Research Article

Bacteriological Diversity and Antibiogram Analysis of Blood Culture Isolates in a Pediatric Setting at Tertiary Care Hospital Karachi

Shaikh Ali Masood[*,1], Shabbir Ahmed Mallick[1], Romana Nisar Ahmed[1], Tooba[1], Haider Abbas[2], Ayesha Samad[3]

[1]*Department of Pediatric Medicine, Liaquat National Hospital & Medical College, Karachi, Pakistan.*
[2]*Department of Pediatric Cardiac, National Institute of Cardiovascular Diseases(NICVD), Karachi, Pakistan.*
[3]*Department of Pediatric Medicine, National Institute of Child Health (NICH), Karachi, Pakistan.*

Abstract: Background: In low-middle income countries multi-drug resistant (MDR) bacteria are considered a health priority. The protocols directed by The Clinical and Laboratory Standards Institute (CLSI) recommend to develop antibiogram in hospital settings.

Objective: To analyze the bacteriological diversity and antibiogram patterns of blood culture isolates in a pediatric settings at a tertiary care hospital in Karachi, Pakistan.

Materials and Methods: This descriptive cross-sectional study was executed at Department of Pediatrics, Liaquat National Hospital during 2nd February, 2025 to 30th September, 2025 after taking formal ethical approval of the hospital committee bearing number App#1152-2024-LNH-ERC. Patients admitted to pediatric department and suspected for blood stream infection (BSI) were included. Standard aseptic measures were used to collect the blood sample. According to the CLSI's breakpoint guidelines, the isolates were classified as susceptible, intermediate, or resistant to the test antibiotics bases on inhibition zone diameter.

Result: A total of 370 patients were enrolled with median age of patients was 35.5 (IQR=12-124) months. BSI was detected in 75 (20%). Out of 75, gram-positive and gram-negative bacteria were found in 17 (22.7%) and 58 (77.3%) patients respectively. Out of total 17 gram positive bacteria, almost half were *Streptococcus pneumoniae* and other half were *Enterococcus species*. Among 58 gram-negative bacteria, the commonest detected pathogen was *Salmonella Typhi* (56.9%). Among gram-positive bacteria, both of pathogens were 100% resistant to meropenem. Resistance of Ciprofloxacin, Ceftriaxone, Cefuroxime was seen in 100% isolates of *Klebsiella pneumoniae*, *E. coli* and *Hafnia alvei*. S. Typhi was least resistant to Cefuroxime (3%), Chloramphenicol (3%) Gentamicin (6%), Imipenem (6%) while highly resistant to Ceftriaxone (75.8%), Ampicillin (72.7%), Amikacin (69.6%).

Conclusion: A remarkable burden of BSI was found in our settings with higher burden of gram-negative bacteria, Enteric fever being the most frequent. Different resistance patterns were observed for different antibiotics, mostly 100% resistance was seen for most of bacterial isolates. This finding underscores the ongoing monitoring of antimicrobial profile to decide the appropriate empirical therapy of antibiotics.

Keywords: Antibiogram, Antimicrobial profile, Antibiotics, Blood stream infections, Low-middle income countries.

INTRODUCTION

Bacteremia refers to the presence of bacteria in the bloodstream. Admitted patients remain vulnerable to morbidity and mortality as a consequence of blood stream infections (BSIs) regardless of advancements in supportive care and therapies [1]. Primarily BSIs are fatal infections as pathogens propagate all over the body through reproducing infections, leading to multiorgan dysfunction [2]. BSIs pose significant health threats, markedly in children. These infections in pediatric patients are associated with deadly consequences [3]. They make up complex series of inflammatory processes extending to systemic inflammatory response syndrome, septic shock, severe sepsis and eventually fatality if not rapidly treated [4].

Primarily antibiograms are utilized for monitoring of local antimicrobial profile in terms of sensitivity and resistance rates, aid in ascertaining the relevant empiric antimicrobial therapy, whilst comparing to different institutions [5]. They are suggested by the Infectious Diseases Society of America and the Centers for Disease Control and Prevention as an essential segment of antibiotic stewardship programs [6]. The protocols directed by The Clinical and Laboratory Standards Institute (CLSI) recommend to develop antibiogram in hospital settings [7]. Data generated by antibiogram can be integrated into local management protocols and patient care plans giving information for treatment options for patients having different infections including community-acquired pneumoniae, urinary tract infections, skin and soft tissue infections [8].

