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Bacterial Etiology and Antimicrobial Susceptibility Patterns of Bloodstream Infections among Pediatric Patients in a Tertiary Care Hospital: A Cross-Sectional Study

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Abstract

Bloodstream infections (BSIs) are an important cause of morbidity and mortality among children, particularly in low- and middle-income countries. Early identification of causative organisms and their antimicrobial susceptibility patterns is essential for appropriate antimicrobial therapy and antimicrobial stewardship. This retrospective cross-sectional study was conducted in the Department of Microbiology and Virology, KPJ Specialized Hospital, Kashimpur, Gazipur, Bangladesh, from January 2025 to September 2025. A total of 609 blood culture specimens obtained from children aged ≤ 18 years with clinically suspected bloodstream infection were retrospectively analyzed. Blood cultures were processed using the automated BD BACTEC FX^{TM} 40 system. Bacterial isolates were identified using conventional microbiological methods, and antimicrobial susceptibility testing (AST) was performed by the Kirby-Bauer disk diffusion method according to the applicable Clinical and Laboratory Standards Institute (CLSI) criteria. Bacterial growth was detected in 69 of

609 blood cultures (11.3%). The majority of children were aged 1 - 5 years (62.4%), and 59.4% were male. Fever was the most common presenting complaint (47.6%), followed by respiratory distress (33.3%). Among culture-positive isolates, Gram-positive and Gram-negative organisms accounted for 50.7% and 49.3%, respectively. *Staphylococcus aureus* was the most frequently reported bacterial isolate, followed by *Klebsiella* spp. and *Acinetobacter* spp. Resistance to several commonly used antimicrobial agents was observed among both Gram-positive and Gram-negative isolates. Susceptibility percentages were interpreted according to the number of isolates tested for each antimicrobial agent, and findings based on very small numbers of isolates were interpreted cautiously. The observed antimicrobial resistance among pediatric bloodstream isolates highlights the importance of routine blood culture testing, continuous local antimicrobial resistance surveillance, and antimicrobial stewardship. Local susceptibility data should be regularly reviewed to support appropriate empirical and definitive antimicrobial treatment.

Keywords

Bloodstream Infection, Blood Culture, Pediatric Sepsis, Antimicrobial Susceptibility, Antimicrobial Resistance

1. Introduction

Bloodstream infections (BSIs) are a major cause of morbidity and mortality worldwide and represent an important clinical manifestation of severe bacterial infection and sepsis. They occur when viable microorganisms gain access to the bloodstream and may progress rapidly to systemic inflammatory responses, organ dysfunction, septic shock, and death. BSIs may arise from primary bloodstream infection or secondary spread from infections involving sites such as the respiratory tract, urinary tract, abdomen, skin, or other tissues [1]-[6].

Children are particularly vulnerable to severe bacterial infections because of age-related differences in immune function, physiological reserves, and host defense mechanisms. The clinical presentation of pediatric bloodstream infection may be nonspecific, particularly in younger children, making early microbiological diagnosis important. Blood culture remains the principal laboratory method for identifying bloodstream pathogens and provides an opportunity to determine antimicrobial susceptibility and guide targeted treatment [7]-[10].

A wide range of Gram-positive and Gram-negative bacteria can cause bloodstream infections in children. Important Gram-negative pathogens include *Escherichia coli*, *Klebsiella* spp., *Acinetobacter* spp., *Pseudomonas aeruginosa*, *Salmonella* spp., and other Enterobacterales. Important Gram-positive pathogens include *Staphylococcus aureus*, coagulase-negative staphylococci (CoNS), streptococci, and enterococci [11] [12]. The relative contribution of individual organisms varies according to patient age, community- or hospital-acquired infection, underlying disease, healthcare exposure, local infection control practices, and antimicrobial use.

