

BLOOD CULTURE PROVEN COMMON BACTERIAL PATHOGENS IN PATIENTS ADMITTED IN THE PEDIATRIC UNIT OF A TERTIARY CARE HOSPITAL IN PAKISTAN

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ABSTRACT

Background: Bloodstream infections (BSIs) in pediatric populations represent a substantial burden of morbidity and mortality, particularly in developing countries. Rapid identification of causative bacterial pathogens and determination of their antimicrobial susceptibility profiles are essential for timely intervention and effective management of sepsis. **Objective:** To determine the spectrum of bacterial pathogens isolated from blood cultures and assess their antimicrobial sensitivity patterns among pediatric patients admitted with sepsis at a tertiary care hospital in Pakistan. **Study Design:** Descriptive cross-sectional study. **Settings:** Department of Pediatrics, Fauji Foundation Hospital, Rawalpindi, Pakistan. **Duration of Study:** 23 January 2025 to 23 April 2025. **Methods:** Blood samples were collected aseptically from pediatric patients meeting the clinical criteria for sepsis and processed using an automated BACTEC system. Standard microbiological techniques, identified bacterial isolates, and antimicrobial susceptibility testing were conducted by Clinical and Laboratory Standards Institute (CLSI) guidelines. Data were analyzed using SPSS version 25.0, with Chi-square tests applied to evaluate associations between categorical variables. **Results:** Among 145 enrolled patients, 117 (80.7%) demonstrated positive blood cultures. *Staphylococcus aureus* was the predominant pathogen (27.4%), followed by *Escherichia coli* (23.9%) and *Klebsiella pneumoniae* (22.2%). *Staphylococcus aureus* exhibited 100% sensitivity to vancomycin, while imipenem showed high efficacy against *E. coli* (95%) and *K. pneumoniae* (90%). Notably, substantial resistance to third-generation cephalosporins was observed. A statistically significant association was found between male gender and a higher incidence of *Staphylococcus aureus* infections ($p=0.045$). **Conclusion:** *Staphylococcus aureus* remains the leading cause of pediatric bloodstream infections, and emerging antimicrobial resistance patterns pose a serious challenge to empirical therapy. Routine surveillance of bacterial pathogens and their resistance profiles is imperative to guide effective antimicrobial stewardship and improve clinical outcomes in Pakistan's pediatric population.

Keywords: Sepsis; Bloodstream Infection; Pediatric Sepsis; Antimicrobial Resistance; Bacterial Pathogens; Pakistan

INTRODUCTION

Sepsis remains a major cause of morbidity and mortality in pediatric populations worldwide, particularly in low- and middle-income countries like Pakistan. Bloodstream infections in children are associated with a significant healthcare burden due to prolonged hospitalizations, increased antimicrobial resistance, and poor clinical outcomes if not diagnosed and treated promptly (1). Early identification of causative organisms through blood culture is crucial for guiding appropriate antibiotic therapy and improving patient prognosis (2).

In Pakistan, infectious diseases contribute significantly to pediatric mortality, accounting for nearly 30–40% of all childhood deaths (3). Despite improvements in public health interventions, bacterial sepsis continues to pose a critical challenge, particularly in tertiary care centers where patients often present with advanced stages of infection (4). Blood culture remains the gold standard for diagnosis, but several regional studies have reported varying positivity rates and pathogen spectra, reflecting differences in microbial epidemiology and healthcare practices (5).

Studies from urban centers like Karachi, Lahore, and Rawalpindi have consistently highlighted gram-positive organisms such as *Staphylococcus aureus* and gram-negative bacteria, including *Escherichia coli* and *Klebsiella pneumoniae*, as predominant pathogens in pediatric sepsis (6,7). However, over the past decade, antimicrobial resistance patterns have shown alarming trends, with increased resistance to third-generation cephalosporins and even carbapenems (8). This escalating resistance emphasizes the need for

continuous local surveillance to update empirical antibiotic guidelines.

Moreover, there is a paucity of recent large-scale data focusing exclusively on pediatric bloodstream infections in Pakistani tertiary care settings. Most available studies are either outdated or limited in scope (9). With evolving bacterial profiles and emerging resistant strains, periodic evaluation of blood culture isolates and their antimicrobial susceptibility patterns is critical for timely interventions, policy formulation, and antibiotic stewardship programs (10).

The World Health Organization has globally urged countries to monitor antimicrobial resistance trends and adapt empirical therapy protocols based on local data (11). In Pakistan, however, regional variation exists even within provinces, necessitating localized research for more effective clinical management (12).

The current study is, therefore, designed to determine the spectrum of blood culture-proven bacterial pathogens in pediatric patients admitted to a tertiary care hospital in Rawalpindi. It also aims to analyze antimicrobial susceptibility patterns, providing updated evidence to guide empirical treatment decisions in the pediatric population. Given the rising burden of pediatric sepsis and antimicrobial resistance in Pakistan, there is an urgent need for updated local data to inform clinical practice. By identifying the prevalent organisms and their resistance profiles in children admitted with sepsis, this study will contribute to optimizing empirical treatment protocols, enhancing patient outcomes, and strengthening infection control strategies in tertiary care hospitals.