In low-middle income countries multi-drug resistant (MDR) bacteria are considered a health priority as resistance rates are generally high in these regions [9]. Limited resources, substandard infrastructure, insufficient health resources and inadequate

* Address correspondence to this author at the Department of Pediatric Medicine, Liaquat National Hospital & Medical College, Karachi, Pakistan.. Email: alimasood146@gmail.com

sanitation and hygiene levels marginally accounts for infection spread and fatal impacts of MDRs bacteria in lower middle income countries (LMICs) [9,10]. Consequently, preemptive diagnosis and empirical antibiotic therapy are important to decelerate the further progression and improve BSIs prognosis. Nonetheless, the selection of presumptive antibiotic therapy must be derived from the patient's health profile, commonly identified isolates, and their antimicrobial profiles in the territory [11]. In several hospitals, management of BSIs imposes a challenge because of growing antibiotic resistance [12].

Similar to the shifts in bacterial patterns, pathogens' antimicrobial susceptibility patterns differ globally and are influenced by regional pathogens and antibiotic usage trends [13]. Even within the same practice region, pathogen susceptibility patterns to drugs can occasionally shift [13]. Furthermore, the World Health Organization (WHO) has distributed an urgency illnesses list, promoted development of new antimicrobials, and guided related directed research [14]. Antimicrobial stewardship programs (ASPs) in particular have grown significantly. The antibiogram is helpful not only for facility-level clinicians but also for ASPs and public health, as there is a growing need to comprehend the collective dynamics of antimicrobial susceptibility in order to confront the concerns of rising antimicrobial resistance.

An important emerging problem in our daily clinical practice is antimicrobial resistance, which has made treating physicians' jobs more difficult while also placing a heavy financial strain on patient families [15]. Antibiotic stewardship programs and periodic antibiograms are necessary to better understand the types of organisms, their susceptibilities, and resistance patterns. In an emergency, this information helps with the start of empirical antibiotics. Thus we planned the current study to analyze the bacteriological diversity and antibiogram patterns of blood culture isolates in a pediatric settings at a tertiary care hospital in Karachi, Pakistan.

MATERIALS AND METHODS

This descriptive cross-sectional study was executed at Department of Pediatrics, Liaquat National Hospital with the formal ethical approval of the hospital committee on institutional letter head bearing number App#1152-2024-LNH-ERC. The study was carried out during 2nd February, 2025 to 30th September, 2025. Patients of age 0-16 years of either gender admitted to pediatric department and suspected for BSI (fever≥38 ◦C, lethargic, presence of hypotension, tachycardia or catheters, central lines) were included. Patients received antibiotics within 48 hours prior to sample collection, viral or fungal infections, congenital abnormalities, antibiogram testing was unable to perform and contaminated specimens were excluded. Patients were enrolled into the study with the written informed consent of their parents.

Sample size of 366 was computed taking 39% prevalence of positive blood culture isolates in pediatric patients [16] at 95% confidence interval and 5% margin error using online available calculator Open-Epi. Patients were enlisted through non-probability consecutive sampling technique.

Standard aseptic measures were used to collect the blood sample. To reduce contamination from skin flora, the venipuncture site was first prepared using sterile cotton wool soaked in 70% alcohol and then 10% Povidone-iodine. After that, the area was left to dry for roughly 30 to 60 seconds. For each patient, blood samples were taken from two distinct locations (an average of 3 mL per location). Note that due to safety concerns, only one site was used to select patients younger than one month. After cleaning the cover cap with alcohol, one milliliter of the blood sample was added to a BACTEC-Ped plus aerobic blood culture vial that was appropriately marked. Blood samples were taken prior to the start of antibiotics. Following rigorous adherence to the manufacturer's instructions, the BACTEC-Ped Plus blood culture bottle was then shipped to the lab to be incubated in the BACTEC 9050 automated system for five days at 37°C. Three different kinds of blood culture plates—MacConkey agar, chocolate agar, and blood agar (5% sheep blood)—were trans-inoculated with positive colonies. For 16–18 hours, each plate was incubated in a microaerophilic environment with 5% CO_2. VITEK-MS (bio Mérieux, France) was used to identify the microorganisms.

