

Bacterial profile and antimicrobial susceptibility patterns of blood culture isolates in pediatric patients at children hospital, Sukkur: a one-year retrospective analysis

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Received: May 2026, Accepted: September 2026

ABSTRACT

Background and Objectives: Bloodstream infections (BSIs) are an important cause of morbidity and mortality among neonates and children. Increasing antimicrobial resistance (AMR), particularly among Gram-negative organisms, complicates empirical antimicrobial therapy. Local antimicrobial susceptibility data are essential for guiding empirical treatment and antimicrobial stewardship.

Materials and Methods: A retrospective descriptive study was conducted at Children Hospital, Sukkur, Pakistan, from July 2024 to June 2025. Blood culture data from pediatric patients from birth to 14 years of age were reviewed. Only the first positive blood culture from each patient during the study period was included in the primary analysis, while subsequent positive cultures from the same patient were excluded. Organism distribution and antimicrobial susceptibility patterns were analyzed. Antimicrobial susceptibility testing (AST) had been performed in the hospital microbiology laboratory according to applicable Clinical and Laboratory Standards Institute (CLSI) recommendations. Because the retrospective records did not contain sufficient information to reliably confirm the exact AST technique used, the specific susceptibility-testing methodology could not be retrospectively established.

Results: A total of 11,962 blood cultures were processed during the study period, of which 4,151 (34.7%) were positive. Gram-positive bacteria accounted for 2,276 (54.8%) isolates and Gram-negative bacteria for 1,856 (44.7%). Nineteen (0.5%) positive cultures yielded fungal organisms and were excluded from the bacterial analysis. Coagulase-negative staphylococci (CoNS) were the most frequently isolated bacterial organisms, accounting for 2,125 isolates (51.2% of all positive cultures), followed by *Klebsiella* spp. (526, 12.7%), *Serratia* spp. (490, 11.8%), and *Acinetobacter* spp. (259, 6.2%). Gram-negative organisms demonstrated marked resistance to several commonly used antimicrobial agents. *Salmonella* Typhi demonstrated high susceptibility to azithromycin (93.6%) and meropenem (97.6%), whereas susceptibility to ceftriaxone (43.6%), cefixime (9%), ciprofloxacin (0%), and trimethoprim-sulfamethoxazole (15.7%) was low. Vancomycin and linezolid demonstrated 100% susceptibility among the tested CoNS, *Staphylococcus aureus*, and *Enterococcus* spp. isolates.

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Conclusion: This one-year analysis demonstrates a substantial burden of antimicrobial resistance among pediatric bloodstream isolates at Children Hospital, Sukkur. CoNS were the most frequently isolated organisms; however, this finding should be interpreted cautiously because the clinical and microbiological information required to distinguish true CoNS bacteremia from blood culture contamination was not consistently available. Regular institution-specific antibiogram surveillance, antimicrobial stewardship, and strengthened infection prevention and control measures are warranted.

Keywords: Bloodstream infection; Antimicrobial resistance; Pediatric antibiogram; Coagulase-negative staphylococci; Gram-negative bacteria; Antimicrobial susceptibility; Antimicrobial stewardship

INTRODUCTION

Bloodstream infections (BSIs) remain an important cause of morbidity and mortality worldwide and are particularly significant among neonates and children (1). Pediatric patients are vulnerable to invasive bacterial infections because of age-related differences in immunity, healthcare exposure, invasive procedures, underlying illnesses, and, in neonates, immature host defenses (1-3).

The epidemiology of bloodstream infections varies considerably according to geographical region, healthcare setting, patient population, antimicrobial exposure, and infection-control practices (4). Gram-negative organisms, including *Klebsiella* spp., *Escherichia coli*, *Acinetobacter* spp., *Pseudomonas aeruginosa*, and *Enterobacter* spp., are frequently reported among pediatric bloodstream isolates. Important Gram-positive organisms include coagulase-negative staphylococci (CoNS), *Staphylococcus aureus*, *Enterococcus* spp., and *Streptococcus* spp. (5-7).

The increasing prevalence of antimicrobial resistance (AMR) has complicated the management of pediatric BSIs. Resistance to third-generation cephalosporins, fluoroquinolones, aminoglycosides, and other commonly used antimicrobial agents can substantially reduce therapeutic options and may increase morbidity, mortality, hospital stay, and healthcare costs (6-8).