Antimicrobial resistance (AMR) has substantially complicated the management of bloodstream infections. Increasing resistance to commonly used β-lactams, fluoroquinolones, aminoglycosides, and other antimicrobial classes may limit empirical treatment options and increase the risk of treatment failure. Consequently, local antimicrobial susceptibility surveillance is essential for selecting appropriate empirical therapy and for updating institutional antimicrobial guidelines [13]-[16].

Data on pediatric bloodstream infections and their antimicrobial susceptibility patterns remain limited in many South Asian settings, including Bangladesh. Differences in bacterial distribution and resistance patterns between hospitals and geographical regions make locally generated microbiological data particularly important for clinical decision-making. Previous studies from Bangladesh and neighboring countries have demonstrated considerable variation in the predominance of Gram-positive and Gram-negative pathogens and in their antimicrobial susceptibility profiles [17]-[23].

Therefore, the present study was undertaken to determine the bacterial etiology and antimicrobial susceptibility patterns of bloodstream infections among pediatric patients attending a tertiary care hospital in Bangladesh.

2. Materials and Methods

2.1. Study Design and Setting

This retrospective cross-sectional study was conducted in the Department of Microbiology and Virology, KPJ Specialized Hospital, Kashimpur, Gazipur, Bangladesh. The study included blood culture specimens obtained from pediatric patients with clinically suspected bloodstream infection during the period from 1 January 2025 to 30 September 2025. Data were retrospectively retrieved from laboratory records, laboratory requisition forms, and available patient records.

The study was conducted in accordance with applicable institutional ethical requirements and the ethical guidelines of the Bangladesh Medical Research Council (BMRC). Ethical approval was obtained from the institutional ethical authority of KPJ Specialized Hospital & Nursing College under approval number KPJSH/CC&RPIC/RPA/2026/001, dated 22 July 2026. The ethical approval letter specified that no participation was permitted without informed consent. As the present study involved a retrospective review of previously collected clinical and laboratory records, the consent procedure applied to the study should be reported in accordance with the approved protocol and institutional requirements. Patient confidentiality was maintained throughout the study by restricting access to study records and using coded/anonymized data for analysis. No personally identifiable information was included in the final analysis or manuscript.

2.2. Study Population

The study included pediatric patients aged ≤ 18 years who underwent blood culture testing as part of their routine clinical evaluations.

2.3. Inclusion Criteria

1) Children aged ≤ 18 years.

2) Patients clinically suspected of having a bloodstream infection for whom blood culture testing was requested.

3) Blood culture specimens were received and processed in the microbiology laboratory between 1 January 2025 and 30 September 2025.

4) Availability of sufficient demographic and microbiological information for analysis.

2.4. Exclusion Criteria

1) Patients aged > 18 years.

2) Duplicate blood culture specimens or duplicate isolates from the same patient during the same infectious episode.

3) Records with insufficient demographic or microbiological information for the intended analysis.

4) Blood cultures are interpreted as contaminants according to predefined clinical and microbiological criteria.

2.5. Clinical Data Collection

Demographic and clinical information was retrospectively obtained from laboratory requisition forms, available patient records, and the laboratory information system. The variables included age, sex, presenting complaints, blood culture result, isolated bacterial pathogen, and antimicrobial susceptibility results.

2.6. Definition and Handling of Blood Culture Contamination

Blood culture isolates considered contaminants were excluded from the final analysis according to the laboratory's predefined clinical and microbiological interpretation criteria. The assessment of contamination was based on the identity of the isolated organism, the clinical context, and, where available, information from repeat blood cultures and the likelihood of true bloodstream infection. No blood culture was excluded because of contamination during the study period.

2.7. Blood Sample Collection

Blood samples were collected by trained healthcare personnel using standard aseptic techniques in accordance with institutional infection-prevention and control procedures. The venipuncture site was disinfected using 70% isopropyl alcohol followed by a chlorhexidine-based antiseptic solution. Two blood culture sets were collected from each patient, with aerobic and anaerobic bottles used for culture. Age- and weight-appropriate blood volumes were collected, with approximately 0.4 - 5 mL collected from infants and 5 - 10 mL from children according to body weight. Blood samples were collected before the initiation of empirical antibiotic therapy and were inoculated directly into the blood culture bottles. The inoculated bottles were then transported to the microbiology laboratory for pro-

cessing.