In accordance with the 2017 Clinical Laboratory Standard Institute (CLSI) recommendation for antimicrobial susceptibility testing [17], the Kirby Bauer disc diffusion method was used to conduct the antibiotic susceptibility test for the various isolates that were found. The inoculum was standardized to the 0.5 McFarland standard, which is equivalent to 1.5 x 108 CFU/ml, the density of a bacterial suspension [18]. Depending on CLSI's guidelines for each isolate, different antibiotic discs were employed for the test. According to the CLSI's breakpoint guidelines, the isolates were classified as susceptible, intermediate, or resistant to the test antibiotics. The inhibition zone diameter (IZD) was measured in millimeters (mm). After initial work-up testing for methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum β-lactamase (ESBL) by Gram-negative organisms. For ESBL detection, isolates with zone diameters <27 mm for cefotaxime, <22 mm for ceftazidime, <25 mm for ceftriaxone, <27 mm for aztreonam and <17 mm for cefpodoxime were presorted as potential ESBL producers on the basis of the most recent CLSI M100 document. For ESBL producers, a 5 mm increase in the zone of inhibition in a disc containing clavulanate as opposed to the medication alone was seen as positive.

STATISTICAL ANALYSIS

Data was analyzed using SPSS version 27. Frequency and percentages were computed for categorical variables. Numerical variable 'age' was first tested for normality assumption using Shapiro-Wilk test which was non-normally distributed and hence was expressed as median with inter-quartile range (IQR). Data is presented in a tabular form.

RESULT

A total of 370 patients were enrolled into the study. Median age of patients was 35.5 (IQR=12-124) months with range of 2-208 months. Approximately two-third of patients were males (67%). Most of the patients were admitted with suspicion of enteric fever (40.8%). Table **1** displays summary of patients' features.

Table 1. Summary of Patients' Features.

Patients' Features	Frequency	Percentage
Age		
0-12 months	102	27.6
12.1-60 months	126	34.0
>60 months	142	38.4
Gender		
Male	248	67
Female	122	33
Admitting diagnosis		
Acute exacerbation of asthma	5	1.4
Acute febrile illness	10	2.7
Acute gastroenteritis	19	5.1
Enteric fever	151	40.8
Sepsis	63	17.0
Pneumoniae	44	11.9
Chronic liver disease	10	2.7
Urinary tract infection	10	2.7
Disseminated MRSA	5	1.4
Enterocutaneous fistula	5	1.4
Fulminant myocarditis	5	1.4
Ileal perforation	5	1.4
infective endocarditis	5	1.4
Measles	5	1.4
Perforated appendix	15	4.1
Pneumoperitoneum	5	1.4
Scorpion bite	3	0.8
Suspected Inborn Error of Metabolism	5	1.4

Out of 370 patients, BSI was detected in 75 (20%). Out of 75, gram-positive and gram-negative bacteria were found in 17 (22.7%) and 58 (77.3%) patients respectively. Out of total 17 gram positive bacteria, almost half were *Streptococcus pneumoniae* and other half were *Enterococcus species*. Among 58 gram-negative bacteria, the commonest detected pathogen was *Salmonella Typhi* (56.9%). Out of 44 *Salmonella Typhi* cases, 36% were XDR and 24% were MDR and 40% were non-MDR /XDR. Table **2** displays the details detected pathogens.

Table 2. Summary Statistics for Detected Pathogens.

Bacteria	Frequency	Percentage
Gram-positive bacteria		
Streptococcus pneumoniae	6	8
Enterococcus species	5	6.7
Methicillin-Susceptible *Staphylococcus aureus* (MSSA)	14	18.7
Staphylococcus aureus (MRSA)	6	8
Gram-negative bacteria		
Salmonella Typhi	33	44
Acinetobacter (MDR)	8	10.7
Burkholderia cepacia	5	6.7
Klebsiella pneumoniae	4	5.3
E.coli	3	4
Serratia marcescens (MDR)	2	2.7
Moraxella species	1	1.3
Hafnia alvei	1	1.3
Pseudomonas aeruginosa	1	1.3

Table **3** shows Antimicrobial resistance profile of gram-positive bacteria against different tested antibiotics. All of the isolates of *Streptococcus pneumoniae* were resistant to linezolid, meropenem and vancomycin while half of the isolates showed resistance to erythromycin and Sulfamethoxazole /trimethoprim. All of the isolates of *Enterococcus species* were completely resistant to meropenem whereas 60% of these isolates were resistant to ampicillin and Erythromycin.

Table 3. Antimicrobial Resistance Profile of Gram-positive Bacteria against different Tested Antibiotics.

Pathogens	Gram Positive Bacteria	
	Streptococcus pneumoniae (MRSA)	*Enterococcus species*
Ampicillin	-	3(60)
Gentamicin	-	0
Clindamycin	4(66.7)	0
Erythromycin	3(50)	3(60)
Linezolid	6(100)	-
Meropenem	6(100)	5(100)
Sulfamethoxazole/ trimethoprim	3(50)	0
Vancomycin	6(100)	0

Data is presented as n(%), - showing antibiotics were not tested for the corresponding pathogen.

