Section: Pediatrics

Original Research Article

BACTERIAL ETIOLOGICAL AGENTS RESPONSIBLE FOR SEPSIS IN CHILDREN AGED 1-36 MONTHS AND SUSCEPTIBILITY PATTERNS OF ISOLATES

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Received *: 17/02/2026*
Received in revised form *: 04/04/2026*
Accepted *: 20/04/2026*

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DOI: 10.70034/ijmedph.2026.2.688

Source of Support: Nil,
Conflict of Interest: None declared

Int J Med Pub Health
2026; 16 (2); 4184-4190

ABSTRACT

Background: Pediatric sepsis remains a major cause of morbidity and mortality, particularly in infants and toddlers. The etiological spectrum and antimicrobial susceptibility profiles vary across regions and time, highlighting the need for periodic local surveillance to guide empirical therapy. **Aim:** To identify the bacterial etiological agents responsible for sepsis in children aged 1–36 months and to determine the antimicrobial susceptibility pattern of isolates in a tertiary care hospital.

Materials and Methods: A cross-sectional study was conducted in the Department of Microbiology of a tertiary care teaching hospital from January 2024 to December 2024. Blood culture samples were collected from 300 suspected sepsis cases aged 1–36 months, admitted to pediatric wards and PICU. Neonates (<1 month) and children already receiving antibiotics were excluded. Samples were processed using the BACTEC system. Isolates were identified by standard microbiological methods, and antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method as per CLSI 2024 guidelines.

Results: Out of 300 blood culture samples, 92 were culture positive, yielding an overall positivity rate of 30.7%. Culture positivity was highest among infants aged 1–11 months (39.3%). Gram-positive cocci predominated, followed by Gram-negative bacilli; Candida spp. were isolated in a small proportion. Staphylococcus aureus was the most common pathogen (55.4%), followed by coagulase-negative Staphylococcus spp. (21.7%). Gram-positive isolates showed high susceptibility to vancomycin and linezolid, while Gram-negative isolates showed maximum susceptibility to colistin and moderate susceptibility to carbapenems and tetracycline/minocycline. Poor susceptibility was observed for commonly used agents such as cephalosporins and fluoroquinolones, indicating increasing antimicrobial resistance.

Conclusion: Pediatric sepsis in children aged 1–36 months showed a moderate blood culture positivity rate, with Gram-positive cocci—especially Staphylococcus aureus—being the predominant pathogens. The observed resistance to commonly prescribed antibiotics highlights the need for strict antibiotic stewardship and continuous monitoring of local etiological trends and antibiograms to guide effective empirical therapy.

Keywords: Pediatric sepsis; infants; blood culture; etiological agents; antimicrobial susceptibility; Staphylococcus aureus; antibiogram; India.

INTRODUCTION

Sepsis is a life-threatening clinical syndrome that results from a dysregulated host response to infection. The resulting uncontrolled inflammatory cascade can rapidly progress to tissue injury, organ dysfunction, septic shock, and ultimately death if not recognized and treated promptly.[1,2] Mortality in severe pediatric sepsis commonly occurs due to refractory shock, multiple organ dysfunction

syndrome (MODS), respiratory failure, and neurological complications.[1,2]

Despite advances in immunization coverage, improved intensive care practices, and availability of standard treatment guidelines, sepsis continues to remain a major public health challenge in developing countries such as India.[3] Sepsis affects all age groups, but the burden is disproportionately higher at the extremes of age, particularly during early childhood. Globally, sepsis affects nearly 50 million individuals annually, with children contributing a substantial proportion of this burden. Recent estimates suggest that pediatric sepsis accounts for approximately 1.2 million cases per year and constitutes more than 8% of pediatric intensive care unit admissions, with reported mortality varying from 1% to 20% depending on severity and clinical setting.[1,3]