2.8. Blood Culture Processing

Blood culture specimens were incubated and continuously monitored for microbial growth using the automated BD BACTEC FX^{TM}40 blood culture system according to the manufacturer's recommended procedures. Bottles flagged as positive were removed for further microbiological processing and subcultured onto appropriate culture media, including Blood Agar, MacConkey Agar, and Chocolate Agar, as indicated. The inoculated media were incubated at 37˚C under appropriate atmospheric conditions and examined for bacterial growth after 18 - 24 hours, with additional incubation when required.

2.9. Identification of Bacterial Isolates

Bacterial isolates were identified using standard conventional microbiological procedures, including colony morphology, Gram staining, and appropriate biochemical reactions. Organism identification was based on the routine laboratory identification procedures applicable during the study period.

2.10. Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed by the Kirby-Bauer disk diffusion method on Mueller-Hinton agar according to the applicable Clinical and Laboratory Standards Institute (CLSI) interpretive criteria in use during the study period. The exact CLSI edition used for each test should be confirmed from the laboratory's records and stated explicitly in the final manuscript.

For Gram-positive organisms, the antimicrobial agents tested included meropenem, ampicillin, oxacillin, moxifloxacin, chloramphenicol, cotrimoxazole, azithromycin, vancomycin, linezolid, amikacin, ciprofloxacin, levofloxacin, amoxicillin-clavulanic acid, gentamicin, piperacillin, ceftazidime, tetracycline, clindamycin, flucloxacillin, penicillin, cefoxitin, and teicoplanin, where applicable to the organism tested.

For Gram-negative organisms, antimicrobial agents tested included meropenem, imipenem, ampicillin, cefixime, ceftriaxone, cefotaxime, cefuroxime, cefepime, cephalexin, ciprofloxacin, levofloxacin, moxifloxacin, chloramphenicol, cotrimoxazole, amikacin, gentamicin, piperacillin, netilmicin, polymyxin, azithromycin, nalidixic acid, tigecycline, tobramycin, and amoxicillin-clavulanic acid, where applicable to the organism tested.

Inhibition-zone diameters were measured and interpreted as susceptible (S), intermediate (I), or resistant (R) according to the applicable CLSI breakpoints. For each organism-antimicrobial combination, the denominator was the number of isolates actually tested against that antimicrobial agent.

2.11. Data Analysis

Data were summarized using descriptive statistics. Categorical variables were ex-

pressed as frequencies and percentages. Antimicrobial susceptibility was reported as the proportion of tested isolates categorized as susceptible, intermediate, or resistant. Because several organism groups contained very small numbers of isolates, particularly single-isolate groups, these percentages were interpreted descriptively and not as stable estimates of population-level susceptibility.

3. Results

Table 1. Distribution of cases according to age group.

Age Group	Frequency	Percent (%)
<1	62	10.2
1 to 5 years	380	62.4
5 to 10 years	136	22.3
>10 Years	31	5.1
Total	609	100.0

Table 1 shows the age distribution of the cases. Among the 609 cases, the majority were aged 1 - 5 years (62.4%), followed by 5 - 10 years (22.3%). Children aged < 1 year accounted for 10.2%, while those aged > 10 years comprised 5.1%.

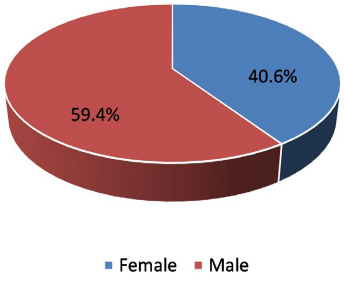

Figure 1. Distribution of cases according to sex.

Figure 1 shows that the distribution of cases according to sex was 59.4% male and 40.6% female, indicating a higher proportion of male cases.