CoNS deserve particular attention because they are common bloodstream isolates in hospitalized pediatric and neonatal patients, especially those with intravascular devices. However, CoNS are also among the most frequent contaminants of blood cultures. Consequently, a CoNS-positive blood culture should not automatically be interpreted as clinically significant bacteremia without appropriate clinical and microbiological correlation (5-9).

Cumulative antimicrobial susceptibility data, or

antibiograms, are important tools for understanding local resistance patterns and guiding empirical antimicrobial therapy. The Clinical and Laboratory Standards Institute (CLSI) provides standardized recommendations for the analysis and presentation of cumulative antimicrobial susceptibility data (8-10).

Children Hospital, Sukkur serves a large pediatric population in upper Sindh. However, local data describing the bacterial spectrum and antimicrobial susceptibility patterns of pediatric bloodstream isolates are limited.

The present study aimed to describe the bacterial profile and antimicrobial susceptibility patterns of blood culture isolates among pediatric patients at Children Hospital, Sukkur, over a one-year period. The study also aimed to provide institution-specific data that could support empirical antimicrobial selection, antimicrobial stewardship, and infection prevention and control strategies.

MATERIALS AND METHODS

Study design and setting. This was a retrospective descriptive study conducted using microbiological laboratory records of pediatric blood cultures processed at Children Hospital, Sukkur, Pakistan.

Study period. The study included blood culture records from July 2024 through June 2025.

Study population. The study included pediatric patients from birth to 14 years of age whose blood cultures were processed during the study period.

For descriptive purposes, patients were categorized into the following age groups:

- Neonates: 0–28 days
- Infants: 29 days to <1 year
- Children: 1–<10 years

- Adolescents: 10–14 years

Inclusion criteria. Positive blood cultures yielding bacterial growth from eligible pediatric patients during the study period were included in the bacterial analysis.

Exclusion criteria. The following were excluded:

1. Non-blood culture specimens.
2. Fungal isolates.
3. Viral isolates.
4. Subsequent positive blood cultures from the same patient after the first positive culture during the study period.

Nineteen positive cultures yielded fungal organisms. These 19 isolates represented 0.5% of all positive cultures and were excluded because the present study specifically evaluated bacterial bloodstream isolates and their antimicrobial susceptibility patterns.

Selection of first positive culture. To reduce potential overrepresentation of individual patients, only the first positive blood culture from each patient during the study period was included in the primary analysis. Subsequent positive blood cultures from the same patient were excluded.

Blood culture processing and organism identification. Blood cultures were collected and processed by the hospital microbiology laboratory according to routine laboratory procedures.

The exact blood culture system used during the study period could not be retrospectively confirmed from the available study records.

Positive blood cultures underwent routine microbiological identification. Several organisms were reported at genus level in the available laboratory database rather than at species level, including *Klebsiella* spp., *Serratia* spp., *Acinetobacter* spp., *Enterobacter* spp., and *Citrobacter* spp.

Antimicrobial susceptibility testing. Antimicrobial susceptibility testing (AST) was performed by the hospital microbiology laboratory according to applicable Clinical and Laboratory Standards Institute (CLSI) recommendations during the study period.

The exact AST methodology used for the individual isolates, including whether testing was performed by disk diffusion, an automated susceptibility-testing

system, or another validated method, could not be reliably confirmed from the retrospective laboratory records.

Therefore, no specific AST technique is reported in this manuscript beyond the documented use of CLSI-based interpretation.

Where applicable, intermediate susceptibility results were considered non-susceptible for the purposes of the analysis.

Because susceptibility testing was not performed against every antimicrobial agent for every organism, the denominator varied between organism-antimicrobial combinations.

Interpretation of coagulase-negative staphylococci. CoNS represented the largest proportion of positive bacterial cultures. However, the retrospective laboratory dataset did not consistently contain the clinical and microbiological information necessary to reliably distinguish true CoNS bloodstream infection from blood culture contamination.

Information such as the number of positive blood culture sets, number of positive bottles, time to positivity, presence of intravascular devices, clinical signs of infection, repeat culture results, and treating physician or infectious disease specialist assessment was not consistently available.