Early diagnosis of pediatric sepsis remains difficult due to its nonspecific clinical presentation, which often overlaps with common febrile illnesses in children.[4] In addition, children may initially compensate physiologically, masking classic signs of sepsis until they present in advanced shock. Several factors increase the risk of sepsis in children, including indwelling medical devices, malignancies, immunosuppressive states, bone marrow or organ transplantation, and chronic underlying diseases.[3,4] Importantly, the causative organisms differ between previously healthy children and those with significant risk factors. Staphylococcus aureus is frequently implicated across both groups. Other commonly reported pathogens in previously healthy children include Escherichia coli and Streptococcus pneumoniae, whereas Candida spp. and Pseudomonas spp. are more frequently isolated in children with chronic illnesses or prolonged hospital exposure.[1,3,5]

Beyond acute mortality, pediatric sepsis is associated with significant long-term consequences. Survivors may develop persistent physical, cognitive, or developmental impairment even after discharge, contributing to long-term morbidity.[1,3,6] In addition, pediatric sepsis imposes a considerable financial burden on families and healthcare systems, particularly in resource-limited settings.[1,3] Since clinical outcomes depend strongly on timely diagnosis and early initiation of appropriate therapy, empirical antibiotics must be started immediately in suspected cases, followed by escalation or de-escalation based on microbiological confirmation and susceptibility results.

The microbial spectrum responsible for pediatric sepsis is known to vary over time and across geographic regions. Therefore, periodic epidemiological surveillance of etiological agents and local antibiograms plays an essential role in guiding evidence-based empirical therapy and improving outcomes. However, limited data are available regarding the microbiological profile of pediatric sepsis and antimicrobial susceptibility patterns in our region. Hence, the present study was undertaken to determine the etiological agents responsible for pediatric sepsis and their antimicrobial susceptibility pattern in a tertiary care hospital setting.

Aim

To determine the etiological agents responsible for pediatric sepsis and to assess their antimicrobial susceptibility pattern among children admitted to pediatric wards and PICU in a tertiary care hospital.

Objectives

1. To identify and determine the frequency of microorganisms isolated from blood culture samples of suspected pediatric sepsis cases.
2. To study the antimicrobial susceptibility pattern of the isolated organisms to commonly used and reserved antimicrobial agents.

MATERIALS AND METHODS

This cross-sectional study was conducted in the Department of Microbiology at a tertiary care teaching hospital from January 2024 to December 2024, after approval from the Institutional Ethics Committee. Written informed consent was obtained from the guardians of all participants. A total of **300 blood culture samples** were collected from suspected sepsis patients aged **1–36 months**, admitted to pediatric wards and the Pediatric Intensive Care Unit (PICU). Neonates (<1 month) and children already receiving antibiotic therapy at the time of sampling were excluded.

Blood samples (approximately **3–5 mL, as feasible by age/weight**) were collected by peripheral venipuncture under strict aseptic precautions and inoculated into pediatric blood culture bottles (BACTEC system) prior to initiation of antimicrobial therapy. Bottles flagged positive were subcultured on blood agar and MacConkey agar and incubated at **37°C for 18–24 hours**. Isolates were identified using standard microbiological procedures (7). Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method, and interpretation was done according to **CLSI 2024** guidelines (8). Data were entered in Microsoft Excel and analyzed using **SPSS version 23.0**. Results were expressed as frequencies and percentages and presented in tables and figures.

RESULTS

A total of 300 blood culture samples were collected during the study period from children aged 1–36 months, admitted to pediatric wards and the Pediatric Intensive Care Unit (PICU). Most of the suspected sepsis cases were observed in the 1–11 months age group.

Demographic profile

Among the 300 suspected sepsis cases, 140 (46.7%) belonged to the 1–11 months group, followed by 95 (31.7%) in the 12–23 months group and 65 (21.6%)

in the 24–36 months group. Male children constituted 172 (57.3%) of the study population.