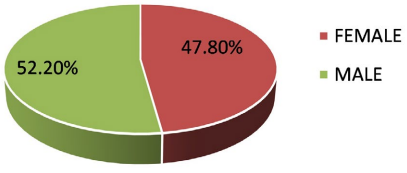

Figure 2. Distribution of growth in culture.

Figure 2 shows the distribution of culture-positive cases according to sex. Among the 69 culture-positive cases, 52.2% (36) were male and 47.8% (33) were

female, indicating a slightly higher proportion of culture-positive cases among male patients.

Table 2. Distribution of cases according to complaints.

Complaint of	Percentage (Frequency)
Fever	47.6% (290)
Respiratory Distress	33.3% (203)
Seizures	2.5% (15)
Vomiting, loose motions, and abdominal pain	7.9% (48)
Others	8.7% (53)
Total	100% (609)

Table 2 shows the distribution of cases according to complaints. Fever was the most common complaint, reported in 47.6% (290) of cases, followed by respiratory distress in 33.3% (203). Vomiting, loose motion, and abdominal pain were reported in 7.9% (48) of cases, while seizures were the least common complaint at 2.5% (15).

Table 3. Distribution of pathogens according to type.

Category	Isolated Organisms	Frequency	Percent (%)
Gram-positive pathogens	Total	35	50.7%
	Staphylococcus aureus	20	29.0%
	Coagulase-Negative Staphylococci (CNS)	9	13.0%
	Other Gram-positive isolates	6	8.7%
Gram-negative pathogens	Total	34	49.3%
	Klebsiella spp.	12	17.4%
	Acinetobacter spp.	11	15.9%
	Salmonella spp.	9	13.0%
	Enterobacter spp.	1	1.4%
	Serratia spp.	1	1.4%
Total	—	69	100%

Table 3 shows the distribution of pathogens according to type. Among the 69 culture-positive specimens, Gram-positive organisms accounted for 35 (50.7%) and Gram-negative organisms for 34 (49.3%). *S. aureus* was the most frequently reported organism (20, 29.0% of positive cultures), followed by *Klebsiella* spp. (12, 17.4%) and *Acinetobacter* spp. (11, 15.9%). Of the 20 *S. aureus* isolates, 6 were reported as MRSA, representing 30.0% of the *S. aureus* isolates. MRSA should therefore be interpreted as a resistance-defined subgroup of *S. aureus* and not as an additional bacterial species/category.

Table 4. Growth of Bacteria according to age.

Growth in culture	<1 yr	1 - 5 yrs	5 - 10 yrs	>10 yrs	Total
NG*	43.5% (27)	93.7% (356)	94.1% (128)	93.5% (29)	88.7% (540)
STAPH AUREUS	19.4% (12)	1.6% (6)	1.5% (2)	0.0% (0)	3.3% (20)
CNS	9.7% (6)	0.8% (3)	0.0% (0)	0.0% (0)	1.5% (9)
MRSA	6.5% (4)	0.5% (2)	0.0% (0)	0.0% (0)	1.0% (6)
ACINETOBACTER SPP.	1.6% (1)	1.8% (7)	2.2% (3)	0.0% (0)	1.8% (11)
KLEBSIELLA SPP.	17.7% (11)	0.3% (1)	0.0% (0)	0.0% (0)	2.0% (12)
ENTEROBACTER SPP.	0.0% (0)	0.3% (1)	0.0% (0)	0.0% (0)	0.2% (1)
SALMONELLA SPP.**	0.0% (0)	1.1% (4)	2.2% (3)	6.5% (2)	1.5% (9)
SERRATIA SPP.	1.6% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.2% (1)
Total	100% (62)	100% (380)	100% (136)	100% (31)	100% (609)

Table 4 shows the growth of bacteria according to age. No bacterial growth was observed in 540 (88.7%) of the 609 cultures. Among the reported isolates, *S. aureus* was the most frequent organism, followed by *Klebsiella* spp. and *Acinetobacter* spp. The largest proportion of *S. aureus* and *Klebsiella* spp. was observed among children aged < 1 year.

