

Bacteriological Profile and Antibiogram of Blood Culture Isolates Using an Automated Blood Culture System in a Tertiary Care Hospital in Jammu, Jammu and Kashmir, India

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ABSTRACT

Bloodstream infections (BSIs) are a major cause of morbidity and mortality worldwide and require prompt diagnosis and appropriate antimicrobial therapy. The emergence of multidrug-resistant organisms has made the management of BSIs increasingly challenging. This study was conducted to determine the bacteriological profile and antimicrobial susceptibility pattern of blood culture isolates using an automated blood culture system. This retrospective cross-sectional study was conducted in the Department of Microbiology, Acharya Shri Chander College of Medical Sciences and Hospital (ASCOMS), Jammu, Jammu and Kashmir, India, over a period of four years from January 2021 to December 2024. Blood culture samples received from patients with suspected BSIs were processed using the BD BACTEC automated blood culture system. Positive cultures were identified using standard microbiological techniques, and antimicrobial susceptibility testing was performed using the BD Phoenix M50 automated identification and susceptibility system in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. A total of 715 blood culture samples were processed, of which 190 (26.6%) yielded significant bacterial growth. Gram-positive organisms predominated, with *Staphylococcus aureus* being the most common isolate (n = 96, 50.5%). Gram-negative organisms included *Escherichia coli* (n = 25, 13.1%) and *Klebsiella pneumoniae* (n = 8, 4.2%). *Staphylococcus aureus* showed high susceptibility to vancomycin (97.9%), linezolid (97.9%), and daptomycin (97.9%). Methicillin-resistant *Staphylococcus aureus* (MRSA) accounted for 72.9% of *S. aureus* isolates. *Escherichia coli* demonstrated high susceptibility to amikacin (100%) and gentamicin (92%), while resistance to cephalosporins and fluoroquinolones was common. *Klebsiella pneumoniae* exhibited extensive multidrug resistance, including resistance to carbapenems. *Staphylococcus aureus* was the predominant pathogen causing bloodstream infections, with a high prevalence of MRSA. The emergence of multidrug-resistant organisms, including carbapenem-resistant *Klebsiella pneumoniae*, underscores the need for continuous surveillance and rational antibiotic use to guide empirical therapy and strengthen antimicrobial stewardship.

Keywords

Bloodstream infections;
BACTEC;
Antibiogram;
Staphylococcus aureus; MRSA;
Multidrug resistance

Article Info

Received:
15 March 2026
Accepted:
22 April 2026
Available Online:
10 May 2026

Introduction

Bloodstream infections (BSIs) remain a major global health concern and are associated with significant morbidity and mortality. BSIs may be caused by bacteria, fungi, or viruses; however, bacteria account for the majority of cases. The clinical manifestations of BSIs range from transient asymptomatic bacteremia to severe sepsis and septic shock, both of which are associated with high mortality rates. Early detection of pathogens and prompt determination of their antimicrobial susceptibility are essential for optimizing patient management and improving clinical outcomes.

The distribution of causative microorganisms and their antimicrobial susceptibility patterns varies over time, even within the same healthcare facility. Continuous surveillance of bloodstream pathogens is therefore essential for updating institutional antibiograms and guiding clinicians in selecting appropriate empirical and prophylactic antimicrobial therapy.

Among bacterial pathogens causing BSIs, Gram-positive organisms such as *Staphylococcus aureus*, coagulase-negative staphylococci, and *Enterococcus* species are frequently isolated. Common Gram-negative pathogens include *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*. Many of these organisms belong to the ESKAPE group, which is recognized for its ability to evade antimicrobial therapy and contribute significantly to antimicrobial resistance.

The spectrum of organisms responsible for BSIs is influenced by several factors, including the type of healthcare facility, use of intravascular catheters, duration of hospitalization, host immune status, underlying comorbidities, adherence to infection prevention practices, and prior antimicrobial exposure.

Timely and appropriate administration of antimicrobial therapy has a substantial impact on patient survival. However, definitive microbiological identification and susceptibility testing require time, leading clinicians to initiate broad-spectrum antibiotics empirically. Inappropriate or prolonged use of such agents contributes to the emergence and spread of antimicrobial resistance.