Table 1: Demographic profile of suspected pediatric sepsis cases (1–36 months) (N = 300)

Age group	Male n (%)	Female n (%)	Total n (%)
1–11 months	82 (58.6)	58 (41.4)	140 (46.7)
12–23 months	54 (56.8)	41 (43.2)	95 (31.7)
24–36 months	36 (55.4)	29 (44.6)	65 (21.6)
Total	**172 (57.3)**	**128 (42.7)**	**300 (100)**

Blood culture positivity

Out of 300 blood culture samples, 92 were culture-positive, yielding an overall blood culture positivity rate of 30.7%. Blood culture positivity was marginally higher among males (30.8%) compared to females (30.5%). [Table 2]

Table 2: Blood culture positivity by gender (N = 300)

Gender	Total suspected (n)	Culture positive n (%)	Culture negative n (%)
Male	172	53 (30.8)	119 (69.2)
Female	128	39 (30.5)	89 (69.5)
Total	**300**	**92 (30.7)**	**208 (69.3)**

Culture positivity was highest in infants aged 1–11 months (39.3%), followed by children aged 12–23 months (26.3%) and 24–36 months (18.5%). [Table 3]

Table 3: Blood culture positivity by age group (1–36 months) (N = 300)

Age group	Total suspected (n)	Culture positive n (%)	Culture negative n (%)
1–11 months	140	55 (39.3)	85 (60.7)
12–23 months	95	25 (26.3)	70 (73.7)
24–36 months	65	12 (18.5)	53 (81.5)
Total	**300**	**92 (30.7)**	**208 (69.3)**

Organism-wise distribution of isolates

Among the 92 culture-positive samples, Gram-positive cocci were predominant, followed by Gram-negative bacilli, while Candida spp. were isolated in a small proportion. The most common isolate was Staphylococcus aureus (55.4%), followed by coagulase-negative Staphylococcus spp. (21.7%). [Table 4]

Table 4: Organism-wise distribution of isolates (n = 92)

Organism	Isolates (n)	Percentage (%)
Staphylococcus aureus	51	55.4
CoNS	20	21.7
Enterococcus spp.	3	3.3
E. coli	6	6.5
Klebsiella spp.	3	3.3
Pseudomonas aeruginosa	2	2.2
Acinetobacter spp.	5	5.4
Candida spp.	2	2.2
Total	**92**	**100**

Antimicrobial susceptibility pattern

Gram-positive isolates demonstrated excellent susceptibility to vancomycin and linezolid, with good activity also observed for doxycycline and minocycline. However, reduced susceptibility was noted for penicillin, erythromycin, and fluoroquinolones.

Among the Staphylococcus aureus isolates, a substantial proportion were methicillin resistant, indicating an important burden of MRSA in this age group.

Gram-negative isolates exhibited maximum susceptibility to colistin, followed by carbapenems and tetracycline/minocycline, while poor susceptibility was observed for cephalosporins and fluoroquinolones, suggesting increased resistance to commonly used antimicrobials.

Candida spp. were isolated in 2 cases, and both isolates showed good susceptibility to azole antifungals and amphotericin B.

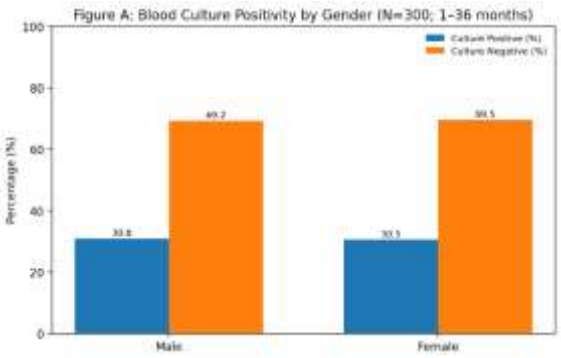

Figure 1: Blood culture positivity by gender (N = 300; 1–36 months)

