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Original Research Article

Bacteremia and antimicrobial resistance among febrile under five children attending pediatric clinic in Bahir Dar, Northwest Ethiopia: a retrospective study (2018–2024)

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ABSTRACT

Background: Bacteremia is a major cause of illness and death in febrile under-five children, particularly in low- and middle-income countries like Ethiopia. Rising antimicrobial resistance (AMR) further complicates treatment. This study assessed bacteremia prevalence and AMR patterns among febrile under-five children at the Amhara Public Health Institute, northwest Ethiopia.
Methods: A retrospective review was conducted using blood culture and antimicrobial susceptibility data (2018–2024) from febrile children under five. Bacterial identification and susceptibility testing followed the modified Kirby–Bauer disk diffusion method per CLSI 2020 guidelines. Data were analyzed with statistical package for the social sciences (SPSS) v26.0.
Results: Of 746 blood cultures, 157 (21.0%) were positive. Gram-negative bacteria predominated (76.5%), with *Klebsiella pneumoniae* (31.8%) most common, followed by *Acinetobacter baumannii* (10.8%) and *Enterococcus spp.* (10.8%). Infants under one year accounted for 82.2% of cases; males comprised 56.1%. High resistance was observed to ampicillin (90.6% Gram-negatives; 79.1% Gram-positives), ceftriaxone (77.6%), cotrimoxazole (72.8%), and gentamicin (60.3%). Meropenem resistance in Gram-negatives was lower (19%). *K. pneumoniae* showed 100% resistance to ampicillin, 88% to ceftriaxone and cotrimoxazole, and 82% to gentamicin. S*taphylococcus aureus* exhibited 100% resistance to ceftazidime and 87.5% to ciprofloxacin.
Conclusion: Bacteremia remains a significant burden in febrile under-five children, with high AMR rates limiting treatment options. Strengthening antimicrobial stewardship, implementing local AMR surveillance, and updating empirical treatment guidelines are critical to improving outcomes and reducing preventable child mortality in Ethiopia.

Keywords: Bacteremia, Antimicrobial resistance, Bloodstream infection, Paediatric infections, Ethiopia

INTRODUCTION

Bacteremia, defined as the presence of bacteria in the bloodstream, is a critical clinical condition that presents significant risks, particularly in pediatric populations under five years of age.[1] This infection can be transient or can lead to severe systemic inflammation and sepsis if not promptly recognized and adequately treated.[2] In children, bacteremia is clinically significant because of their immature immune systems, which are less capable of mounting effective defenses against invasive pathogens. The illness can rapidly progress, causing substantial morbidity characterized by prolonged hospitalization, invasive interventions, and potentially long-term health sequelae.[3] Mortality associated with pediatric bacteremia remains worryingly high, particularly in low- and middle-income countries where diagnostic and therapeutic resources may be limited.[4]

Globally, bloodstream infections (BSIs) account for a major portion of pediatric infectious disease morbidity and mortality, representing a challenging public health issue.

The epidemiology of bacteremia reveals wide geographic variations influenced by socio-economic status, healthcare infrastructure, and prevalent pathogens.[5] In sub-Saharan Africa, a region burdened by infectious diseases and systemic healthcare delivery challenges, bacteremia has particularly grave consequences in young children.[6] Empirical treatment strategies based on outdated resistance profiles can result in poor outcomes and increased healthcare costs.[7]

In Ethiopia, several studies have reported rising levels of resistance among common bloodstream pathogens, including *Klebsiella pneumoniae, Escherichia coli, Staphylococcus aureus*, and *Acinetobacter baumannii*, with many isolates showing resistance to first-line antibiotics such as ampicillin, cotrimoxazole, and even third-generation cephalosporins.[8-10] Resistance to first-line antibiotics, including ampicillin, amoxicillin-clavulanic acid, tetracycline, and trimethoprim-sulfamethoxazole, is reported at high rates in bacterial isolates from pediatric bloodstream and urinary tract infections. Multidrug resistance (MDR) and extended-spectrum beta-lactamase (ESBL) production have been observed in *Klebsiella pneumoniae, Escherichia coli*, and other Gram-negative isolates, complicating treatment choices.[11]

Despite the severity of the problem, there is limited published data on the burden of bacteremia and antimicrobial resistance patterns among febrile children under five in Bahir Dar.