Blood culture remains the gold standard for the diagnosis of bacteremia. Automated blood culture systems offer advantages over conventional manual methods, including

reduced time to detection and improved recovery of pathogens. The present study was undertaken to determine the bacteriological profile and antimicrobial susceptibility pattern of blood culture isolates obtained from patients with suspected bloodstream infections in a tertiary care hospital in Jammu, Jammu and Kashmir, India.

The present study aimed to characterize the bacteriological profile of isolates responsible for bloodstream infections among clinically suspected cases and to evaluate their antimicrobial resistance patterns. Specifically, the study focused on identifying the bacterial organisms isolated from blood culture samples and assessing their antimicrobial susceptibility patterns (antibiogram) to understand the prevailing trends of antimicrobial resistance and support effective clinical and therapeutic management of bloodstream infections. The findings of this study may contribute to the early diagnosis and appropriate selection of antimicrobial therapy, thereby reducing morbidity and improving patient outcomes associated with bloodstream infections.

Materials and Methods

Study Design: Retrospective cross-sectional study.

Study Duration: January 2021 to December 2024.

Study Setting: Department of Microbiology, Acharya Shri Chander College of Medical Sciences and Hospital (ASCOMS), Jammu, Jammu and Kashmir, India.

Study Population: Blood samples received from inpatients with clinically suspected bloodstream infections during the study period.

Inclusion Criteria: All blood samples received from clinically suspected cases of bloodstream infection during the study period.

Exclusion Criteria: Blood culture samples yielding contaminants or mixed bacterial growth.

Ethical Clearance

Ethical approval was obtained from the Institutional Ethics Committee of Acharya Shri Chander College of Medical Sciences and Hospital, Jammu, prior to the commencement of the study. Patient confidentiality was maintained throughout the study.

Methods for Processing of Samples

Specimen Collection

A total of 715 blood samples were collected aseptically prior to initiation of antibiotic therapy. The venipuncture site was disinfected using 70% alcohol followed by 2% tincture of iodine.

Blood Volume Collected

- **Adults:** 8–10 mL of blood inoculated into BD BACTEC Plus Aerobic vials
- **Pediatric patients:** 1–3 mL of blood inoculated into BD BACTEC Plus Aerobic vials

All inoculated vials were transported promptly to the microbiology laboratory.

Processing of Samples

Blood culture vials were incubated in the BD BACTEC automated blood culture system.

Vials showing no growth after 5 days were reported as sterile for aerobic organisms.

Positive bottles were subjected to: 1. Gram staining 2. Subculture onto:

- 5% sheep blood agar
- Chocolate agar
- MacConkey agar

Culture plates were incubated at 37°C for 18–24 hours.

Identification of isolates was based on colony morphology and Gram staining characteristics. A 0.5 McFarland suspension was prepared from isolated colonies, and identification and antimicrobial susceptibility testing were performed using the BD Phoenix M50 automated system according to CLSI guidelines and the manufacturer's instructions.

Results and Discussion

Culture Positivity

Of the 715 blood culture samples processed, 190 (26.6%) yielded significant bacterial growth.

Gender Distribution

Among the culture-positive cases, 102 (53.7%) were male and 88 (46.3%) were female.

Gram-positive organisms were more frequently isolated than Gram-negative organisms. *Staphylococcus aureus* was the predominant pathogen, followed by *Escherichia coli* and *Klebsiella pneumoniae*. A high prevalence of MRSA and extensive multidrug resistance among Gram-negative isolates were observed.

Bloodstream infections remain a major cause of morbidity and mortality and require early diagnosis and appropriate antimicrobial therapy. In the present study, *Staphylococcus aureus* was the most frequently isolated organism, followed by Gram-negative bacilli such as *Escherichia coli* and *Klebsiella pneumoniae*. Similar findings have been reported in previous studies.