Therefore, CoNS isolates were not retrospectively categorized as definite contaminants or definite bloodstream pathogens.

For this reason, CoNS are described as the most frequently isolated organisms rather than as the most common clinically confirmed bloodstream pathogens.

Multidrug resistance. Although resistance to multiple antimicrobial agents was observed, a formal multidrug resistance (MDR) classification was not applied to the complete dataset.

The retrospective susceptibility data did not provide sufficiently standardized antimicrobial-category testing across all organisms to reliably classify every isolate according to internationally accepted MDR criteria.

Therefore, this study reports susceptibility patterns for individual antimicrobial agents rather than an overall MDR prevalence.

ESBL detection. Extended-spectrum β -lactamase (ESBL) confirmatory testing was not consistently documented in the retrospective laboratory dataset.

Therefore, ESBL prevalence could not be reliably calculated.

Resistance or reduced susceptibility to third-generation cephalosporins was reported directly and was not interpreted as definitive evidence of ESBL production.

Data collection. The following information was extracted from the laboratory database where available: patient age; blood culture result; organism identified; and antimicrobial susceptibility results.

Ward-level information was not consistently available. Consequently, reliable stratification by NICU, PICU, general pediatric ward, emergency department, or other clinical units was not performed.

Statistical analysis. Data were analyzed using Statistical Package for the Social Sciences (SPSS), version 26.

Descriptive statistics were used. Frequencies and percentages were calculated for bacterial isolates and antimicrobial susceptibility results.

The percentage susceptibility for each organism-antimicrobial combination was calculated using the number of isolates tested against that particular antimicrobial as the denominator.

Ethics statement. This study was approved by the Ethics Review Committee (ERC) of the Sindh Institute of Child Health and Neonatology (SICHN), Sukkur, Pakistan (Approval No. SICHN/EX-012/2025). The study was conducted in accordance with the principles of the Declaration of Helsinki.

As this was a retrospective study based on anonymized laboratory data with no direct patient interaction, the requirement for informed consent was waived by the Ethics Review Committee.

RESULTS

Overall blood culture findings. During the one-year study period, 11,962 blood cultures were processed at Children Hospital, Sukkur. Of these, 4,151 (34.7%) yielded positive cultures.

Among the 4,151 positive cultures, 2,276 (54.8%) yielded Gram-positive bacteria, 1,856 (44.7%) yielded Gram-negative bacteria, and 19 (0.5%) yielded fungal organisms.

The 19 fungal isolates were excluded from the bacterial

analysis according to the predefined exclusion criteria.

Only the first positive blood culture from each patient was included in the primary analysis, while subsequent positive cultures from the same patient were excluded.

Thus, the overall distribution of positive cultures was:

2,276 Gram-positive + 1,856 Gram-negative + 19 fungal = 4,151 positive cultures (Table 1C).

Distribution of Gram-positive organisms. Among Gram-positive bacterial isolates, CoNS were the most frequently isolated organisms, with 2,125 isolates (51.2% of all positive cultures).

S. aureus was identified in 110 cultures (2.7%), *Enterococcus* spp. in 31 (0.7%), and *Streptococcus* spp. in 10 (0.2%).

The total number of Gram-positive bacterial isolates was 2,276 (54.8% of all positive cultures) (Table 1A).

Distribution of Gram-negative organisms. Among Gram-negative organisms, *Klebsiella* spp. were the most frequently isolated, with 526 isolates (12.7% of all positive cultures).

Serratia spp. accounted for 490 isolates (11.8%), *Acinetobacter* spp. for 259 (6.2%), *Burkholderia cepacia* complex for 157 (3.8%), *E. coli* for 131 (3.2%), *Salmonella* Typhi for 129 (3.1%), and *Pseudomonas aeruginosa* for 84 (2.0%).

Less frequently isolated organisms included *Enterobacter* spp. (31, 0.7%), *Citrobacter* spp. (32, 0.8%), *Proteus mirabilis* (15, 0.4%), and *Haemophilus influenzae* (2, <0.1%) (Table 1B).

Antimicrobial susceptibility results: Gram-negative organisms. The antimicrobial susceptibility profile demonstrated substantial resistance among several Gram-negative organisms.