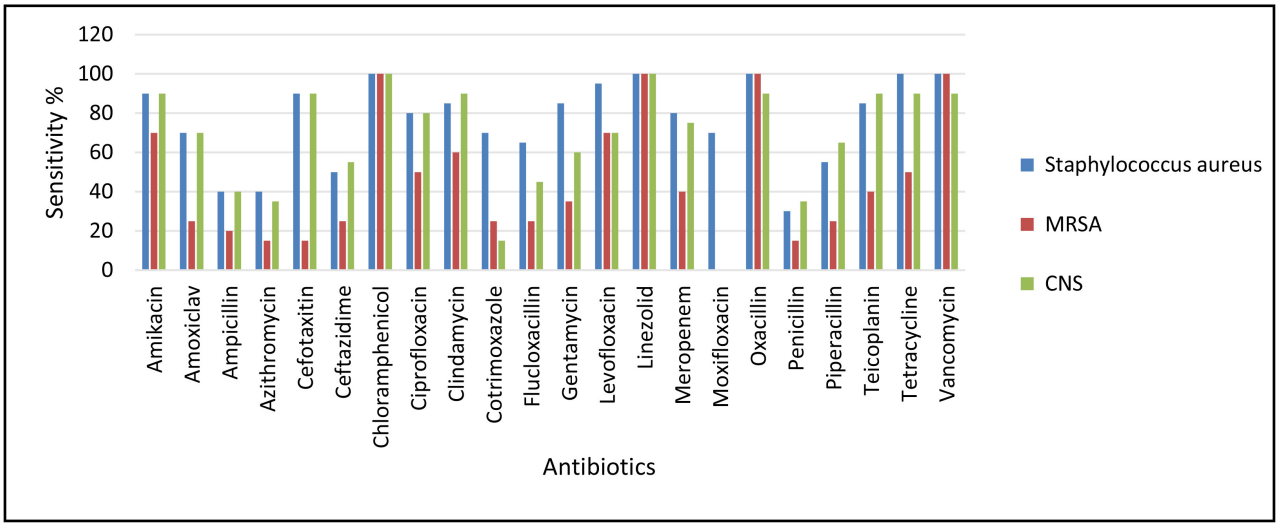

Figure 3. Sensitivity pattern of gram-positive isolates.

Figure 3 demonstrates the antimicrobial susceptibility patterns of the Gram-positive isolates. *Staphylococcus aureus* showed high susceptibility to linezolid, vancomycin, chloramphenicol, tetracycline, oxacillin, levofloxacin, and amikacin, whereas comparatively lower susceptibility was observed to ceftazidime, penicillin, ampicillin, azithromycin, ciprofloxacin, cotrimoxazole, and other tested antimicrobial agents. MRSA isolates showed high susceptibility to vancomycin, linezolid, and chloramphenicol, while greater resistance was observed against several fluoroquinolones and β-lactam antibiotics. CoNS isolates demonstrated high sus-

ceptibility to linezolid, chloramphenicol, amikacin, vancomycin, and tetracycline, whereas relatively high resistance was observed to cotrimoxazole, ceftazidime, and moxifloxacin. Overall, the Gram-positive isolates demonstrated variable antimicrobial susceptibility patterns, with relatively preserved activity of linezolid and vancomycin. The susceptibility percentages should be interpreted cautiously because the number of isolates tested varied between antimicrobial agents and some organism groups were small.