A high prevalence of methicillin-resistant *Staphylococcus aureus* (72.9%) was observed. This finding is comparable to reports from tertiary care centers in India and highlights the importance of strict infection control practices and antimicrobial stewardship programs. Most *S. aureus* isolates remained highly susceptible to vancomycin, linezolid, and daptomycin.

Among Gram-negative isolates, *Escherichia coli* showed high susceptibility to aminoglycosides, particularly amikacin and gentamicin, while substantial resistance to cephalosporins and fluoroquinolones was noted. These findings are consistent with the increasing prevalence of extended-spectrum β -lactamase-producing strains.

Klebsiella pneumoniae demonstrated extensive multidrug resistance, including complete resistance to carbapenems. The emergence of carbapenem-resistant *K. pneumoniae* is a serious clinical concern because of limited therapeutic options and increased mortality.

The antimicrobial susceptibility patterns observed in this study underscore the growing burden of multidrug resistance among both Gram-positive and Gram-negative organisms. The continued effectiveness of vancomycin, linezolid, tigecycline, and aminoglycosides supports their role in managing severe bloodstream infections.

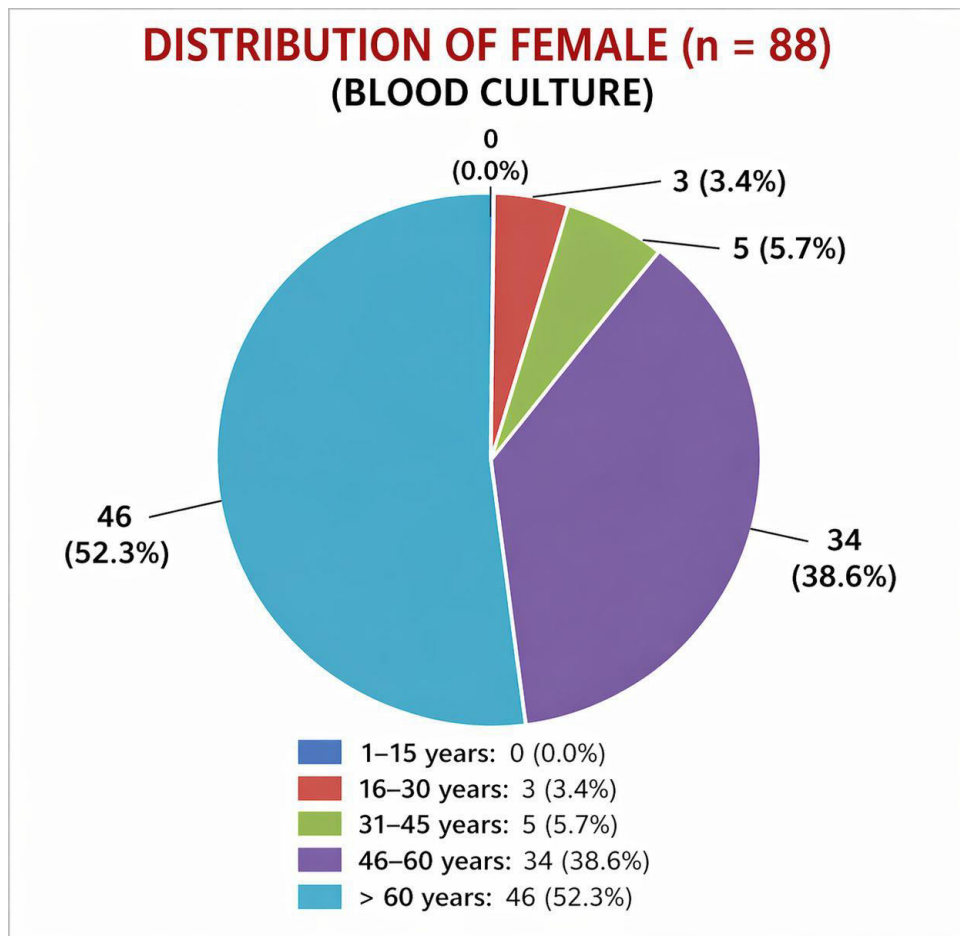
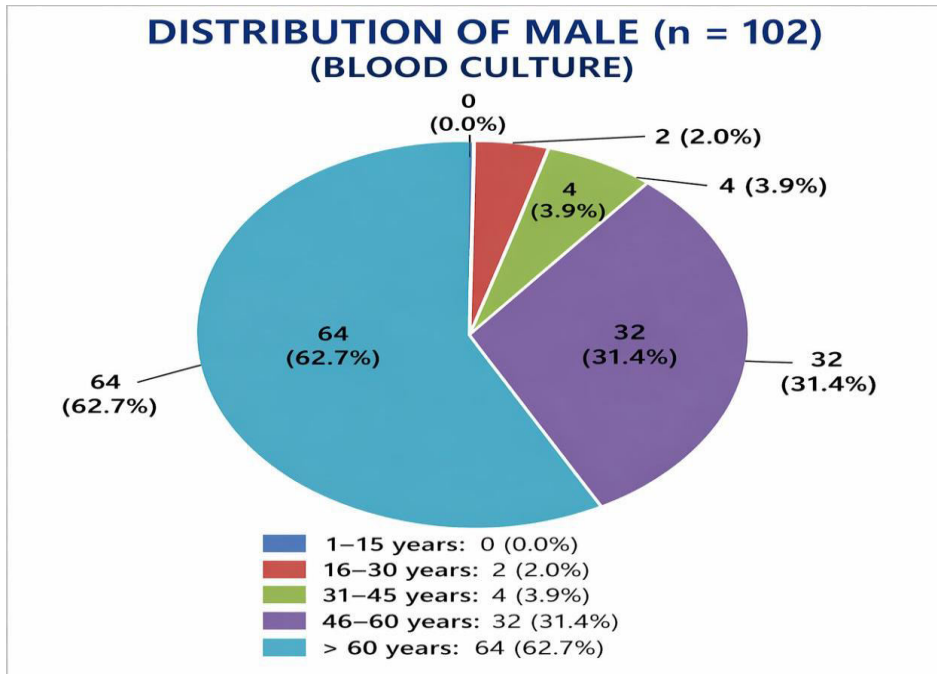