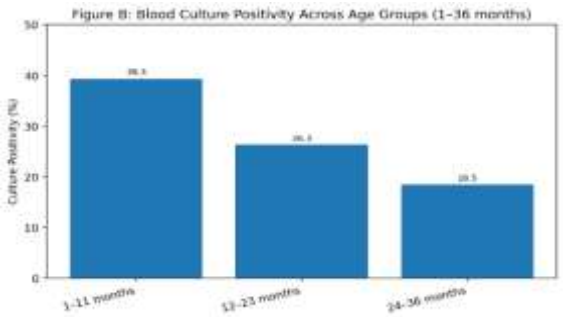

Figure 2: Blood culture positivity across age groups (1–36 months)

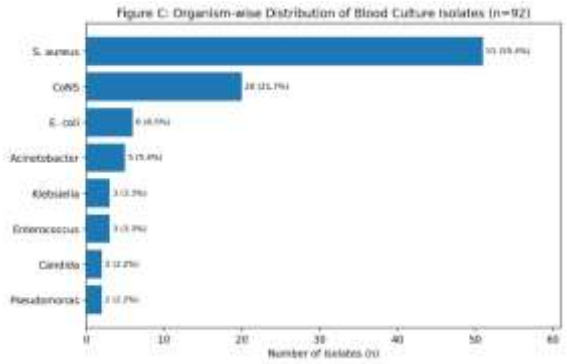

Figure 3: Organism-wise distribution of blood culture isolates (n = 92)

Organism distribution

Table 5: Organism-wise distribution of isolates (n = 86)

Organism	Isolates (n)	Percentage (%)
Staphylococcus aureus	47	54.7
Coagulase-negative Staphylococcus spp. (CoNS)	19	22.1
Enterococcus spp.	3	3.5
Escherichia coli	5	5.8
Klebsiella spp.	3	3.5
Pseudomonas aeruginosa	2	2.3
Acinetobacter spp.	5	5.8
Candida spp.	2	2.3
Total	86	100

Table 6: Group-wise distribution of isolates (n = 86)

Category	Isolates (n)	Percentage (%)
Gram-positive cocci	69	80.2
Gram-negative bacilli	15	17.4
Candida spp.	2	2.3
Total	86	100

Antimicrobial susceptibility pattern of Gram-positive isolates

Gram-positive isolates showed excellent susceptibility to vancomycin and linezolid, with good activity also observed for doxycycline and minocycline. However, susceptibility was poor for commonly used agents such as penicillin, erythromycin, and fluoroquinolones. Among *Staphylococcus aureus* isolates, 19 out of 47 (40.4%) were identified as methicillin-resistant *Staphylococcus aureus* (MRSA). [Table 6 and Table 7]

Table 6: Antibiotic susceptibility pattern of major Gram-positive isolates

Antibiotic	*S. aureus* (n = 47) Sensitive n (%)	CoNS (n = 19) Sensitive n (%)
Vancomycin	47 (100)	19 (100)
Linezolid	45 (95.7)	17 (89.5)
Doxycycline	44 (93.6)	17 (89.5)
Minocycline	46 (97.9)	19 (100)
Fluoroquinolones	18 (38.3)	7 (36.8)
Penicillin	6 (12.8)	3 (15.8)
Erythromycin	13 (27.7)	6 (31.6)
Clindamycin	—	8 (42.1)

Table 7: MRSA prevalence among Staphylococcus aureus isolates (n = 47)

Parameter	Isolates (n)	Percentage (%)
MRSA	19	40.4
MSSA	28	59.6
Total	47	100

Antimicrobial susceptibility pattern of Gram-negative isolates

Gram-negative isolates exhibited the highest susceptibility to colistin, followed by carbapenems and tetracycline/minocycline. Both enteric coliforms and non-fermenters demonstrated poor sensitivity to cephalosporins and fluoroquinolones, reflecting increased resistance to commonly prescribed antimicrobial agents. [Table 8]