This study aims to determine the prevalence of bacteremia and assess the antimicrobial resistance profiles of bacterial isolates among febrile under-five children from laboratory investigations performed at Amhara Public Health Institute, Bahir Dar, northwest Ethiopia.

METHODS

Study design and period

An institution based retrospective study was conducted at Amhara Public Health Institute which is found in Bahir Dar, Amhara National regional state to analyze laboratory data on bacterial isolates among febrile under-five children from clinical samples collected from 2018 to 2024.

Sample size

This study included all available microbiological culture and antimicrobial susceptibility testing results from febrile children under five years of age processed at the Amhara Public Health Institute between January 2018 and December 2024.

In total, 746 blood culture records meeting the inclusion criteria were analyzed to determine the antimicrobial resistance patterns of bacterial bloodstream infections to commonly used antimicrobial agents.

Data sources

Socio-demographic data and laboratory data for microbiological cultures and antibiotic susceptibility testing were retrieved from archived medical records of microbiology reference laboratory, Amhara Public Health Institute.

Inclusion criteria

All data from isolates tested for antibiotic susceptibility using standard methods and with confirmed samples taken from febrile under-five children patients during the study period was included.

Exclusion criteria

Incomplete records lacking susceptibility data were excluded from the study.

Data collection and analysis

Demographic information extracted for analysis included age, gender and address. Microbiological data, including bacteria identified, and antibiotic resistance profiles based on microbiological analysis of patient samples, were extracted. The bacterial isolates were identified and tested for antibiotic susceptibility using the modified Kirby–Bauer disc diffusion method on Mueller–Hinton agar plates, following the guidelines outlined in the Clinical and Laboratory Standards Institute (CLSI) guideline of 2020.[25] The collected data were checked; coded and entered into Epi info version 7.2.5 and exported to statistical package for the social sciences (SPSS) version 26.0 for further analysis. Characteristics of antibiotic resistance were analyzed using descriptive statistics for demographic and clinical variables were carried out to summarize data. The results were presented using tables. The overall resistance of bacterial strains and individual resistance profile of each strain to various antibiotics were presented using tables.

Ethical considerations

Ethical approval was obtained from the institutional review board of Amhara Public Health Institute. Patient confidentiality was maintained by unique identification to all records. The study poses no direct risk to participants as it uses secondary data. This study involved the collection of existing data and records. Informed consent was exempted according to the decision of institutional review board.

RESULTS

Distribution of organisms isolated

In our study, we analyzed a total of 746 data for antimicrobial resistance of blood stream bacterial infections to common antimicrobial agents from 2018 to 2024, of these 157 (21.04%) were culture positive. Of

these, *Klebsiella pneumoniae* is the most frequently isolated organism, accounting for 31.8% (50 cases) of the total isolates, followed by *Acinetobacter baumannii* and *Enterococcus spp.* are tied for the second most frequent, each at 10.8% (17 cases), *Enterobacter cloacae* follow at 9.6% (15 cases).

Coagulase-negative *Staphylococci* (CoNS) and *Escherichia coli* are next, each at 7.6% (12 cases), whereas *K. oxytoca* (2.5%), *K. ozaenae* (4.5%), *Pseudomonas aeruginosa* (4.5%), *S. aureus* (5.1%), and *Enterobacter aerogenes* (5.1%) are relatively less common but still significant. One hundred twenty (76.5%) of the infections were due to Gram negative bacteria whereas 37 (23.5%) of them were Gram positive bacteria, and these data are summarized in Table 1.