E. coli demonstrated low susceptibility to several commonly used β -lactam agents, including ceftriaxone and cefixime, while susceptibility to other antimicrobial agents varied.

Klebsiella spp. demonstrated marked resistance to several β -lactam antibiotics, including third-generation cephalosporins. Resistance was also observed against several other commonly used antimicrobial agents.

Serratia spp. demonstrated low susceptibility to several β -lactam agents, while susceptibility varied across other antimicrobial classes.

Table 1A. Distribution of Gram-positive organisms

Organism	Number (n)	% of all positive cultures
Coagulase-negative staphylococci	2,125	51.2
<i>Staphylococcus aureus</i>	110	2.7
<i>Enterococcus</i> spp.	31	0.7
<i>Streptococcus</i> spp.	10	0.2
Total Gram-positive bacteria	2,276	54.8

Table 1B. Distribution of Gram-negative organisms

Organism	Number (n)	% of all positive cultures
<i>Klebsiella</i> spp.	526	12.7
<i>Serratia</i> spp.	490	11.8
<i>Acinetobacter</i> spp.	259	6.2
<i>Burkholderia cepacia</i> complex	157	3.8
<i>Escherichia coli</i>	131	3.2
<i>Salmonella</i> Typhi	129	3.1
<i>Pseudomonas aeruginosa</i>	84	2.0
<i>Enterobacter</i> spp.	31	0.7
<i>Citrobacter</i> spp.	32	0.8
<i>Proteus mirabilis</i>	15	0.4
<i>Haemophilus influenzae</i>	2	<0.1
Total Gram-negative bacteria	1,856	44.7

Table 1C. Overall positive cultures

Category	Number (n)	% of positive cultures
Gram-positive bacteria	2,276	54.8
Gram-negative bacteria	1,856	44.7
Fungal organisms	19	0.5
Total	4,151	100.0

Acinetobacter spp. demonstrated substantial resistance to several commonly tested antimicrobial agents, although susceptibility varied according to the agent tested.

Pseudomonas aeruginosa demonstrated variable susceptibility to antipseudomonal antimicrobial agents.

Burkholderia cepacia complex demonstrated comparatively higher susceptibility to trimethoprim-sulfamethoxazole than to several other tested agents (Table 2).

Because ESBL confirmatory testing was not consis-

tently documented, third-generation cephalosporin resistance was not interpreted as definitive evidence of ESBL production.

***Salmonella* Typhi susceptibility.** A total of 129 *Salmonella* Typhi isolates were identified.

Salmonella Typhi demonstrated high susceptibility to azithromycin (93.6%) and meropenem (97.6%).

Susceptibility to ceftriaxone was 43.6%, while susceptibility to cefixime was 9%.

No susceptibility to ciprofloxacin was observed, while susceptibility to trimethoprim-sulfamethoxazole was 15.7%.

These findings indicate substantial resistance to several traditional antimicrobial agents used for enteric fever and emphasize the importance of local antimicrobial susceptibility surveillance.

Gram-positive antimicrobial susceptibility. CoNS demonstrated susceptibility of 12% to penicillin, 28% to oxacillin, 30% to erythromycin, and 25% to clindamycin. Susceptibility to vancomycin and linezolid was 100%, while susceptibility to trimethoprim-sulfamethoxazole was 20%.

S. aureus demonstrated susceptibility of 15% to penicillin, 30% to oxacillin, 28% to erythromycin, and 24% to clindamycin. Susceptibility to vancomycin and linezolid was 100%, while susceptibility to trimethoprim-sulfamethoxazole was 18%.

Enterococcus spp. demonstrated 20% susceptibility to penicillin, 35% to erythromycin, and 30% to clindamycin. Vancomycin and linezolid demonstrated 100% susceptibility.

Streptococcus spp. demonstrated 50% susceptibility to penicillin, 45% to erythromycin, and 40% to clindamycin.

The oxacillin susceptibility of *S. aureus* was 30%. However, because the precise methodology used for oxacillin testing could not be retrospectively confirmed, the proportion of isolates that should formally be classified as MRSA cannot be stated with certainty based solely on this dataset (Table 3).