Table **4** shows Antimicrobial resistance profile of MRSA and MSSA against different tested antibiotics. MRSA was highly

resistant to ciprofloxacin (83.3%) and clindamycin (50%). MSSA was less resistant to clindamycin, tetracycline and Trimethoprim-Sulfamethoxazole with only one case resistant to these antibiotics out of 14 cases.

Table 4. Antimicrobial resistance profile of MRSA and MSSA against different tested antibiotics.

Antibiotic	MRSA	MSSA
Clindamycin	3(50)	1(7.1)
Erythromycin	-	-
Gentamicin	2(33.3)	1(7.1)
Ciprofloxacin	5(83.3)	2(14.2)
Trimethoprim-Sulfamethoxazole	1(16.7)	1(7.1)
Tetracycline	2(33.3)	1(7.1)
Vancomycin	0(0)	0(0)
Linezolid	0(0)	0(0)

Data is presented as n(%), - showing antibiotics were not tested for the corresponding pathogen

Table **5** outlines antimicrobial resistance profile of gram-negative organisms against different tested antibiotics. Resistance of Ciprofloxacin, Ceftriaxone, Cefuroxime was seen in 100% isolates of *Klebsiella pneumoniae*, *E.coli* and *hafnia alvei*. *S.Typhi* was least resistant to Cefuroxime (3%), Chloramphenicol (3%) Gentamicin (6%), Imipenem (6%) while highly resistant to Ceftriaxone (75.8%), Ampicillin (72.7%), Amikacin (69.6%).

Table 5. Antimicrobial Resistance Profile of Gram-negative against Different Tested Antibiotics.

Pathogens	*Staphylococcus aureus*	*Salmonella Typhi*	*Klebsiella pneumoniae*	*acinetobacter (MDR)*	*E.coli*	*Burkholderia cepacia*	*Pseudomonas aeruginosa*	*Serratia marcescens ((MDR))*	*Moraxella species*	*hafnia alvei*
Amikacin	-	23(69.6)	3(75)	7(87.5)	0	-	0	1(50)	-	0
Amoxicillin–clavulanate	-	4(12.1)	4(100)	1(12.5)	3(100)	-	-	2(100)	0	1(100)
Ampicillin	0	24(72.7)	-	-	3(100)	-	-	2(100)	-	1(100)
Ciprofloxacin	5(83.3)	29(87.8)	4(100)	7(87.5)	3(100)	-	0	1(50)	1(100)	1(100)
Gentamicin	1(16.7)	2(6)	3(75)	6(75)	0	-	-	1(50)	-	0
Ceftriaxone	-	25(75.8)	4(100)	8(100)	3(100)	-	-	0	0	1(100)
Cefuroxime	-	1(3)	4(100)	1(12.5)	3(100)	-	-	2(100)	0	1(100)
Cefixime	-	16(48.5)	-	-	-	-	-	-	-	-
Imipenem	-	2(6)	1(25)	7(87.5)	1(33.3)	-	0	-	-	0
Meropenem	-	-	1(25)	2(25)	1(33.3)	2(40)	-	1(50)	-	-
Piperacillin–tazobactam	-	2(6)	3(75)	7(87.5)	1(33.3)	-	0	1(50)	-	0
Tetra cycline	2(33.3)	-	-	-	-	-	-	-	0	-
Fusic acid	1(16.7)	-	-	-	-	-	-	-	-	-
Cloxacillin	3(6)	-	-	-	-	-	-	-	-	-
Sulfamethoxazole/trimethoprim	1(16.7)	23(69.6)	4(100)	-	2(66.7)	0	-	0	1(100)	1(100)
Chloramphenicol	-	1(3)	0	-	0	-	-	1(50)	-	0
Erythromycin	-	4(12.1)		-	-	-		-	1(100)	

Data is presented as n(%), - showing antibiotics were not tested for the corresponding pathogen.

DISCUSSION

In our research, blood stream infection (BSI) was observed in 75 patients out of 370 patients which is equivalent to 20 percent. This is rather an impressive level of prevalence in comparison to the high-income countries. An example is that of 1,809,751 encounters in 162 hospitals in the United States in which only 0.3% or 18 were found to have the positivity rate [19], whereas a study done in Saudi Arabia showed that the positivity rate was 3.5% in 83,605 blood cultures in children [20]. Swedish data also showed that even though the overall incidence was lower, neonates exhibited an outsize burden of disease and 34.4% of the total number of BSI episodes occurred in neonates aged 0-2 months [21]. On the same note, a Chinese study reported 2544

isolates of 2368 patients in the span of 5 years and this also indicates a relatively lower prevalence as compared to ours [22]. On the contrary, in a low and middle-income country, the research presents a higher degree, which would be more likely to correspond to our results. As an example a study done in Tanzania recorded a prevalence of 14.2 amongst children [23]. The differences indicate that the prevalence of BSI is generally lower in the high-income environment and the prevalence rates are higher in the resource-limited areas which can be probably attributed to the differences in the access to healthcare, infection control measures as well as the susceptibility of the patients. Moreover, study design, population and diagnostic criteria differences can also be causal factors of difference in BSI prevalence between settings.