Distribution of isolates by age and sex

Most infections occur in infants <1 year (82.2%), with only 17.8% in children aged 1-5 years. *K. pneumoniae* (94% of its cases), *E. cloacae* (93.3%), *K. ozaenae* (100%) and *P. aeruginosa* (85.7%) were the highest prevalent isolates among <1 year group, whereas *K. oxytoca* is more common in 1-5-year-olds (75%). Out of 157 total isolates; 88 (56.1%) were from males whereas 69 (43.9%) were from females. *P. aeruginosa* (85.7% male), *K. oxytoca* (75%) and *K. pneumoniae* (64%) show male predominance, whereas *S. aureus* (75%) and *A. baumannii* (58.8%) skewed toward females. The details are presented in Table 2.

Table 1: Distribution of organisms isolated.

Isolated organisms	Frequency	%
Acinetobacter baumannii	17	10.8
CoNS	12	7.6
Enterobacter aerogenes	8	5.1
Enterobacter cloacae	15	9.6
Entrococuss spps	17	10.8
Escherchia coli	12	7.6
K. oxytoca	4	2.5
K. ozaenae	7	4.5
K. pneumonia	50	31.8
Pseudomonas aeruginosa	7	4.5
S. aureus	8	5.1
Total	157	100.0

Table 2: Distribution of isolates by age and sex.

Isolated organisms	Age category		Sex	
	<1 year (%)	**1-5 year (%)**	**Female (%)**	**Male (%)**
A. baumannii	13 (76.5)	4 (23.5)	10 (58.8)	7 (41.2)
CoNS	10 (83.3)	2 (16.7)	4 (33.3)	8 (66.7)
E. aerogenes	5 (62.5)	3 (37.5)	3 (37.5)	5 (62.5)
E. cloacae	14 (93.3)	1 (6.7)	9 (60.0)	6 (40.0)
Entrococuss spps	12 (70.6)	5 (29.4)	9 (52.9)	8 (47.1)
E. coli	8 (66.7)	4 (33.3)	4 (33.3)	8 (66.7)
K. oxytoca	1 (25.0)	3 (75.0)	1 (25.0)	3 (75.0)
K. ozaenae	7 (100.0)	0 (0.0)	4 (57.1)	3 (42.9)
K. pneumoniae	47 (94.0)	3 (6.0)	18 (36.0)	32 (64.0)
P. aeruginosa	6 (85.7)	1 (14.3)	1 (14.3)	6 (85.7)
S. aureus	6 (75.0)	2 (25.0)	6 (75.0)	2 (25.0)
Total	129 (82.2)	28 (17.8)	69 (43.9)	88 (56.1)

Antimicrobial resistance of bacterial isolates

The resistance profiles of all isolates against antimicrobials from blood sample showed significant differences in response to all antimicrobial agents. We retrospectively analyzed the differences in antimicrobial susceptibility of *Acinetobacter baumannii, Citrobacter species, Enterobacter aerogenes, Enterobacter Cloacae, Escherchia Coli, Klebsiella oxytoca, Klebsiella ozaenae, Klebsiella pneumonia, S. aureus, Coagulase* Negative *Staphylococus spp, Entrococuss spps,* and *Pseudomonas aeruginosa*. *Klebsiella pneumonia* had high resistance to Ampicillin (100%), Ceftraiaxone (88%), Co-trimoxazole (88%), Gentamicin (82%) and Tobramycin (70%) nevertheless it was sensitive to Ceftazidime (34%) and Meropenom (14%). *Escherchia coli* showed high resistance to Ampicillin (100%), Tobramycin (91.7%), Co-trimoxazole (91.7%), Chloramphenicol (75%), Ceftazidime (75%) and Ciprofloxacin (75%) nevertheless it was sensitive to Meropenem (16.7%). *Acinetobacter baumannii* had high resistance to Ceftriaxone (76.5%) however it was sensitive to Cefoxitin (11.8%), Tetracycline (35.3%) and Meropenem (29.4%). *Enterobacter aerogenes* had high resistance to Ampicillin (100%), Tobramycin (100%), Co-trimoxazole (100%), Ceftraiaxone (76.5%) and Chloramphenicol (75%) however sensitive to Cefoxitin (12.5%) and Meropenem (25%). *Pseudomonas aeruginosa* had high resistance to Ceftriaxone (71.4%) however sensitive to Tobramycin (28.6%), Ceftazidime (14.3%), Gentamicin (28.6%), Tetracycline (14.3%) and Meropenem (14.3%). *S. aureus* had high resistance to Ciprofloxacin (87.5%) and Co-trimoxazole (87.5%) nevertheless it was sensitive to Tetracycline (37.5%). Coagulase negative *Staphylococus*