Table 8: Antibiotic susceptibility pattern of Gram-negative isolates

Antibiotic	Enteric GNB (*E. coli* + *Klebsiella*) (n = 8) Sensitive n (%)	Non-fermenters (*Pseudomonas* + *Acinetobacter*) (n = 7) Sensitive n (%)
Colistin	8 (100)	7 (100)
Carbapenems	6 (75.0)	4 (57.1)
Minocycline/Tetracycline	7 (87.5)	5 (71.4)
Aminoglycosides	6 (75.0)	5 (71.4)
Piperacillin–Tazobactam	3 (37.5)	5 (71.4)
Cefepime	—	4 (57.1)
Cephalosporins (overall)	2 (25.0)	2 (28.6)
Fluoroquinolones	2 (25.0)	2 (28.6)
Amoxycillin–Clavulanate	2 (25.0)	—

Fungal isolates

Two blood culture isolates were identified as *Candida* spp. (2.3%). Both isolates demonstrated good susceptibility to azole group antifungals and amphotericin B.

DISCUSSION

In the present study, the overall blood culture positivity rate among suspected sepsis cases in children aged 1–36 months was 30.7%. This moderate culture positivity is comparable to findings from several tertiary care studies where similar yields have been reported among hospitalized infants and toddlers.[13] Differences in blood culture positivity across studies may be explained by variations in study design, case definitions, timing of sample collection, volume of blood obtained, severity of illness at presentation, and differences in healthcare-seeking behavior and referral patterns.[12]

Age-wise distribution showed that suspected sepsis cases were more frequently observed among infants (1–11 months) than older toddlers. Importantly, culture positivity was also highest in this age group (39.3%), followed by the 12–23 months and 24–36 months groups. This pattern is consistent with earlier reports demonstrating that infants have a higher risk of culture-confirmed sepsis and bloodstream infections.[12] The increased susceptibility in early infancy is biologically plausible due to immaturity of innate and adaptive immune responses, limited ability to localize infection, and reduced physiological reserve. In addition, infants are more likely to require hospitalization and invasive procedures, which may further predispose them to bloodstream infections.

The microbiological profile in this study demonstrated a clear predominance of Gram-positive cocci, with Staphylococcus aureus being the most common isolate (55.4%), followed by coagulase-negative Staphylococcus spp. (CoNS) (21.7%). Similar organism patterns have been reported in pediatric sepsis studies from ward and PICU settings, where S. aureus continues to remain a major cause of bloodstream infections.[12,13] The predominance of Gram-positive organisms may reflect increasing healthcare exposure, frequent use of intravenous cannulas, and the contribution of healthcare-associated bloodstream infections in hospitalized children.

CoNS constituted a substantial proportion of isolates in the present study. Although CoNS is often regarded as a commensal organism and a frequent blood culture contaminant, it can act as an important pathogen in infants and young children, especially in the presence of invasive devices, prolonged hospitalization, malnutrition, and immunocompromised states.[12,13] Therefore, CoNS isolation should be interpreted cautiously with clinical correlation, and repeat cultures are recommended where feasible to differentiate contamination from true bacteremia. The proportion of CoNS isolates in this study also emphasizes the importance of strict aseptic precautions during blood sample collection.

Gram-negative bacilli constituted a smaller but clinically significant proportion of isolates. The major Gram-negative pathogens included E. coli, Klebsiella spp., Acinetobacter spp., and Pseudomonas aeruginosa, which is concordant with findings reported from similar tertiary care settings.[12] However, some studies have reported Gram-negative bacilli as the predominant causative agents of pediatric sepsis.[14] Such variability across studies likely reflects differences in institutional antibiotic policies, infection prevention practices, patient population, and local endemic organisms. Despite their relatively lower proportion in our study, Gram-negative infections remain clinically important due to rapid progression, risk of septic shock, and higher likelihood of multidrug resistance.

