Section: Microbiology

Original Research Article

COMPARISON BETWEEN CONVENTIONAL BLOOD CULTURE AND PCR FOR DIAGNOSIS OF SEPSIS IN A TERTIARY CARE HOSPITAL

Priyanka Mategadikar[1], Sundaram Supare[2], Dilip Gedam[3], Sarfaraz Ahmed[3], Gopal Agrawal[4]

[1]*Senior Resident, Department of Microbiology, IGGMC, Nagpur, India.*
[2]*Assistant Professor, Department of Microbiology, IGGMC, Nagpur, India.*
[3]*Associate Professor, Department of Microbiology, IGGMC, Nagpur, India.*
[4]*Professor and Head, Department of Microbiology, IGGMC, Nagpur, India.*

Received *: 20/04/2026*
Received in revised form *: 10/06/2026*
Accepted *: 26/06/2026*

Corresponding Author:
Dr. Dilip Gedam,
Associate Professor, Department of Microbiology IGGMC, Nagpur, India.
Email: gedam_dilip74@rediffmail.com

DOI: 10.70034/ijmedph.2026.3.123

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

Int J Med Pub Health
2026; 16 (3); 758-762

ABSTRACT

Background: Sepsis remains a major cause of morbidity and mortality, particularly among critically ill patients. Early identification of causative organisms is essential for timely initiation of appropriate antimicrobial therapy. Conventional blood culture, though considered the gold standard, is limited by prolonged turnaround time and reduced sensitivity. Molecular sepsis panels have emerged as rapid diagnostic tools enabling early pathogen detection and improved clinical decision-making. The aim and objective is to compare the positivity rate and etiological spectrum of pathogens detected by molecular sepsis panel and conventional blood culture in clinically suspected sepsis cases, and to evaluate their distribution across different clinical care units in a tertiary care hospital.

Materials and Methods: This descriptive observational study included clinically suspected sepsis cases. A total of 246 samples were tested using a molecular sepsis panel. Out of these, 116 samples were simultaneously subjected to conventional blood culture. Pathogens identified by both methods were analyzed and compared, along with their distribution across different clinical care units.

Results: Among the 116 paired samples, the sepsis panel detected 27 (23.3%) positive cases, whereas blood culture detected 13 (11.2%) positive cases, demonstrating a higher detection yield with the molecular method. Overall positivity of the sepsis panel was 27/246 (11.0%). Blood culture positivity was 13/116 (11.2%). Klebsiella pneumoniae was the most frequently isolated organism in both methods, accounting for 62.96% of sepsis panel detections and 53.84% of blood culture isolates. The Neonatal Intensive Care Unit (NICU) contributed the highest number of positive cases.

Conclusion: Klebsiella pneumoniae was the predominant pathogen associated with sepsis, with the NICU showing the highest burden. Molecular sepsis panels demonstrated a higher diagnostic yield and faster detection compared to conventional blood culture, supporting their role as a valuable adjunct in critical care settings.

Keywords: Conventional Blood Culture, PCR.

INTRODUCTION

Bloodstream infections and sepsis are major causes of morbidity and mortality and represent a significant global public health concern. Sepsis is defined as life-threatening organ dysfunction caused by a dysregulated host response to infection.[1] Organ dysfunction is assessed using the Sequential Organ Failure Assessment (SOFA) score, or its simplified version, the quick SOFA (qSOFA) score. Sepsis is suspected when there is an increase of ≥2 points in the SOFA score, or when ≥2 clinical criteria of qSOFA are present, including hypotension (systolic blood pressure ≤100 mmHg), tachypnea (respiratory

rate ≥22 breaths/min), or altered mental status (Glasgow Coma Scale <15).

Patients who survive sepsis often experience long-term physical, psychological, and cognitive impairments, collectively referred to as post-sepsis syndrome, which significantly reduces quality of life and productivity.[2] Early and appropriate antimicrobial therapy is critical, as delays in treatment initiation are associated with increased mortality, particularly in patients with septic shock.[1,3]

Despite its importance, causative microorganisms cannot be identified in a substantial proportion of suspected sepsis cases due to the limited sensitivity of conventional blood culture. Even when pathogens are detected, empirical antimicrobial therapy is often initiated because culture-based identification typically requires at least 48 hours. In sepsis, timely and appropriate empirical therapy has been shown to significantly reduce mortality.[4]

In neonatal populations, the burden of sepsis is particularly high, with up to 20% of very low birth weight infants (VLBWI) experiencing at least one episode of culture-proven sepsis during hospitalization, and up to 50% developing clinical sepsis without microbiological confirmation.[5–7]

The increasing prevalence of antimicrobial resistance has further reduced the effectiveness of empirical antibiotic therapy.[8,9] Therefore, rapid and accurate identification of causative pathogens, along with detection of antimicrobial resistance genes, is essential for guiding targeted therapy and improving patient outcomes in bloodstream infections.[10,11]

Against this background, the present study was undertaken to compare the positivity rate and etiological spectrum of pathogens detected by a molecular sepsis panel and conventional blood culture among clinically suspected sepsis cases, and to evaluate their distribution across different clinical care settings in a tertiary care hospital.