spp. showed high resistance to Co-trimoxazole (75%) and Ciprofloxacin (66.7%) nevertheless it was sensitive to Cefoxitin (8.3%), Gentamicin (25%) and Tetracycline (41.7%). *Entrococuss spp.* showed high resistance to Co-trimoxazole (88.2%), Ciprofloxacin (88.2%), Ampicilin (82.4%), and Gentamicin (76.5 nevertheless it was sensitive to Tobramycin (29.4%) and Ceftraiaxone (35.3%). The details of resistance of all pathogens are presented in Tables 3-5.

Table 3: Overall antimicrobial resistance rate of gram-positive and gram-negative bacteria.

Antimicrobials	Gram -positive bacteria	Gram -negative bacteria
	% Resistance	% Resistance
Ampicilin	78.7	90.6
Amox/Clav	48.4	75.0
Chloramphenicol	63.0	67.2
Tobramycin	58.4	64.7
Ceftraiaxone	52.0	77.6
Ceftazidime	70.6	53.6
Ciprofloxacin	80.8	58.6
Cefoxitin	41.3	33.8
Co-trimoxazole	83.6	72.8
Gentamicin	46.3	60.3
Tetracycline	48.0	57.6
Meropenem	68.0	19.0

Table 4: Antimicrobial resistance rate of gram-positive bacteria.

Antimicrobials	Gram-positive bacteria		
	CONS	***Enterococcus spps.***	***S. aureus***
Ampicillin	Not tested	82.4	75
Amox/Clav	41.7	Not tested	62.5
Chloramphenicol	50.0	Not tested	Not tested
Tobramycin	58.3	29.4	Not tested
Ceftraiaxone	58.3	35.3	62.5
Ceftazidime	Not tested	70.6	Not tested
Ciprofloxacin	66.7	88.2	87.5
Cefoxitin	8.3	52.9	62.5
Co-trimoxazole	75.0	88.2	87.5
Gentamicin	25.0	76.5	Not tested
Tetracycline	41.7	64.7	37.5
Meropenem	58.3	70.6	75

Table 5: Antimicrobial resistance rate of gram-negative bacteria.

Antimicrobials	Gram-negative bacteria							
	A. baumannii	***E. aerogenes***	***E. cloacae***	***E. coli***	***K. oxytoca***	***K. ozaenae***	***K. pneumoniae***	***P. aeruginosa***
Ampicillin	Not tested	100	100	100	25	100	100	Not tested
Amox/Clav	Not tested	75	100	66.7	16.7	71.4	74	Not tested
Chloramphenicol	Not tested	75	80	75	18.8	71.4	60	Not tested
Tobramycin	58.8	100	60	91.7	22.9	85.7	70	28.6
Ceftriaxone	76.5	87.5	93.3	83.3	20.8	100	88	71.4
Ceftazidime	58.8	62.5	80	75	18.8	85.7	34	14.3
Ciprofloxacin	58.8	62.5	73.3	75	18.8	85.7	66	28.6
Cefoxitin	11.8	12.5	81.0	58.3	14.6	14.3	46	32.0
Co-trimoxazole	64.7	100	86.7	91.7	22.9	100	88	Not tested
Gentamicin	Not tested	75	73.3	58.3	14.6	85.7	82	28.6
Tetracycline	35.3	75	53.3	100	25	85.7	72	14.3
Meropenem	29.4	25	20	16.7	4.2	28.6	14	14.3