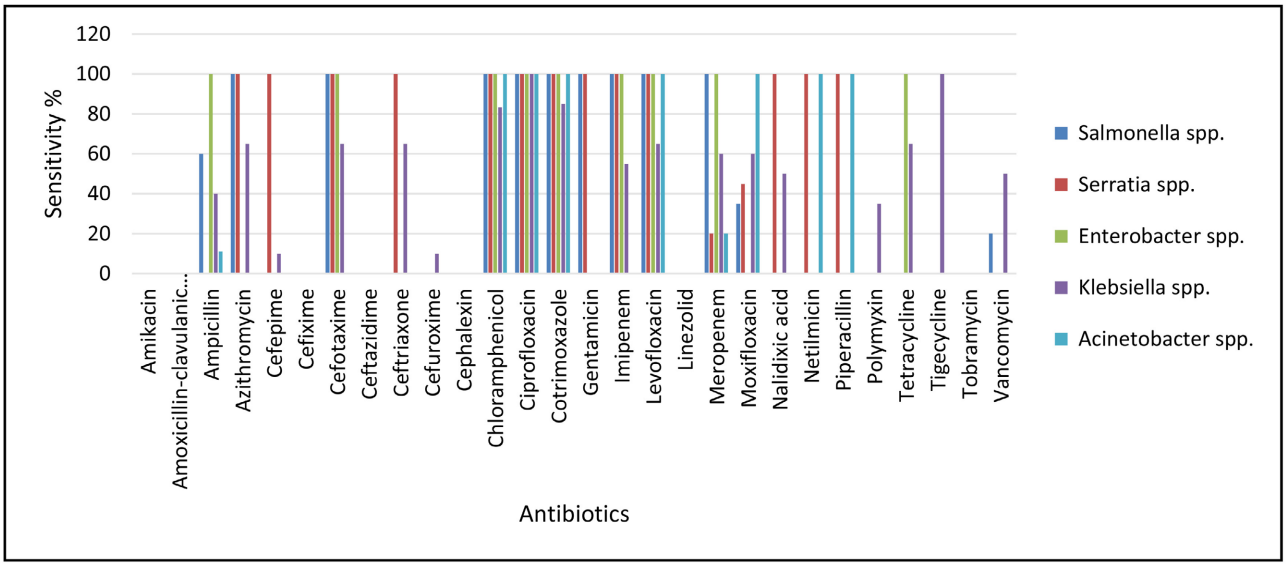

Figure 4. Sensitivity pattern of gram-negative isolates.

Figure 4 demonstrates the antimicrobial sensitivity patterns of the Gram-negative bacterial isolates against the tested antibiotics. *Acinetobacter* spp. showed 100% sensitivity to moxifloxacin, levofloxacin, cotrimoxazole, piperacillin, and netilmicin, while 100% resistance was observed to ceftazidime, cefuroxime, and amoxicillin-clavulanic acid. Resistance was also high to ampicillin (88.89%) and meropenem (80%). *Klebsiella* spp. showed 100% sensitivity to tigecycline and 83.33% sensitivity to cotrimoxazole, whereas 100% resistance was observed to ampicillin, cefepime, cephalexin, piperacillin, and tobramycin. *Salmonella* spp. demonstrated 100% sensitivity to chloramphenicol, cotrimoxazole, ciprofloxacin, levofloxacin, cefotaxime, imipenem, azithromycin, and gentamicin, but showed 100% resistance to cephalexin, piperacillin, polymyxin, linezolid, and netilmicin. *Enterobacter* spp. exhibited 100% sensitivity to meropenem, chloramphenicol, cotrimoxazole, ciprofloxacin, levofloxacin, imipenem, and tetracycline, while 100% resistance was observed to ceftriaxone, vancomycin, amoxicillin-clavulanic acid, cefuroxime, cefepime, cephalexin, nalidixic acid, polymyxin, and amikacin. *Serratia* spp. showed 100% sensitivity to ceftriaxone, chloramphenicol, cotrimoxazole, azithromycin, ciprofloxacin, cefotaxime, levofloxacin, imipenem, gentamicin, cefepime, and piperacillin, with 100% resistance to ampicillin, cephalexin, and amoxicillin-clavulanic acid.