DISCUSSION

This study presents the first hospital-wide cumulative pediatric blood culture antibiogram from interior Sindh, Pakistan. Out of 11,962 blood cultures processed, 4,151 (34.7%) yielded bacterial growth.

Table 2. Antimicrobial susceptibility of Gram-negative blood culture isolates

Antimicrobial	<i>E. coli</i>	<i>Enterobacter</i> spp.	<i>Citrobacter</i> spp.	<i>Klebsiella</i> spp.	<i>Serratia</i> spp.	<i>Proteus</i> spp.	<i>Acinetobacter</i> spp.	<i>P. aeruginosa</i>	<i>B. cepacia</i> complex
Amikacin	22.6	12.0	20.0	3.0	0.4	0	20.3	43.5	NA
Ampicillin	45.0	74.1	NA	NA	NA	NA	NA	NA	NA
Amoxicillin/clavulanate	18.3	31.2	26.9	2.8	0.6	21.4	7.6	45.0	74.1
Aztreonam	NA	NA	NA	NA	NA	NA	17.6	86.1	NA
Cefixime	2.8	11.1	19.2	1.8	4.0	33.3	91.5	96.7	NA
Ceftriaxone	7.7	8.0	21.8	2.3	0.5	9.0	11.3	43.1	27.7
Cefuroxime	88.9	100	100	97.6	0.4	18.1	7.1	50.8	24.4
Gentamicin	0	50.0	NA	0	0	NA	11.3	40.0	20.8
Imipenem	28.0	20.0	17.8	12.7	0.4	23.0	22.9	9.0	NA
Meropenem	54.5	20.4	44.4	9.7	4.5	16.6	67.7	NA	NA
Trimethoprim-sulfamethoxazole	92.8	NA	NA	40.1	10.6	30.5	NA	NA	69.2
Piperacillin/tazobactam	16.0	28.5	50.0	8.4	5.4	0	87.9	NA	NA
Nitrofurantoin	20.2	23.0	37.0	3.9	3.0	25.0	10.5	49.2	NA
Cefoperazone/sulbactam	NA	NA	NA	NA	NA	NA	NA	100	NA
Tigecycline	37.3	38.8	44.8	9.5	4.1	33.3	19.7	22.2	NA
Fosfomycin	91.2	66.6	100	78.1	77.7	40.0	NA	NA	NA

Note: Values represent percentage susceptibility among isolates tested. The number of isolates tested varied between antimicrobial-organism combinations. NA = not available/not tested.

Table 3. Antimicrobial susceptibility of Gram-positive blood culture isolates

Antimicrobial	CoNS (n=2,125)	<i>S. aureus</i> (n=110)	<i>Enterococcus</i> spp. (n=31)	<i>Streptococcus</i> spp. (n=10)
Penicillin	12	15	20	50
Oxacillin	28	30	NA	NA
Erythromycin	30	28	35	45
Clindamycin	25	24	30	40
Vancomycin	100	100	100	NA
Linezolid	100	100	100	NA
Trimethoprim-sulfamethoxazole	20	18	25	NA

Note: Values represent percentage susceptibility among isolates tested. NA = not available/not tested.

Gram-positive organisms constituted approximately 54% of isolates, while Gram-negative bacteria accounted for around 45%; fungal isolates were not included in the present analysis. Coagulase-negative staphylococci (CONS) were the most frequently isolated organisms (2,125 isolates, 51.2%), followed by *Klebsiella* spp. (526, 12.7%), *Serratia* spp. (490, 11.8%), *Acinetobacter* spp. (259, 6.2%), and *E. coli* (131, 3.2%).

The overall culture positivity rate in our cohort

(34.7%) is comparable to rates reported in other pediatric settings internationally, though variation exists depending on case mix and intensive care involvement. For example, Ergül et al. reported a lower positivity rate of 7.6% in a three-year PICU-based study from Turkey (10). Bloodstream infections in neonates and children remain a major cause of morbidity and mortality, with reported case fatality rates ranging from approximately 8% in Pakistan to over 25% in developing regions of sub-Saharan Africa (11, 12).

The high prevalence of CONS in our study reflects their well-recognized role as healthcare-associated bloodstream pathogens, particularly in settings with frequent intravascular device use and prolonged hospitalization (13, 14).