MATERIALS AND METHODS

Study Design and Setting: This was a retrospective observational single-centre study conducted in the Department of Microbiology, Indira Gandhi Government Medical College and Hospital, Nagpur, after approval from the Institutional Ethics Committee. The study aimed to compare the diagnostic performance of conventional blood culture and a PCR-based sepsis panel for the detection of bloodstream infections in patients clinically suspected of sepsis. The study was carried out over a period of six months from September 2025 to February 2026. Ethical clearance was obtained from the Institutional Ethics Committee.

Study Population: A total of 353 blood samples from clinically suspected sepsis patients were included in this study. Only those samples for which blood was simultaneously submitted for both conventional blood culture and PCR-based sepsis panel testing were included. Samples submitted exclusively for either blood culture or molecular testing were excluded from the analysis.

Sample Collection and Processing: Blood samples received in the Department of Microbiology for culture were processed using standard conventional microbiological techniques. Samples received at the Viral Research and Diagnostic Laboratory (VRDL) for molecular diagnosis were processed using a multiplex PCR-based sepsis panel for rapid pathogen detection.

Conventional Blood Culture: Approximately 5–10 mL of blood from adults and 1–2 mL from paediatric patients was aseptically inoculated into trypticase soy broth (TSB) and incubated at 37°C. Subcultures were performed on blood agar and MacConkey agar at 24 hours, 48 hours, and subsequently up to 7 days, or earlier if visible growth was detected. Isolates were identified based on Gram staining, colony morphology, culture characteristics, and standard biochemical tests.

Molecular Detection by Sepsis Panel: Samples subjected to molecular testing underwent nucleic acid extraction followed by multiplex real-time PCR-based sepsis panel analysis. The assay enabled rapid detection and identification of common bacterial and fungal pathogens directly from clinical specimens, according to the manufacturer's instructions.

Data Collection: Demographic details, clinical information, laboratory findings, and microbiological results were retrieved from laboratory records. Data regarding pathogen detection by both diagnostic modalities and distribution of positive cases across various clinical care units, including intensive care units and inpatient wards, were collected and analyzed.

RESULTS

A total of 353 patients clinically suspected of sepsis were included in the study. Both conventional blood culture and molecular sepsis panel testing were performed and compared.

Table 1: Comparison of Conventional Blood Culture and PCR-Based Sepsis Panel Results in Clinically Suspected Sepsis Cases (n = 353)

Result	Conventional blood culture	Sepsis panel
Negative	328	319
Positive	25	34
Total	353	353

Values are expressed as number of cases. The sepsis panel demonstrated higher positivity compared to conventional blood culture. Differences were not statistically significant ($\chi^2 = 1.20$, $p > 0.05$).

The difference in positivity between the two methods was not statistically significant ($\chi^2 = 1.20$, $p > 0.05$). Conventional blood culture detected 25 (7.1%) positive cases, whereas the PCR-based sepsis panel detected 34 (9.6%) positive cases, identifying 9 additional cases that were negative by blood culture.

Using blood culture as the reference standard, PCR demonstrated a sensitivity of 100%, specificity of 97.3%, positive predictive value (PPV) of 73.5%, and negative predictive value (NPV) of 100%. The overall diagnostic accuracy was 97.5%. Cohen's kappa showed strong agreement between the two methods ($\kappa = 0.82$).

Table 2: Age-wise Distribution of Results by Conventional Blood Culture and PCR-Based Sepsis Panel in Clinically Suspected Sepsis Cases

Age group	Negative		Positive	
	Sepsis	Blood culture	Sepsis	Blood culture
0-20 yrs	114	122	30	22
21-40 yrs	55	56	2	1
41-60	78	78	1	1
61-80	63	63	1	1
>80	9	9	0	0
Total	319	328	34	25

values are expressed as number of cases. Sepsis panel showed higher positivity in most age groups compared to conventional blood culture. No positive cases were observed in patients above 80 years by either method.