4. Discussion

In the present study, bacterial growth was detected in 69 of 609 blood cultures (11.3%). This finding is broadly comparable with previously reported culture-positivity rates in pediatric populations, although the observed proportion varies considerably according to patient selection, clinical setting, blood-volume adequacy, prior antimicrobial exposure, laboratory methods, and definitions of contamination [17]-[21].

Among the culture-positive patients, the original manuscript reported 52.2% males and 47.8% females. These proportions correspond to approximately 36 males and 33 females among 69 culture-positive cases. The previously reported values of 50 males and 30 females were incorrect because they total 80 patients rather than 69 and have therefore been removed.

The predominance of younger children among culture-positive cases is clinically plausible because infants and younger children may have increased susceptibility to invasive bacterial infection due to age-related differences in immune function and host defense. Similar age-related patterns have been reported in previous pediatric bloodstream infection studies [17]-[21]. However, age-specific culture positivity should be interpreted with caution because the number of blood cultures performed in each age group and the clinical threshold for requesting cultures may differ.

In the present study, Gram-positive organisms accounted for 50.7% of culture-positive isolates, whereas Gram-negative organisms accounted for 49.3%. This distribution differs from some recent studies from Bangladesh and other regions in which Gram-negative bacteria predominated [22]. For example, a 2026 Bangladeshi study reported a predominance of Gram-negative organisms among pediatric bacterial infections, although that study included multiple clinical specimen types and therefore is not directly comparable with the present blood-culture-only study [23].

Among the reported organisms, *S. aureus* was the most frequent, followed by *Klebsiella* spp. and *Acinetobacter* spp. The predominance of *S. aureus* among Gram-positive isolates is consistent with reports from several pediatric settings, whereas the relative contribution of individual Gram-negative organisms varies between geographical regions and healthcare facilities [17]-[25].

A major methodological issue identified during revision was the reporting of MRSA as a separate organism in addition to *S. aureus*. Because MRSA is a methicillin-resistant phenotype of *S. aureus*, it should be reported as a subgroup of the total *S. aureus* isolates rather than as a separate organism when calculating the overall bacterial distribution. The present manuscript therefore reports 20 *S. aureus* isolates, of which six were classified as MRSA. The remaining six Gram-positive isolates in the original Gram-positive total of 35 require confirmation from the original laboratory records before the final organism distribution can be considered fully reconciled.

The antimicrobial susceptibility findings demonstrate substantial resistance

among several commonly used antimicrobial agents. Among the Gram-positive isolates, linezolid and vancomycin retained high activity according to the available results. Similar high susceptibility to vancomycin and linezolid has been reported in previous pediatric bloodstream infection studies [17] [26]-[28]. However, the small number of isolates in the present study limits the precision and generalizability of organism-specific susceptibility estimates.

The reported oxacillin susceptibility of MRSA was identified as an internal inconsistency and should not be retained without verification. Since MRSA is defined by resistance to methicillin-class agents, including oxacillin, a finding of oxacillin susceptibility would conflict with the MRSA classification. The original laboratory records should, therefore, be reviewed to determine whether the organism classification, oxacillin result, or data-entry process was responsible for the discrepancy.

Among Gram-negative organisms, *Acinetobacter* spp. demonstrated high resistance to several β-lactam agents, including carbapenems, in the reported dataset. Carbapenem resistance among *Acinetobacter* spp. is an important clinical concern because carbapenems are often used for severe infections caused by multidrug-resistant Gram-negative bacteria. Differences between the present findings and studies reporting greater carbapenem susceptibility may reflect differences in hospital antimicrobial exposure, infection-control practices, patient populations, and local resistance mechanisms [17] [20] [26].

The susceptibility pattern of *Klebsiella* spp. showed complete resistance to several commonly tested antimicrobial agents, whereas tigecycline and cotrimoxazole demonstrated comparatively greater activity in the available dataset. Studies from other countries have similarly documented substantial resistance among *Klebsiella pneumoniae*, particularly to β-lactam antibiotics [19] [29]. Nevertheless, organism-specific percentages based on only 12 isolates should not be interpreted as definitive estimates of local susceptibility.