DISCUSSION

Antibiotic-resistant bacterial infections are an increasing cause of morbidity and mortality worldwide.[12] AMR poses a significant public health challenge, with serious clinical and economic consequences.[13] This retrospective, institution-based study was conducted from 2018 to 2024 to determine the prevalence of bacteremia and assess antimicrobial resistance patterns among bacterial isolates from febrile children under five, based on laboratory investigations at the Amhara Public Health Institute in Bahir Dar, northwest Ethiopia.

The result of this study identified a bacteremia prevalence of 21.04% (157 cases). This prevalence is comparable to a study from Gondar, Ethiopia that reported bloodstream infection prevalence of 20.7% and another Ethiopian study in which culture-positive bacteria causing pediatric sepsis were present in 21.6% of cases, suggesting a consistent pattern of bacteremia among pediatric patients in the country.[14,15]

Klebsiella pneumoniae was the most frequently isolated organism, accounting for 31.8% (50 cases), consistent with a study from Tanzania (26.9%).[16] Its high prevalence may be attributed to its nosocomial potential, environmental persistence, and increasing resistance, complicating treatment efforts. Similar findings were reported in a Tanzanian study indicating *K. pneumoniae* (26.9%) as the most common bacterial pathogen.[16]

The high frequency of *K. pneumoniae* may reflect its strong nosocomial potential, ability to survive in hospital environments, and growing antimicrobial resistance. In this study, *Acinetobacter baumannii, Enterococcus spp., Enterobacter cloacae,* CONS, *Escherichia coli, K. oxytoca, K. ozaenae, Pseudomonas aeruginosa, S. aureus*, and *Enterobacter aerogenes* were also identified as causes of bacteremia. These findings were similar to a study from Bahir Dar, Ethiopia reporting *S. aureus, K. pneumoniae, A. baumannii, P. aeruginosa*, and Enterobacter species as part of the ESKAPE pathogens, the leading cause of hospital-acquired infections.[17]

This study also revealed a higher proportion of Gram-negative isolates (76.5%) compared to Gram-positive ones (23.5%). Gram-negative bacteria, especially *Enterobacteriaceae*, are often associated with more severe infections and higher mortality due to their virulence factors and resistance mechanisms. This result was consistent with previous studies showing Gram-negative bacteria cause a higher rate of BSI than Gram-positive bacteria.[18,19]

Bacteremia was more prevalent in males than females, consistent with an Ethiopian study reporting 23.8% in males versus 19.2% in females.[1] In our study, most infections occurred in infants under one year (82.2%), with only 17.8% in children aged 1–5 years. This aligns with reports that neonates and young infants are at higher risk due to immature immune systems, perinatal risk factors, and frequent hospital exposure, such as an Ethiopian study in which 73.8% of infections occurred in children under one year.[15]

Our findings showed *K. pneumoniae* had high resistance to ampicillin, ceftriaxone, cotrimoxazole, gentamicin, and tobramycin but was sensitive to ceftazidime and meropenem. This mirrors a Rwandan study reporting 100% resistance to ampicillin, 42.8% to ciprofloxacin, 77.3% to gentamicin, and 33.3% to cefotaxime.[20]

E. coli showed significant resistance to ampicillin, tobramycin, cotrimoxazole, chloramphenicol, ceftazidime, and ciprofloxacin, but remained sensitive to meropenem. These results align with a Rwandan study reporting >90% resistance to tetracycline and ampicillin, 83.3% to amoxicillin–clavulanic acid, 79.3% to cefadroxil, and 78.6% to ceftazidime.[21]