In our research among 75 culture-proven BSI cases gram-negative bacteria were the most common, meaning that we observed 58 (77.3) cases of gram-negative bacteria and 17 (22.7) cases of gram-positive bacteria. This is in line with the results of Tanzania where 78.5% BSIs were found to be caused by organisms of gram-negative shape compared to gram-positive organisms [23] and a study in Saudi Arabia where the gram-negative organisms were found to cause 61% of the infection [20]. But opposite findings have been perceived in the other areas. An example is a study carried out in China which showed that the gram-positive isolates were most common with the proportion of 54.6 (as a proportion of the isolates) among the isolates [22]. Equally, a study carried out in Sweden, showed that theiture percentage of gram positive infections (59.7) was before gram negative (35.4) [21]. Nigerian data also showed that it was variable with 20/30 isolates being gram-positive [24]. These dissimilarities point to the geographical variations of the BSI pathogen spread, which could be conditioned by population dissimilarities, medical care procedures, antimicrobial intake as well as regional epidemiological trends.

Salmonella Typhi was the most abundant organism followed by multidrug-resistant (MDR) *Acinetobacter* spp. (10.7%), methicillin-resistant *Staphylococcus aureus* (MRSA) and *Streptococcus pneumoniae* (8%) followed by *Enterococcus* spp. and *Burkholderia cepacia* (6.7%) in inpatient pediatric patients in our study. These results largely agree with research conducted in the region. Indicatively, a research conducted in Peshawar had indicated that Gram-negatives were constituting 71.1 percent bloodstream infections with *S. Typhi* having highest prevalence of 31.5 percent followed by *E. coli* and *Staphylococcus aureus* [25]. A similar study by Peshawar (Fauji Foundation Hospital, Rawalpindi) however gave different results with the *Staphylococcus aureus* (27.4%), *Escherichia coli* (23.9%) and *Klebsiella pneumoniae* (22.2%) being the most common isolate in pediatric case of BSI. This could be explained by difference in the population under study, type of hospital [e.g. tertiary care vs. general care), season or the local burden of the disease such as lack of enteric fever outbreaks during that time could explain the lower prevalence of *Salmonella Typhi* in that cohort [26].

Comparisons of the international kind suggest some differences. In a Saudi multicenter study which included between 2015-2021, Gram- negative bacteria was approximately six one-fifth of the pediatric bloodstream isolates of which *Klebsiella* spp. were the most common followed by *E. coli* and *Acinetobacter* [20]. A more recent Saudi study was able to specifically comment on *K. pneumoniae* as the most prevalent MDR isolate in hospitalized children [27]. Conversely in a quaternary referral hospital study from Brazil, the most common pathogens of childhood infections were *Escherichia coli* 23% and *Staphylococcus aureus* (17.9%) with *Klebsiella pneumoniae* coming in at the third-largest (12.8%). Interestingly, their cohort did not bear *Salmonella Typhi*, and the regional epidemiology could be discriminated by differences with ours findings [28]. These differences highlight the contribution of the local epidemiology. *Salmonella Typhi* is the dominating strain in our environment and it may be an indication of endemics and regional specifics of our health. Therefore, the empirical treatment programs have to be specific to the local microbial trend rather than the international guidelines only.

In this particular research, there was an alarming trend of resistance among the gram-positive isolates. The 100 percent of all *Streptococcus pneumoniae* isolates showed resistance to linezolid and meropenem and high resistance was found to the antibiotics, clindamycin (66.7 percent), erythromycin and trimethoprim-sulfamethoxazole (50 percent each). A study of BSI in Beijing pediatrics has reported similar high prevalence of macrolide resistance in which more than 95 percent of the *S. pneumoniae* were resistant to clindamycin and erythromycin, but resistant to linezolid and vancomycin [22]. On the contrary, the Swedish and US studies, had low resistance rates in general and *S. pneumoniae* was sensitive to the reserve antibiotics, such as linezolid and meropenem [19, 21]. Those results could be an indication of excessive use of broad-spectrum antibiotics on the local level and the need for effective antimicrobial stewardship.