The antimicrobial susceptibility findings of this study have important implications for empirical management. Gram-positive isolates demonstrated excellent susceptibility to vancomycin and linezolid, suggesting that these agents remain reliable options for severe infections caused by resistant Gram-positive organisms. Similar high susceptibility to vancomycin and linezolid has been reported in other pediatric sepsis studies.[12,14] In addition, doxycycline and minocycline showed good activity, indicating potential usefulness in selected cases based on culture results and clinical judgment. In contrast, reduced susceptibility to commonly used agents such as penicillin, erythromycin, and fluoroquinolones reflects increasing resistance and reduced effectiveness of these drugs for empirical therapy.

A substantial proportion of S. aureus isolates in this study were methicillin resistant, indicating a significant burden of MRSA in children aged 1–36

months. Comparable MRSA prevalence has been documented in previous studies, suggesting that MRSA continues to remain a persistent challenge in both hospital and community settings.[12] This has direct therapeutic implications, as MRSA infections frequently require treatment with reserved antibiotics such as vancomycin or linezolid, which increases treatment cost and limits alternative options.

Among Gram-negative isolates, maximum susceptibility was observed to colistin, followed by carbapenems and tetracycline/minocycline, whereas poor susceptibility was noted for cephalosporins and fluoroquinolones. Similar resistance patterns have been reported in earlier studies, reflecting the rising burden of multidrug-resistant Gram-negative pathogens.[12] The poor activity of commonly prescribed antibiotics is particularly concerning because cephalosporins and fluoroquinolones remain widely used as first-line agents in many clinical settings. These findings strongly support the need for antibiotic stewardship, rational prescription practices, and periodic updating of institutional antibiograms to guide evidence-based empirical therapy.

Candida spp. were isolated in a small proportion of cases, indicating that fungal bloodstream infections, although less frequent, remain clinically relevant in pediatric sepsis. Such infections are more likely in critically ill children with prolonged hospitalization, indwelling devices, and prior exposure to broad-spectrum antibiotics.[15,17] Therefore, fungal sepsis should be considered in high-risk infants who do not respond adequately to antibacterial therapy, particularly in intensive care settings.

Overall, this study demonstrates that pediatric sepsis in children aged 1–36 months is associated with a moderate blood culture positivity rate, with Gram-positive organisms—particularly S. aureus—being predominant. The observed resistance to commonly used antimicrobials among both Gram-positive and Gram-negative isolates highlights the importance of continuous local surveillance and updated antibiograms. Regular monitoring of etiological trends and susceptibility patterns is essential for timely initiation of appropriate empirical antimicrobial therapy and for improving clinical outcomes in pediatric sepsis.

CONCLUSION

Pediatric sepsis in children aged 1–36 months remains an important cause of morbidity among hospitalized patients. The present study demonstrated a moderate blood culture positivity rate, with a clear predominance of Gram-positive cocci. Staphylococcus aureus was the most common etiological agent, followed by coagulase-negative Staphylococcus spp. A considerable proportion of isolates showed resistance to commonly used antimicrobials such as penicillin, cephalosporins, and fluoroquinolones. Vancomycin and linezolid retained excellent activity against Gram-positive isolates, while colistin and carbapenems showed the best effectiveness against Gram-negative isolates. These findings emphasize the importance of periodic institutional surveillance of etiological agents and antimicrobial susceptibility patterns, along with strict antibiotic stewardship, to guide appropriate empirical therapy and improve outcomes in pediatric sepsis.

Limitations

This study has certain limitations. As it was conducted in a single tertiary care hospital, the findings may not be generalizable to other institutions with different microbial ecology and antibiotic practices. Repeat blood cultures were not routinely performed, which may have influenced the interpretation of CoNS isolates in distinguishing contamination from true bloodstream infection. In addition, the study did not categorize cases into community-acquired and hospital-acquired sepsis, and clinical outcome correlation such as mortality, duration of hospitalization, and complication rates was not assessed. Larger multicentric studies with standardized protocols and outcome-based analysis are required to develop robust region-specific evidence for empirical treatment guidelines in pediatric sepsis.

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