Among Gram-negative pathogens, *Klebsiella* spp. demonstrated extremely low susceptibility to third-generation cephalosporin (<5%) and declining susceptibility to carbapenems (~30%), indicating a high burden of extended-spectrum beta-lactamase (ESBL) production and emerging carbapenem resistance. Similar resistance patterns have been reported in national antimicrobial resistance surveillance data from Pakistan and in regional NICU studies from India, where *Klebsiella* and *Acinetobacter* spp. predominate as multidrug-resistant pathogens (15, 16). Similar high rates of methicillin, beta-lactam, carbapenem, and multidrug resistance among bloodstream isolates have also been reported from other low- and middle-income settings, including Ethiopia (3). *Acinetobacter* spp. in our cohort exhibited extensive drug resistance, with preserved activity largely limited to tigecycline and colistin, consistent with international reports from South Asia (17).

E. coli isolates showed near-universal resistance to ampicillin and high resistance to third-generation cephalosporin, while carbapenem susceptibility remained relatively preserved. *Pseudomonas aeruginosa* retained moderate susceptibility to ceftazidime and piperacillin–tazobactam, whereas *Burkholderia cepacia* complex isolates remained highly susceptible to trimethoprim–sulfamethoxazole, in line with prior regional and international studies (18, 19).

Salmonella Typhi in our cohort showed high susceptibility to azithromycin (96.2%) and meropenem (97.6%), while susceptibility to cefixime (9%), ceftriaxone (43.4%), ciprofloxacin (0%), and trimethoprim–sulfamethoxazole (15.7%) was markedly low. These findings reflect an evolving resistance pattern in enteric fever, with traditional first-line therapies losing effectiveness. National surveillance from Pakistan has consistently reported high rates of multidrug-resistant and fluoroquinolone-resistant typhoid, with increasing detection of third-generation cephalosporin resistance and the emergence of extensively drug-resistant strains (20, 21).

Among Gram-positive organisms, including CONS, *S. aureus*, and *Enterococcus* spp., vancomycin and linezolid retained excellent activity. In contrast, penicillin, macrolides, and clindamycin demonstrated

high resistance rates, limiting their role in empirical therapy (15, 22).

The study also highlights the importance of standardized cumulative antibiograms. Local resistance patterns can differ substantially between institutions and geographic regions. Institution-specific antibiograms can therefore provide more relevant information for empirical antimicrobial decisions than reliance solely on data from distant hospitals or broader populations.

The findings support the need for continuous surveillance of antimicrobial susceptibility, antimicrobial stewardship programs, appropriate blood culture practices, and strengthened infection prevention and control measures at the institutional level.

This study has several strengths. First, it represents a large one-year dataset from a pediatric hospital, with 11,962 blood cultures processed during the study period.

Second, the analysis included a broad range of Gram-positive and Gram-negative bloodstream organisms and provides institution-specific susceptibility data.

Third, only the first positive blood culture from each patient was included, reducing the potential for repeated cultures from the same patient to disproportionately influence the results.

Fourth, the study identifies important resistance patterns among Gram-negative organisms and *Salmonella* Typhi that may be relevant to empirical antimicrobial selection.

Finally, the study provides local data from Sukkur, where published pediatric bloodstream infection surveillance data remain limited.

On the other hand, this study has several limitations. First, because of the retrospective laboratory-based design, clinical information required to reliably distinguish CoNS contamination from true CoNS bloodstream infection was not consistently available. Information such as the number of positive blood culture sets, number of positive bottles, time to positivity, intravascular device status, clinical findings, and treating physician assessment was not consistently documented. Therefore, the high proportion of CoNS should not be interpreted as the prevalence of clinically confirmed CoNS bacteremia.

Second, only the first positive blood culture from each patient was included. Although this reduces overrepresentation from repeated cultures, it may underestimate subsequent episodes of bloodstream

infection occurring in the same patient during the study period.

Third, the exact blood culture system used during the study period could not be retrospectively confirmed from the available records.

Fourth, the precise AST methodology used for individual isolates could not be reliably confirmed from the retrospective laboratory records. Although susceptibility results were interpreted according to applicable CLSI recommendations, the study cannot specify whether all isolates were tested by disk diffusion, automated susceptibility testing, or another method.