The *Enterococcus species* was resistant to ampicillin (60 percent) and erythromycin (60 percent) and universal resistance to meropenem. Gentamicin, clindamycin, Trimethoprim-Sulfamethoxazole and vancomycin did not present any resistance to infections but sample size was small. Patterns were found to be similar in a study carried out in Beijing, *E. faecium* was high-resistant to ampicillin, yet all the isolates were sensitive to vancomycin and linezolid [22]. Preserved vancomycin susceptibility of *Enterococcus* was also shown in data from the US although resistance to beta-lactam was increasing [19]. The local pressure of the antibiotic or nosocomial spread may be the cause for the high resistance to meropenem in our location.

Salmonella Typhi was the commonest organisms that were isolated in this study and it has alarming rates of resistance to various popular antibiotics. The resistance was significantly high (87.8%), ceftriaxone (75.8%), ampicillin (72.7%) and trimethoprim-sulfamethoxazole (69.6%) some of the main types of drug used in treatment of typhoid. However, gentamicin (94% sensitive) and imipenem (94% sensitive) had a relatively good sus-

ceptibility. This resistance to first line antibiotics is high which is consistent with the reports from South Asia on the same problem, and indicates that the problem of extensively drug resistant strains of *Salmonella Typhi* in children has continued [19, 25].

In case of *Staphylococcus aureous* (MRSA) there was resistance to ciprofloxacin (83.3) and moderate resistance to tetracycline (33.3) but a relatively maintained susceptibility to gentamicin and cloxacillin. This is the same case as seen in Saudi Arabia and the U.S where the MRSA strains showed the same resistance profiles with more focus of the global burden of MRSA infecting the pediatric patients [19, 20].

The *Klebsiella pneumoniae* was found to have very high resistance to most of the antibiotics tested (amoxicillin -clavulanate, ceftriaxone, cefuroxime, ciprofloxacin, merpenem, univariate 100% resistant, imipenem 25, merpenem 25). *E. coli* isolates also showed complete resistance to amoxicillin-clavulanate, ampicillin and ciprofloxacin however amikacin and gentamicin showed resistance. These results are in line with the trends of resistance in Pakistan and China whereby multidrug-resistant Enterobacterales is becoming more frequent in pediatrics [22, 25].

Non-fermenters such as *Acinetobacter* (MDR) were highly resistant with high resistance to amikacin (87.5%), ceftriaxone (100%), ciprofloxacin (87.5%) and carbapenems such as imipenem (87.5%), and meropenem (25%). The relative susceptibility of *Pseudomona aeruginosa* and *Burkholderia cepacia* were relatively better and were limited by small sample sizes. These resistance profiles are consistent with the international publications which reveal the high risk of MDR non-fermenters in BSIs of pediatric origin [22, 25].

Lastly, the less frequent organisms like *serratia marcescens* (MDR), *Moraxella species* and *Hafnia alvei* showed different resistance with serratia having a high resistance towards different antibiotics such as amoxicillin-clavulanic acid (100% each). Though they are less common, these species have also been reported to have been more frequently reported as multi-drug-resistant causative agents of bloodstream infections in children in the hospital setting, thus making the choice of treatment more difficult in the hospital setting [20,22].

CONCLUSION

A remarkable burden of BSI was found in our settings with higher burden of gram-negative bacteria, Enteric fever being the most frequent. Different resistance patterns were observed for different antibiotics, mostly 100% resistance was seen for most of bacterial isolates. This finding underscores the ongoing monitoring of antimicrobial profile to decide the appropriate empirical therapy of antibiotics.

LIST OF ABBREVIATIONS

ASPs: Antimicrobial stewardship programs.

BSIs: Blood stream infections.

CLSI: Clinical and Laboratory Standards Institute.

IZD: Inhibition zone diameter.

MDR: Multi-drug resistant.

MRSA: Methicillin-resistant *Staphylococcus aureus*.

WHO: World Health Organization.

AUTHORS' CONTRIBUTION

Shaikh Ali Masood: Conceptualization, Study Design, and Writing draft.

Shabbir Ahmed Mallick: Conceptualization, Study Design, Critical review and revision the manuscript and Final approval, final proof to be published.

Romana Nisar Ahmed and **Tooba**: Study Design, and Writing draft.

Haider Abbas and **Ayesha Samad**: Methodology, Data analysis and interpretation.

ACKNOWLEDGEMENTS

Declared none.

ETHICAL DECLARATIONS

Data Availability

Data will be available from the corresponding author upon a reasonable request.

