2** *Esc* (66.7)
Netilmicin (n = 6)	**2** *Sa* (33.3)	0 (0)	**2** *Fb* +**2** *Esc* (66.7)
Amikacin	**2** *Sa* (33.3)	0 (0)	**2** *Fb* +**2** *Esc* (66.7)
Nitrofurantoin (n = 2)	**2** *Ec* (100)	0 (0)	0 (0)
Piperacillin-tazobactam(n = 1)	*Fb* (100)	0 (0)	0 (0)

* Hi=*Haemophilus influenza*, Sp=*Streptococcus pneumonie*, Sa= *Staphylococcus aureus*, Ec= *Enterococcus spp*. Fb= *Flavobacterium spp*. Esc= *Escherichia coli*

Double bacterial growth was observed in four samples, all of which yielded *Acinetobacter spp*. and *Klebseilla pneumoniae*. Both organisms were resistant to most of the tested antibiotics. Cotrimoxazole was susceptible to *Acinetobacter spp*. but resistant to *Klebsiella pneumoniae* (Table VII).

Table VII: Antibiotic susceptibility pattern of *Acinetobacter spp*. (n=4) + *Klebsiella pneumoniae* (n=4)

Antibiotic name	Susceptible, n (%)	Intermediate, n (%)	Resistant, n (%)
Ceftriaxone	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Cefepime	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Meropenem	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Amikacin	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Levofloxacin	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Piperacillin-tazobactum	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Ceftazidime	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Imipenem	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Gentamicin	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Ciprofloxacin	0 (0)	0 (0)	4 *Aci* +4*Kl* (100)
Cotrimoxazole	**4** (50)	0 (0)	4*Kl* (50)

* Aci represents *Acinetobacter spp.* and Kl represents *Klebsiella pneumoniae*

Discussion

This study demonstrates a high blood culture positivity rate (43.6%), indicating a substantial burden of blood stream infections in the study population. The overwhelming predominance of Gram-negative bacilli (96.6%) highlights a marked epidemiological shift toward Gram-negative pathogens, consistent with trends reported from tertiary care hospitals in South Asia. *Klebsiela pneumoniae* emerged as the leading isolate, followed by *Acinetobacter spp*. and *Pseudomonas aeruginosa*, underscoring the growing clinical importance of multi-drug resistant (MDR) non-fermenting and *Enterobacter spp*. in blood stream infections.[3, 8]

The detection of double bacterial growth in a small proportion of samples (2.3%), exclusively involving *Klebsiella pneumoniae* and *Acinetobacter spp*. suggests possible polymicrobial sepsis, which is often associated with severe illness, prolonged hospitalization, and prior antibiotic exposure. The relatively low isolation rate of Gram-positive cocci contrasts with earlier reports but may reflect differences in patient demographics, antimicrobial practices, and local infection control measures.[9,10]

Antibiotic susceptibility patterns revealed an alarming degree of resistance among Gram-negative isolates. *Klebsiella pneumoniae* demonstrated resistance to almost all tested antibiotics, with Chloramphenicol showing the highest sensitivity, suggesting limited therapeutic options and possible widespread extended-spectrum β-lactamese or Carbapenemese production. Similarly *Acinetobacter spp*. exhibited extensive resistance, with only modest sensitivity to Cotrimoxazole and Fluroquinolones, aligning with its well recognized MDR phenotype. Although *Pseudomonas aeruginosa* showed comparatively better susceptibility to Ciprofloxacin and Levofloxacin, the reduced effectiveness of commonly used agents such as Piperacillin-Tazobactum and Ceftazidime is clinically concerning.[11,12]

In contrast, Gram-positive cocci retained complete susceptibility to Chloramphenicol, Vancomycin, and Linezolid, indicating preserved efficacy of these agents against invasive Gram-positive infections. Overall, the findings emphasize the urgent need for continuous local surveillance, judicial antimicrobial use, and strengthened antibiotic stewardship programs to curb the rising threat of antimicrobial resistance and to guide empirical therapy for bloodstream infections.[13,14]

Conclusion

This study demonstrates a high prevalence of Gram-negative bacteremia, with *Klebsiella pneumoniae* emerging as the most common pathogen, followed by *Acinetobacter spp*. and *Pseudomonas aeruginosa*. Overall antibiotic susceptibility was low, with chloramphenicol showing the highest activity against the isolated organisms, while susceptibility to commonly used agents such as Fluoroquinolones and Cotrimoxazole remained limited. Gram-positive cocci displayed excellent susceptibility to Chloramphenicol, Vancomycin, and Linezolid. These findings highlight the predominance of multidrug- resistant Gram-negative pathogens and underscore the need for strengthened antimicrobial stewardship and targeted therapy guided by local susceptibility patterns.

Conflict of interest

None

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