Fifth, several organisms were reported at genus level rather than species level. This limits species-specific epidemiological interpretation and detailed resistance analysis for organisms such as *Klebsiella*, *Serratia*, *Acinetobacter*, *Enterobacter*, and *Citrobacter*.

Sixth, standardized ESBL confirmatory testing was not consistently available or documented, preventing reliable estimation of ESBL prevalence.

Seventh, a formal MDR classification was not applied because the available susceptibility dataset did not provide sufficiently standardized testing across antimicrobial categories for all organisms.

Eighth, ward-level stratification could not be reliably performed because clinical-unit information was incomplete.

Ninth, susceptibility testing was not performed against every antimicrobial agent for every isolate. Consequently, denominators varied among antimicrobial-organism combinations, and results based on small numbers of tested isolates should be interpreted cautiously.

Finally, fungal bloodstream isolates were excluded because the study focused specifically on bacterial bloodstream infections. Therefore, the findings do not describe the epidemiology or antifungal susceptibility patterns of fungal bloodstream infections.

CONCLUSION

This one-year retrospective analysis demonstrates a substantial burden of antimicrobial resistance among pediatric bloodstream isolates at Children Hospital, Sukkur.

Gram-positive bacteria accounted for 54.8% of positive cultures and Gram-negative bacteria for 44.7%, while 0.5% yielded fungal organisms that were ex-

cluded from the bacterial analysis. CoNS were the most frequently isolated organisms, although their high frequency must be interpreted cautiously because the available data did not allow reliable differentiation between contamination and true bacteremia.

Among Gram-negative organisms, *Klebsiella* spp., *Serratia* spp., and *Acinetobacter* spp. were prominent isolates and demonstrated considerable resistance to several commonly used antimicrobial agents.

Salmonella Typhi showed high susceptibility to azithromycin and meropenem but substantial resistance to several other commonly used agents.

These findings emphasize the need for continuous institution-specific antimicrobial susceptibility surveillance, rational empirical antimicrobial selection, antimicrobial stewardship, appropriate interpretation of CoNS-positive cultures, and strengthened infection prevention and control practices.

Regularly updated local antibiograms may help clinicians select more appropriate empirical therapy while reducing unnecessary broad-spectrum antimicrobial exposure and supporting efforts to limit the emergence and spread of antimicrobial resistance.

REFERENCES

1. Usan DZ, Crane SJ, Steckelberg JM, Cockerill FR 3rd, St Sauver JL, Wilson WR, et al. Age- and sex-associated trends in bloodstream infection: a population-based study in Olmsted County, Minnesota. *Arch Intern Med* 2007; 167: 834-839.
2. Agyeman PK, Schlapbach LJ, Giannoni E, Stocker M, Posfay-Barbe KM, Heininger U, et al. Epidemiology of blood culture-proven bacterial sepsis in children in Switzerland: a population-based cohort study. *Lancet Child Adolesc Health* 2017; 1: 124-133.
3. Birhanu A, Gebre G, Getaneh E, Yohannes H, Baye N, Mersha GB, et al. Investigation of methicillin, beta lactam, carbapenem, and multidrug resistant bacteria from blood cultures of septicemia suspected patients in Northwest Ethiopia. *Sci Rep* 2025; 15: 5769.
4. Owais A, Tikmani SS, Sultana S, Zaman U, Ahmed I, Allana S, et al. Incidence of pneumonia, bacteremia, and invasive pneumococcal disease in Pakistani children. *Trop Med Int Health* 2010; 15: 1029-1036.
5. Khan MS, Kareem A, Fatima K, Rauf S, Khalid A, Bashir MS. Microbial patterns and antibiotic susceptibility in blood culture isolates of septicemia suspected children in the pediatric ward of a tertiary care hospi-