Ethical Approval

The study received formal ethical approval of the hospital committee on institutional letter head bearing number App#1152-2024-LNH-ERC.

Consent to Participate

The written informed consent was obtained from parents/guardians.

Consent for Publication

All authors give consent fot the publication of this work.

Conflict of Interest

The authors declare that they have no competing interests.

Competing Interest/Funding

Declared none.

Use of AI-Assisted Technologies

QuillBot, an AI-based software, was utilized exclusively for language refinement, including improvement of readability and correction of grammatical and punctuation errors. The authors assume full responsibility for the accuracy, integrity, and originality of the manuscript.

REFERENCES

[1] Smith DA, Nehring SM. Bacteremia. Treasure Island (FL): StatPearls Publishing 2025.

[2] Allel K, Stone J, Undurraga EA, Day L, Moore CE, Lin L, *et al.* The impact of inpatient bloodstream infections caused by antibiotic-resistant bacteria in low- and middle-income countries: A systematic review and meta-analysis. PLoS Med 2023; 20(6): e1004199. doi: 10.1371/journal.pmed.1004199.

[3] Thaulow CM, Lindemann PC, Klingenberg C, Berild D, Salvesen Blix H, Myklebust TÅ, *et al.* Epidemiology and Antimicrobial susceptibility of invasive bacterial infections in children—a population-based study from Norway. Pediatr Infect Dis J 2021; 40: 403-10. doi: 10.1097/INF.0000000000003013.

[4] Seni J, Mwakyoma AA, Mashuda F, Marando R, Ahmed M, DeVinney R, *et al.* Deciphering risk factors for blood stream infections, bacteria species and antimicrobial resistance profiles among children under five years of age in North-Western Tanzania: a multicentre study in a cascade of referral health care system. BMC Pediatr 2019; 19(1): 32. doi: 10.1186/s12887-019-1411-0.

[5] Yogeshwari S, Devanath I, Annalakshmi S, Singh P. The utility, development and interpretation of antibiograms: A review on their role in empirical antibacterial selection amidst escalating antimicrobial resistance. J Nenonatal Surg 2025; 14(8S): 368-76.

[6] Core Elements of Hospital Antibiotic Stewardship Programs. Centers for Disease Control and Prevention. 2025; Available at: https://www.cdc.gov/antibiotic-use/hcp/core-elements/hospital.html

[7] Hindler JA, Lubbers BV. M39 Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data. 5th ed. USA: Clinical and Laboratory Standards Institute 2022; Available at: https://cdn.bfldr.com/YLD4EVFU/at/35ksm8xm67nh525bbnn6k/m39ed5_sample.pdf

[8] Organisation for Economic Cooperation and Development. Stemming the Superbug Tide: Just a Few Dollars More: Paris: OECD Publishing 2019. https://doi.org/10.1787/9789264307599-en

[9] Okeke IN, Laxminarayan R, Bhutta ZA, Duse AG, Jenkins P, O'Brien TF, *et al.* Antimicrobial resistance in developing countries. Part I: recent trends and current status. Lancet Infect Dis 2005; 5(8): 481-93.

[10] Ehsan H. Antibiotic resistance in developing countries: Emerging threats and policy responses. Public Health Challenges 2025; 4(1): e70034.

[11] Freifeld AG, Bow EJ, Sepkowitz KA, Boeckh MJ, Ito JI. Clinical practice guideline for the use of antimicrobial agents in neutropenic patients with cancer: 2010 update by the Infectious Diseases Society of America. Infect Dis Soc Am 2011; 52: 427.

[12] Radhakrishnan V, Vijaykumar V, Ganesan P, Rajendranath R, Trivadi G. Bloodstream infections in pediatric patients at cancer institute. Ind J Cancer 2014; 51: 418.

[13] Khursheed N, Adnan F, Khan MA, Hatif R. Regional insights on the prevalence and antimicrobial susceptibility pattern of carbapenem and colistin-resistant gram-negative bacteria: an observational cross-sectional study from Karachi, Pakistan. BMC Infect Dis 2025; 25(1): 186. doi: 10.1186/s12879-025-10535-z.

[14] World Health Organization. WHO bacterial priority pathogens list 2024: Bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance. 2024; Available at: https://iris.who.int/server/api/core/bitstreams/1a41ef7e-dd24-4ce6-a9a6-1573562e7f37/content

[15] Safdar N, Saleem S, Salman M, Tareq AH, Ishaq S, Ambreen S, *et al.* Economic burden of antimicrobial resistance on patients in Pakistan. Front Public Health 2025; 13: 1481212. doi: 10.3389/fpubh.2025.1481212.