A. baumannii was highly resistant to ceftriaxone, but sensitive to cefoxitin, tetracycline, and meropenem. E. aerogenes showed complete resistance (100%) to ampicillin, tobramycin, and cotrimoxazole, and high resistance to ceftriaxone (76.5%) and chloramphenicol (75%), with partial sensitivity to cefoxitin (12.5%) and meropenem (25%). These results match an Ethiopian study where *E. aerogenes* showed 90.9% resistance to ampicillin, 100% to amoxicillin, 62.5% to ceftriaxone, and high resistance to multiple other antibiotics.[14]

Enterococcus spp. showed high resistance to cotrimoxazole, ciprofloxacin, ampicillin, and gentamicin, while remaining sensitive to tobramycin and ceftriaxone. Similar resistance patterns have been reported in Myanmar, where ampicillin resistance ranged from 68% to 89%, with high resistance to erythromycin, tetracycline, and ciprofloxacin.[22] A study from Bangladesh also found high resistance to ampicillin and ciprofloxacin among *Enterococcus* isolates.[23]

S. aureus showed high resistance to ciprofloxacin and cotrimoxazole but was sensitive to tetracycline. *Coagulase-negative staphylococci* showed high resistance to cotrimoxazole and ciprofloxacin but were sensitive to cefoxitin, gentamicin, and tetracycline. These results agree with an Ethiopian study in which *S. aureus* showed the highest resistance to penicillin (92.3%), followed by ampicillin (84.6%), cotrimoxazole (61.5%), and tetracycline (53.8%). *Coagulase-negative staphylococci* exhibited 81.8% resistance to penicillin and cotrimoxazole, and 100% to ampicillin. Serratia marcescens showed 100% resistance to ampicillin, followed by gentamicin, tetracycline, and cotrimoxazole (91.7% each).[24]

Limitations

This study had some limitations. First, its retrospective design relied on existing laboratory records, which may be

subject to incomplete documentation and missing variables such as prior antibiotic use, clinical presentation, and patient outcomes. Second, the data were obtained from a single reference laboratory, which may not fully represent bacteremia prevalence and antimicrobial resistance patterns in other healthcare settings within the region. Third, only culture-confirmed cases were included, potentially underestimating the true burden of bacteremia, as culture-negative infections and fastidious organisms could not be captured. Finally, antimicrobial susceptibility testing was limited to the antibiotics routinely included in the laboratory panel, and molecular mechanisms of resistance were not investigated. These factors should be considered when interpreting the findings, and future studies with a prospective, multicenter design and expanded laboratory analyses are recommended.

CONCLUSION

This study provides important insights into the burden of bacteremia and AMR among febrile under-five children in northwest Ethiopia. The overall prevalence of culture-confirmed bacteremia was 21.04%, aligning with findings from other regions of Ethiopia. The dominant bacterial isolates identified were *Klebsiella pneumoniae, Acinetobacter baumannii, and Enterococcus spp*., with a notable predominance of Gram-negative bacteria (76.5%) over Gram-positive ones (23.5%). Infants under one year of age and male children were disproportionately affected, emphasizing the vulnerability of this age group and gender. A key finding from this study is the alarmingly high rate of resistance to commonly used antibiotics, including ampicillin, ceftriaxone, gentamicin, and co-trimoxazole, across most bacterial isolates. Resistance to meropenem, although relatively lower in Gram-negative isolates, remains a concerning development, signaling potential emergence of carbapenem-resistant strains. The high level of drug resistance observed in both Gram-negative and Gram-positive bacteria poses a serious therapeutic challenge and underscores the urgent need for enhanced antimicrobial stewardship and effective infection control policies. Furthermore, the absence of robust antimicrobial resistance surveillance systems in the region hampers timely detection of resistance trends and formulation of evidence-based empirical treatment guidelines.

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