The *Salmonella* isolates showed high susceptibility to several antimicrobial agents in the present dataset. Previous studies from Bangladesh have also reported susceptibility of enteric *Salmonella* isolates to selected third-generation cephalosporins and fluoroquinolones, although resistance patterns have changed over time [30]-[32]. Because the present study did not provide molecular characterization or serotyping data, the *Salmonella* findings should be interpreted as species-group susceptibility results.

The single-isolate findings for *Enterobacter* and *Serratia* spp. require particular caution. A susceptibility percentage derived from one isolate is mathematically 0% or 100%, but does not represent a reliable estimate of the susceptibility of that organism in the wider pediatric population. Therefore, these results should be presented as individual isolate findings rather than generalized antimicrobial susceptibility patterns.

The study findings emphasize the importance of local antibiograms for empirical treatment decisions. However, susceptibility results should be interpreted in conjunction with clinical severity, infection source, prior antimicrobial exposure,

patient-specific risk factors, and current CLSI breakpoints, rather than used in isolation to recommend a specific empirical regimen.

5. Limitations

This study has several limitations. First, it was a retrospective, single-center study, which limits the generalizability of the findings to other hospitals and regions. Second, the study was based on routinely collected laboratory and clinical records, and some potentially relevant variables, including prior antimicrobial exposure, blood-volume adequacy, number of culture sets obtained, and timing of blood collection relative to antimicrobial administration, were not available in the supplied dataset. Third, the overall number of culture-positive isolates was relatively small (n = 69), and several organism-specific groups contained very few isolates. Therefore, antimicrobial susceptibility percentages, particularly those based on one or a small number of isolates, should be interpreted cautiously. Fourth, the study did not include molecular characterization of antimicrobial resistance mechanisms. Finally, the organism categorization requires reconciliation of the MRSA subgroup with the total *S. aureus* count before final publication.

6. Conclusion

This retrospective cross-sectional study identified bacterial growth in 11.3% of blood cultures obtained from pediatric patients with clinically suspected bloodstream infection. Gram-positive and Gram-negative organisms were almost equally represented among culture-positive specimens, with *S. aureus*, *Klebsiella* spp., and *Acinetobacter* spp. being the leading reported pathogens. Several isolates demonstrated resistance to commonly used antimicrobial agents. These findings support the importance of routine blood culture-based diagnosis, continuous local antimicrobial resistance surveillance, and antimicrobial stewardship. However, organism-specific susceptibility results based on small numbers of isolates should be interpreted cautiously. Regular updating of institutional antibiograms and empirical treatment guidelines based on current local susceptibility data may improve antimicrobial selection and help limit the further development of antimicrobial resistance.

Ethics Approval

Ethical approval for this retrospective study was obtained from the KPJ Hospital Ethics Committee. Ethics approval/reference number: KPJSH/CC&RPJC/RPA/2026/001. The requirement for individual informed consent was waived because the study used previously collected clinical and laboratory records. Patient confidentiality was maintained by restricting access to study data and using coded/anonymized information for analysis.

Data Availability

The data underlying this study are not publicly available because they contain pa-

tient-related clinical and laboratory information. De-identified data may be made available from the corresponding author upon reasonable request and subject to institutional and ethical restrictions.

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Author Contributions

Conceptualization, K.N. and M.M.S.; methodology, K.N., R.H., and A.Y.; software, M.A.U.Z.; validation, K.N., T.I., and M.H.S.; formal analysis, K.N. and M.A.U.Z.; investigation, K.N., R.H., A.Y., and T.F.; resources, K.N. and M.M.S.; data curation, K.N., T.I., R.S., and M.A.U.Z.; writing—original draft preparation, K.N.; writing—review and editing, R.H., A.Y., T.I., T.F., R.S., M.H.S., and M.M.S.; visualization, M.A.U.Z. and K.N.; supervision, M.M.S.; project administration, K.N.; funding acquisition, K.N. All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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