[16] Kolesnichenko SI, Lavrinenko AV, Akhmaltdinova LL. Bloodstream infection etiology among children and adults. Int J Microbiol 2021; 2021: 6657134. doi: 10.1155/2021/6657134.

[17] Clinical and Laboratory Standards Institute (CLSI). Performance Standards for Antimicrobial Disk Susceptibility Tests. 12th ed. Wayne, PA: Clinical and Laboratory Standards Institute 2017.

[18] Patel J, Weinstein MP, Eliopoulos G. Performance standards for antimicrobial susceptibility testing. In: Clinical and Laboratory Standards Institute (ed.) CLSI Supplement M100. 27th ed. Wayne, PA: Clinical and Laboratory Standards Institute 2017; pp. 278-82.

[19] Spaulding AB, Watson D, Dreyfus J, Heaton P, Grapentine S, Bendel-Stenzel E, *et al.* Epidemiology of bloodstream infections in hospitalized children in the United States, 2009-2016. Clin Infect Dis 2019; 69(6): 995-1002. doi: 10.1093/cid/ciy1030. PMID: 30534940.

[20] Basnawi F, Essa RA, Alosaimi A, Alrshaid B, Alshuhri S, Almazrua A, *et al.* Bacterial bloodstream infections in a pediatric population: A 7-year experience at a tertiary care center in Saudi Arabia. Infect Dis Health 2025; 30(4): 290-8. doi: 10.1016/j.idh.2025.03.006.

[21] Luthander J, Bennet R, Giske CG, Eriksson M, Nilsson A. Trends of pediatric bloodstream infections in stockholm, sweden: A 20-year retrospective study. Pediatr Infect Dis J 2020; 39(12): 1069-74. doi: 10.1097/INF.0000000000002850.

[22] Lyu ZY, Zhen JH, Meng QY, Zhou W, An JY, Dong F. Bacterial etiology and antimicrobial resistance pattern of pediatric bloodstream infections in Beijing, 2015-2019. Infect Drug Resist 2023; 16: 6297-6308. doi: 10.2147/IDR.S426000.

[23] Seni J, Mwakyoma AA, Mashuda F, Marando R, Ahmed M, DeVinney R, *et al.* Deciphering risk factors for blood stream infections, bacteria species and antimicrobial resistance profiles among children under five years of age in North-Western Tanzania: A multicentre study in a cascade of referral health care system. BMC Pediatr 2019; 19(1): 32. doi: 10.1186/s12887-019-1411-0.

[24] Nnamani KO, Nnamani CP, Iloh KK, Aghanya IN, Ushie SN, Ofiaeli OC, *et al.* Bacterial isolates, antibiogram and outcomes of blood culture proven sepsis in neonates at a tertiary institution in South East Nigeria: A cross-sectional study. Ther Adv Infect Dis 2022; 9: 20499361221122479. doi: 10.1177/20499361221122479.

[25] Muhammad A, Noor Khan S, Jamal T, Ul Haq I, Jabbar A, Ali I. Bacterial spectrum and antimicrobial profile of pediatric blood stream infection at a tertiary care hospital in Pakistan. Chin Med Sci J 2020; 35(4): 315-22. doi: 10.24920/003675.

[26] Khan M, Haider S. Blood culture proven common bacterial pathogens in patients admitted in the pediatric unit of a tertiary care hospital in Pakistan. Pak J Intensive Care Med 2025; 67: 1-4.

[27] Saeedi FA, Hegazi MA, Alsaedi H, Alganmi AH, Mokhtar JA, Metwalli EM, *et al.* Multidrug-resistant bacterial infections in pediatric patients hospitalized at King Abdulaziz University Hospital, Jeddah, Western Saudi Arabia. Children (Basel) 2024; 11(4): 444. doi: 10.3390/children11040444.

[28] Pinheiro FR, Rozza-de-Menezes RE, Blum MC, Pereira RFA, Rocha JA, Guedes Pinto MCF, *et al.* Evaluation of changes in antimicrobial susceptibility in bacteria infecting children and their mothers in pediatric, neonatal-intensive care unit, and gynecology/obstetrics wards of a quaternary referral hospital during the COVID-19 pandemic. Front Microbiol 2023; 14: 1096223. doi: 10.3389/fmicb.2023.1096223.

Received: November 07, 2025 Revised: December 31, 2025 Accepted: January 05, 2026

© 2026. The Authors, National Journal of Health Sciences.
This is an open access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY- NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non- commercially, and license their derivative works on different terms, provided the original work is properly cited, appropriate credit is given, any changes made indicated, and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/.