Age-wise analysis showed that the majority of positive cases occurred in the 0–20 years age group, followed by a marked decline in older age groups. PCR detected a higher number of positive cases in most age groups compared to blood culture. No positive cases were detected in patients above 80 years by either method.

Table 3: Organism-wise Distribution of Pathogens Detected by Conventional Blood Culture and PCR-Based Sepsis Panel

Organism	Sepsis panel	Blood culture
Stenotrophomonas maltophila	1	1
Staphylococcus aureus	2	2
Streptococcus pneumoniae	1	0
Klebsiella pneumoniae	24	16
E. coli	1	1
Acinetobacter baumanii	2	2
Candida albicans	3	3

Values are expressed as number of isolates. PCR-based sepsis panel detected a broader spectrum of pathogens compared to conventional blood culture, including additional detection of Streptococcus pneumoniae not identified by culture.

Klebsiella pneumoniae was the most frequently detected organism, identified in 24 cases by the PCR-based sepsis panel and 16 cases by conventional blood culture. Other organisms detected included Staphylococcus aureus (2 cases each by both methods), Acinetobacter baumannii (2 cases each), Candida albicans (3 cases each), and Escherichia coli (1 case each). Notably, Streptococcus pneumoniae was detected in one case by the PCR-based sepsis panel but was not identified by blood culture. Overall, the PCR-based method demonstrated a broader detection spectrum compared to conventional blood culture.

Table 4: Department-wise Distribution of Positive and Negative Cases Detected by PCR-Based Sepsis Panel and Conventional Blood Culture

Department	Sepsis		Blood culture	
	Negative	Positive	Negative	Positive
MICU	34	2	34	2
PICU	92	27	101	18
RICU	10	1	10	1
SICU	5	0	5	0
Medicine	49	1	49	1
Paediatrics	129	3	129	3

values are expressed as number of cases. The Paediatric Intensive Care Unit (PICU) showed the highest number of positive cases in both diagnostic methods. Overall, PCR-based sepsis panel demonstrated higher positivity in PICU compared to conventional blood culture.

PICU contributed the highest proportion of positive cases in both methods. Other departments showed low and comparable positivity rates. Overall, PCR consistently detected more positive cases across clinical settings, although the differences were not statistically significant ($p > 0.05$).

DISCUSSION

Early and accurate diagnosis of sepsis remains a major clinical challenge, and comparison between conventional blood culture and molecular diagnostic methods such as PCR-based sepsis panels has gained increasing attention. In the present study, the sepsis panel demonstrated a higher positivity rate (9.6%) compared to conventional blood culture (7.1%), indicating improved detection capability. The positivity rate observed in blood culture in this study is lower when compared with previous reports, such as 20% by Baltimore et al,[12] and Gladstone et al.[13] Higher culture positivity rates of 26% by Ahmed et al,[14] 51% by Karthikeyan et al,[15] and 64% by Tallur et al,[16] have also been documented. This variation may be attributed to differences in patient populations, prior antibiotic exposure, and laboratory practices. The improved detection by molecular methods is consistent with previous studies demonstrating their ability to identify fastidious and non-viable organisms that may not grow in conventional culture systems.[17,18]

The high proportion of negative results in both diagnostic modalities reflects a well-recognized limitation in sepsis diagnostics, where a substantial number of clinically suspected cases remain microbiologically unconfirmed. Similar findings were reported by Opota et al., who observed that blood culture positivity in sepsis ranges between 30–40%, largely due to prior antimicrobial therapy and low circulating pathogen load.[17] The slightly higher detection rate by PCR in the present study suggests that molecular assays may serve as a useful adjunct to conventional methods rather than a replacement.

Age-wise analysis revealed that the majority of positive cases occurred in the 0–20 years age group, with a higher detection rate observed using the sepsis panel [Table 2]. This may reflect a greater burden of sepsis in the paediatric population or improved sensitivity of molecular techniques in detecting low-level bacteraemia. Similar observations have been reported by Blauwkamp et al., who demonstrated enhanced pathogen detection using molecular assays in paediatric patients, particularly in cases with low microbial load.[19] The lower positivity observed in older age groups may be related to smaller sample size and variability in clinical presentation.