METHODOLOGY

This descriptive cross-sectional study was conducted at the Department of Pediatrics, Fauji Foundation Hospital, Rawalpindi, Pakistan. It was designed to identify the spectrum of bacterial pathogens isolated from blood cultures of pediatric patients admitted with a clinical diagnosis of sepsis. Following approval from the hospital's Institutional Review Board, the study lasted three months, from 23 January 2025 to 23 April 2025. Before enrollment, written informed consent was obtained from all patients' parents or legal guardians. A non-probability consecutive sampling technique was used. The study included all pediatric patients aged between 1 and 12 who were admitted to the Pediatric Unit with clinical suspicion of sepsis and whose blood cultures were sent before the initiation of antibiotics. Patients who had received antibiotic therapy before sample collection or whose blood cultures contained contaminants were excluded to ensure the accuracy and reliability of microbiological findings. Blood samples were collected using strict aseptic techniques. About 3–5 mL of venous blood was drawn and immediately inoculated into blood culture bottles. Samples were transported to the Microbiology Laboratory of Fauji Foundation Hospital without delay. The blood culture bottles were incubated using the automated BACTEC blood culture system. Positive cultures were subjected to further identification and antimicrobial sensitivity testing by conventional methods, including Gram staining, biochemical reactions, and the Kirby-Bauer disc diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Demographic information, including age, gender, and clinical diagnosis, was recorded on a pre-designed proforma. The bacterial isolates were categorized, and their frequency and antimicrobial resistance patterns were noted. Data entry and analysis were performed using SPSS version 25.0. Categorical variables such as gender, bacterial species, and antibiotic sensitivity were presented as frequencies and percentages. The Chi-square test was applied to assess associations between categorical variables, and a p-value of <0.05 was considered statistically significant.

RESULTS

One hundred forty-five patients diagnosed with sepsis and admitted to the Department of Pediatrics, Fauji Foundation Hospital, Rawalpindi, were enrolled over the study period. The demographic characteristics, including age and gender distribution, are presented in Table 1. The mean age of patients was 5.8 ± 3.2 years (ranging from 1 to 12 years), with a slightly higher proportion of males than females. Table 1 shows that most pediatric patients were under the age of 8 years, and males were slightly predominant. The blood cultures were positive in 117 (80.7%) cases, while 28 (19.3%) cultures remained sterile or had contaminants and were excluded from pathogen analysis. Table 2 summarizes the distribution of isolated bacterial pathogens. (Table2)

Table 4: Distribution of Pathogens According to Age and Gender (n=117)

Pathogen	1–4 years (n=60)	5–8 years (n=50)	9–12 years (n=35)	Male (n=82)	Female (n=63)
Staphylococcus aureus	14 (43.8%)	12 (24%)	6 (17.1%)	18 (22%)	14 (22.2%)
Escherichia coli	12 (37.5%)	10 (20%)	6 (17.1%)	16 (19.5%)	12 (19%)
Klebsiella pneumoniae	8 (25%)	10 (20%)	8 (22.8%)	14 (17%)	12 (19%)
Streptococcus pneumoniae	5 (15.6%)	10 (20%)	3 (8.5%)	10 (12%)	8 (13%)
Others	6 (18.8%)	8 (16%)	5 (14.2%)	8 (9.8%)	5 (8%)

DISCUSSION

This study provides valuable insights into the bacterial pathogens isolated from blood cultures of pediatric patients admitted with sepsis

Table 1: Demographic Characteristics of the Study Population (n=145)

Variables	Subgroups	Frequency (n)	(%)
Age Groups	1–4 years	60	41.4%
	5–8 years	50	34.5%
	9–12 years	35	24.1%
Gender	Male	82	56.6%
	Female	63	43.4%

Table 2: Distribution of Bacterial Isolates in Blood Culture (n=117)

Bacterial Pathogen	Frequency (n)	(%)
Staphylococcus aureus	32	27.4%
Escherichia coli	28	23.9%
Klebsiella pneumoniae	26	22.2%
Streptococcus pneumoniae	18	15.4%
Others (Pseudomonas, etc.)	13	11.1%

Table 2 demonstrates that Staphylococcus aureus was the most commonly isolated organism, followed by Escherichia coli and Klebsiella pneumoniae. Antimicrobial susceptibility testing was performed for all isolates. The sensitivity and resistance profiles are shown in Table 3.