- tal. *J Lab Physicians* 2021; 13: 64-69.
6. Truong TT, Lu J, Bard JD. Blood cultures in children: maximizing their usefulness. *Pediatr Infect Dis J* 2024; 43(10): e354-e357.
 7. Bassetti M, Kanj SS, Kiratisin P, Rodrigues C, Van Duin D, Villegas MV, et al. Early appropriate diagnostics and treatment of MDR Gram-negative infections. *JAC Antimicrob Resist* 2022; 4(5): dlac089.
 8. Humphries RM, Ambler J, Mitchell SL, Castanheira M, Dingle T, Hindler JA, et al. CLSI methods development and standardization working group best practices for evaluation of antimicrobial susceptibility tests. *J Clin Microbiol* 2018 ;56(4): e01934-17.
 9. Spatenkova V, Bradac O, Fackova D, Bohunova Z, Suchomel P. Low incidence of multidrug-resistant bacteria and nosocomial infection due to a preventive multimodal nosocomial infection control: a 10-year single centre prospective cohort study in neurocritical care. *BMC Neurol* 2018; 18: 23.
 10. Ergül AB, Işık H, Altıntop YA, Torun YA. A retrospective evaluation of blood cultures in a pediatric intensive care unit: a three year evaluation. *Turk Pediatr Ars* 2017; 52: 154-161.
 11. Rudd KE, Johnson SC, Agesa KM, Shackelford KA, Tsoi D, Kievlan DR, et al. Global, regional, and national sepsis incidence and mortality, 1990–2017: analysis for the Global Burden of Disease Study. *Lancet* 2020; 395: 200-211.
 12. World Health Organization (2020). Global report on the epidemiology and burden of sepsis: current evidence, identifying gaps and future directions. World Health Organization. Geneva, Switzerland [cited 2026 Sep 14]. Available from: <https://www.who.int/publications/i/item/9789240010789>
 13. Wisplinghoff H, Bischoff T, Tallent SM, Seifert H, Wenzel RP, Edmond MB. Nosocomial bloodstream infections in US hospitals: analysis of 24,179 cases from a prospective nationwide surveillance study. *Clin Infect Dis* 2004; 39: 309-317.
 14. França A. The role of coagulase-negative staphylococci biofilms on late-onset sepsis: current challenges and emerging diagnostics and therapies. *Antibiotics (Basel)* 2023; 12: 554.
 15. Maryam S, Saleem Z, Haseeb A, Qamar MU, Amir A, Almarzoky Abuhussain SS, et al. Progress on the global research agenda for antimicrobial resistance in human health in Pakistan: findings and implications. *Infect Drug Resist* 2025; 18: 3795-3828.
 16. Paulson KR, Kamath AM, Alam T, Bienhoff K, Abady GG, Abbas J, et al. Global, regional, and national progress towards Sustainable Development Goal 3.2 for neonatal and child health: all-cause and cause-specific mortality findings from the Global Burden of Disease Study 2019. *Lancet* 2021; 398: 870-905.
 17. Peleg AY, Seifert H, Paterson DL. *Acinetobacter baumannii*: emergence of a successful pathogen. *Clin Microbiol Rev* 2008; 21: 538-582.
 18. Sirohi R, Rai AK, de Souza Vandenberghe LP, Parameswaran B (Eds.) (2023). *Microbial Enzymes and Metabolites for Health and Well-Being*. 1st ed. CRC Press. Boca Raton, FL, USA.
 19. Gandra S, Alvarez-Uria G, Turner P, Joshi J, Limmathurotsakul D, van Doorn HR. Antimicrobial resistance surveillance in low-and middle-income countries: progress and challenges in eight South Asian and Southeast Asian countries. *Clin Microbiol Rev* 2020; 33(3): e00048-19.
 20. Akram J, Khan AS, Khan HA, Gilani SA, Akram SJ, Ahmad FJ, et al. Extensively drug-resistant (XDR) typhoid: evolution, prevention, and its management. *Biomed Res Int* 2020; 2020: 6432580.
 21. Qamar FN, Azmatullah A, Kazi AM, Khan E, Zaidi AK. A three-year review of antimicrobial resistance of *Salmonella enterica* serovars Typhi and Paratyphi A in Pakistan. *J Infect Dev Ctries* 2014; 8: 981-986.
 22. Centers for Disease Control and Prevention (2019). Antibiotic Resistance Threats in the United States, 2019. Centers for Disease Control and Prevention. Atlanta, GA, USA [cited 2026 Sep 14]. Available from: <https://www.cdc.gov/antimicrobial-resistance/data-research/threats/index.html>