Organism-wise analysis showed that Klebsiella pneumoniae was the most frequently detected pathogen in both methods, with higher detection by the sepsis panel (24 vs 16 cases). This is consistent with epidemiological patterns in developing countries, where Gram-negative organisms, particularly Klebsiella spp., are leading causes of bloodstream infections.[20] The detection of Streptococcus pneumoniae exclusively by the molecular assay highlights the advantage of PCR-based methods in identifying fastidious organisms that may be missed by culture. Similar findings have been reported by Dark et al., who demonstrated improved detection of difficult-to-culture organisms using molecular diagnostics.[18]

Concordant detection of organisms such as Staphylococcus aureus, Acinetobacter baumannii, and Candida albicans by both methods indicates that conventional blood culture remains reliable for commonly cultivable pathogens. However, the additional yield observed with PCR supports its role in improving early pathogen detection and guiding timely antimicrobial therapy.

Department-wise distribution showed that the highest number of positive cases originated from the Paediatric Intensive Care Unit (PICU), followed by the Medical Intensive Care Unit (MICU) (Table 4). This reflects the increased vulnerability of critically ill patients and the higher risk of sepsis in intensive care settings. Similar trends have been reported in ICU-based studies, where invasive procedures, prolonged hospitalization, and immunocompromised status contribute to higher sepsis incidence.[21] The higher detection rate in PICU using the sepsis panel further emphasizes its clinical utility in paediatric critical care.

Overall, the findings of this study are consistent with existing literature supporting the integration of molecular diagnostics into routine sepsis evaluation. While blood culture remains the reference standard due to its ability to provide antimicrobial susceptibility profiles, its limitations in sensitivity and turnaround time are well recognized. PCR-based sepsis panels offer rapid and enhanced pathogen detection, which may facilitate earlier initiation of targeted antimicrobial therapy and potentially improve patient outcomes.

This study has several limitations. Firstly, it is a single-centre study with a relatively limited sample size, which may affect the generalizability of the findings. Secondly, blood culture was considered the reference standard; however, it is well known to have limited sensitivity, which may have influenced the calculated diagnostic performance of the PCR-based sepsis panel. Thirdly, prior antibiotic exposure, which is common in suspected sepsis cases, was not fully controlled and may have contributed to reduced culture positivity. Additionally, the molecular sepsis panel detects pathogen DNA, which may not always represent viable organisms, potentially leading to overestimation of active infection. Finally, antimicrobial susceptibility testing was not available through the PCR method, limiting its role in guiding definitive therapy.

CONCLUSION

The present study demonstrates that the PCR-based sepsis panel has a higher diagnostic yield compared to conventional blood culture in clinically suspected sepsis cases. It enables rapid and broader detection of pathogens, including organisms not identified by culture. Klebsiella pneumoniae was the most common pathogen detected, with the highest burden

observed in the PICU. Although blood culture remains essential for antimicrobial susceptibility testing and definitive diagnosis, molecular methods serve as a valuable adjunct in the early detection of bloodstream infections. Integration of PCR-based sepsis panels with conventional microbiological methods may improve diagnostic efficiency and support timely initiation of appropriate antimicrobial therapy in critically ill patients.