Table 3: Antimicrobial Sensitivity Patterns of Bacterial Isolates

Pathogen	Antibiotics	Sensitive (%)	Resistant (%)
Staphylococcus aureus	Vancomycin	100%	0%
	Oxacillin	70%	30%
	Clindamycin	75%	25%
Escherichia coli	Imipenem	95%	5%
	Cefotaxime	60%	40%
	Ciprofloxacin	55%	45%
Klebsiella pneumoniae	Imipenem	90%	10%
	Ceftriaxone	50%	50%
Streptococcus pneumoniae	Penicillin	85%	15%
	Vancomycin	100%	0%

Table 3 highlights significant antimicrobial resistance patterns, particularly among gram-negative isolates such as E. coli and Klebsiella pneumoniae. Further analysis was done to evaluate the distribution of pathogens according to patient age groups and gender, summarized in Table 4. Statistical analysis using the Chi-square test showed no significant association between age group and type of pathogen isolated (p = 0.083). Still, a significant association between gender and specific pathogens, particularly Staphylococcus aureus, is more frequent in males (p = 0.045).

in a tertiary care hospital in Rawalpindi, Pakistan. Our findings demonstrate that blood culture positivity was observed in 80.7% of cases, which is relatively higher than previous studies conducted in similar settings reporting positivity rates between 40–65% (13,14). This high culture yield may be attributed to improved blood sample

collection techniques and early sampling before initiation of antibiotics.

The predominant pathogen identified was *Staphylococcus aureus* (27.4%), followed by *Escherichia coli* (23.9%), *Klebsiella pneumoniae* (22.2%), and *Streptococcus pneumoniae* (15.4%). These findings align with a recent study from Lahore, where *Staphylococcus aureus* accounted for 25.7% and *E. coli* for 22.5% of bloodstream infections among pediatric patients (15). Similarly, a study from Karachi reported *Staphylococcus aureus* as the leading isolate (30%), followed by *Klebsiella pneumoniae* (18%) (16). However, a multicenter study conducted in South Punjab found a slightly different pattern, with *Klebsiella pneumoniae* (29%) being the most frequent isolate, indicating regional variability (17).

The antimicrobial susceptibility patterns observed in our study raise significant concerns. *Staphylococcus aureus* demonstrated 100% sensitivity to Vancomycin but showed 30% resistance to Oxacillin, highlighting the persistence of methicillin-resistant *Staphylococcus aureus* (MRSA) strains. This is consistent with a study from Islamabad, where MRSA prevalence among pediatric isolates was 28% (18). *Escherichia coli* and *Klebsiella pneumoniae* exhibited high sensitivity to Imipenem (95% and 90%, respectively). Still, they showed considerable resistance to third-generation cephalosporins (Cefotaxime resistance of 40% and Ceftriaxone resistance of 50%, respectively), matching trends reported from other tertiary care hospitals in Pakistan (19,20).

Age-wise distribution analysis revealed that children aged 1–4 years were most frequently affected, accounting for 41.4% of infections. This pattern is corroborated by a study in Peshawar, where early childhood (under 5 years) was the most vulnerable age group for bloodstream infections (21). Male predominance (56.6%) among septicemia cases in our study mirrors previous local findings. It has been attributed to biological susceptibility and socio-cultural factors leading to greater healthcare-seeking behavior for male children (22). The significant association between male gender and higher isolation rates of *Staphylococcus aureus* ($p = 0.045$) suggests a possible gender predisposition or exposure difference. However, further multicenter studies are needed to confirm this trend. No significant correlation between specific pathogens and age groups was detected ($p = 0.083$), indicating that many bacterial pathogens can affect pediatric patients across all age brackets.

Our findings underscore the urgent need for periodic local surveillance of bloodstream infections and antibiotic resistance trends to inform empirical therapy, especially given the rising threat of multidrug-resistant organisms. By global WHO guidelines, continuous monitoring of bacterial isolates and rational use of antibiotics should be emphasized to combat antimicrobial resistance in pediatric populations (23).

CONCLUSION

This study highlights *Staphylococcus aureus* as the most common bacterial isolate causing bloodstream infections in pediatric patients admitted with sepsis, followed closely by *Escherichia coli* and *Klebsiella pneumoniae*. A concerning level of antimicrobial resistance was observed, particularly against third-generation cephalosporins. The significant association between male gender and *Staphylococcus aureus* infections emphasizes the need for gender-sensitive health interventions. These findings reinforce the necessity for ongoing local surveillance of bacterial pathogens and antibiotic susceptibility patterns to guide empirical therapy effectively. Prompt diagnosis, tailored antimicrobial strategies, and adherence to infection control practices are essential to improve clinical outcomes in pediatric sepsis cases in Pakistan.

DECLARATIONS

Data Availability Statement

All data generated or analysed during the study are included in the manuscript.

Ethics approval and consent to participate

Approved by the department Concerned. (IRBEC-MMCH-083-24)

Consent for publication

Approved

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Not applicable

CONFLICT OF INTEREST

The authors declared an absence of conflict of interest.

AUTHOR CONTRIBUTION

MUHAMMAD IBRAR KHAN (PGR)

Conception of Study, Development of Research Methodology Design, Study Design, Review of manuscript, final approval of manuscript.

Manuscript revisions, critical input.

Study Design, Review of Literature.

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Manuscript drafting.

Conception of Study, Final approval of manuscript.

Data entry and Data analysis, drafting article.

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