REFERENCES

1. Evans L, Rhodes A, Alhazzani W, Antonelli M, Coopersmith CM, French C, Machado FR, Mcintyre L, Ostermann M, Prescott HC, Schorr C, Simpson S, Wiersinga WJ, Alshamsi F, Angus DC, Arabi Y, Azevedo L, Beale R, Beilman G, Belley-Cote E, Burry L, Cecconi M, Centofanti J, Coz Yataco A, De Waele J, Dellinger RP, Doi K, Du B, Estenssoro E, Ferrer R, Gomersall C, Hodgson C, Møller MH, Iwashyna T, Jacob S, Kleinpell R, Klompas M, Koh Y, Kumar A, Kwizera A, Lobo S, Masur H, McGloughlin S, Mehta S, Mehta Y, Mer M, Nunnally M, Oczkowski S, Osborn T, Papathanassoglou E, et al. 2021. Surviving Sepsis Campaign: international guidelines for management of sepsis and septic shock 2021. Intensive Care Med 47:1181–1247. https://doi .org/10.1007/s00134-021-06506-y.
2. Van der Slikke EC, An AY, Hancock REW, Bouma HR. Exploring the pathophysiology of post-sepsis syndrome to identify therapeutic opportunities. EBioMedicine. 2020;61:103044.
3. Seymour CW, Gesten F, Prescott HC, Friedrich ME, Iwashyna TJ, Phillips GS, Lemeshow S, Osborn T, Terry KM, Levy MM. 2017. Time to treatment and mortality during mandated emergency care for sepsis. N Engl J Med 376:2235–2244. https://doi.org/10.1056/NEJMoa1703058.
4. Dellinger RP, Levy MM, Rhodes A, Annane D, Gerlach H, opal sM, et al. Surviving Sepsis Campaign: International guidelines for management of severe sepsis and septic shock, 2012. Intensive Care Med 2013;39:165- 228.
5. Hornik CP, Fort P, Clark RH, Watt K, Benjamin DK Jr, Smith PB, et al. Early and late onset sepsis in very-low-birth-weight infants from a large group of neonatal intensive care units. Early Hum Dev. 2012; 88 Suppl 2: S69–S74.
6. Tsai MH, Hsu JF, Chu SM, Lien R, Huang HR, Chiang MC, et al. Incidence, clinical characteristics and risk factors for adverse outcome in neonates with late-onset sepsis. Pediatr Infect Dis J. 2014; 33: e7– e13. https://doi.org/10.1097/INF.0b013e3182a72ee0 PMID: 23899966
7. Perlman SE, Saiman L, Larson EL. Risk factors for late-onset health care-associated bloodstream infections in patients in neonatal intensive care units. Am J Infect Control. 2007; 35: 177–182. https:// doi.org/10.1016/j.ajic.2006.01.002 PMID: 17433941
8. Peralta G, Sanchez MB, Garrido JC, De Benito I, Cano ME, Martinez-Martinez L, Roiz MP. 2007. Impact of antibiotic resistance and of adequate empirical antibiotic treatment in the prognosis of patients with Escherichia coli bacteraemia. J Antimicrob Chemother 60:855–863. https://doi.org/10.1093/jac/dkm279.
9. Tamma PD, Cosgrove SE, Maragakis LL. 2012. Combination therapy for treatment of infections with gram-negative bacteria. Clin Microbiol Rev 25:450–470. https://doi.org/10.1128/CMR.05041-11.
10. Lamy B, Sundqvist M, Idelevich EA, ESCMID Study Group for Bloodstream Infections, Endocarditis and Sepsis (ESGBIES). 2020. Bloodstream infections: standard and progress in pathogen diagnostics. Clin Microbiol Infect 26: 142–150. https://doi.org/10.1016/j.cmi.2019.11.017.
11. Timsit J-F, Ruppé E, Barbier F, Tabah A, Bassetti M. 2020. Bloodstream infections in critically ill patients: an expert statement. Intensive Care Med 46:266–284. https://doi.org/10.1007/s00134-020-05950-6.
12. Baltimore RS, Huie SM, Meek JI, Schuchat A, O'Brein KL: Early-onset neonatal sepsis in the era of group B Streptococcal prevention. Pediatrics 2001, 108:1094-1098.
13. Gladstone IM, Ehrenkranz RA, Edberg SC, Baltimore RS: A ten-year review of neonatal sepsis and comparison with the previous fifty-year experience. Pediatr Infect Dis J 1990, 9:819-825.
14. Ahmed NU, Chowdhury MA, Hoque M, Darmstadt GL: Clinical and bacteriological profile of neonatal septicemia in a tertiary level pediatric hospital in Bangladesh. Indian Pediatr 2002, 39:1034-1039.
15. Karthikeyan G, Premkumar K: Neonatal sepsis: Staphylococcus aureus as the predominant pathogen. Indian J Pediatr 2001, 68:715-717.
16. Tallur SS, Kasturi AV, Nadgir SD, Krishna BVS: Clinico-bacteriological study of neonatal septicemia in Hubli. Indian J Pediatr 2000, 67:169-174
17. Opota O, Croxatto A, Prod'hom G, Greub G. Blood culture based diagnosis of bacteraemia: state of the art. Clin Microbiol Infect. 2015;21(4):313-322
18. Dark P, Blackwood B, Gates S, McAuley D, Perkins GD, McMullan R, et al. Accuracy of LightCycler SeptiFast for the detection and identification of pathogens in blood of patients with suspected sepsis: A systematic review and meta-analysis. Intensive Care Med. 2015;41(1):21-33
19. Blauwkamp TA, Thair S, Rosen MJ, Blair L, Lindner MS, Vilfan ID,et al. Analytical and clinical validation of a microbial cell-free DNA sequencing test for infectious disease. Nat Microbiol. 2019;4(4):663-674.
20. Fleischmann C, Scherag A, Adhikari NKJ, Hartog CS, Tsaganos T, Schlattmann P, et al. Assessment of global incidence and mortality of hospital-treated sepsis. Am j Respir Crit Care Med. 2016;193(3):259-272.
21. Vincent JL, Rello J, Marshall J, Silva E, Anzuueto A, Martin CD et al. international study of the prevalence and outcomes of infection in intensive care units. JAMA 2009;302(21):2323-2329.