Table.1 Gender Distribution of Culture-Positive Cases (n = 190)

| Gender | Number | Percentage (%) |
|--------|--------|----------------|
| Male | 102 | 53.7 |
| Female | 88 | 46.3 |

Table.2 Distribution of Organisms Isolated from Positive Blood Cultures (n = 190)

| Organism | Number | Percentage (%) |
|---|--------|----------------|
| <i>Staphylococcus aureus</i> | 96 | 50.5 |
| Coagulase-negative staphylococci | 24 | 12.6 |
| <i>Staphylococcus argenteus</i> | 1 | 0.5 |
| <i>Streptococcus</i> spp. | 2 | 1.1 |
| <i>Enterococcus</i> spp. | 7 | 3.6 |
| <i>Aerococcus viridans</i> | 2 | 1.1 |
| <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> | 1 | 0.5 |
| <i>Escherichia coli</i> | 25 | 13.1 |
| <i>Klebsiella pneumoniae</i> | 8 | 4.2 |
| <i>Pseudomonas</i> spp. | 13 | 6.8 |
| <i>Salmonella</i> spp. | 2 | 1.1 |
| <i>Stenotrophomonas maltophilia</i> | 4 | 2.1 |
| <i>Acinetobacter baumannii</i> | 3 | 1.6 |
| <i>Burkholderia cepacia</i> | 2 | 1.1 |

Table.3 Antibiotic Susceptibility Pattern of *Escherichia coli* Isolates (n = 25)

| Antibiotic | Sensitive n (%) | Resistant n (%) |
|-------------------------|-----------------|-----------------|
| Amikacin | 25 (100) | 0 (0) |
| Gentamicin | 23 (92) | 2 (8) |
| Tigecycline | 23 (92) | 2 (8) |
| Imipenem | 18 (72) | 7 (28) |
| Meropenem | 18 (72) | 7 (28) |
| Ertapenem | 18 (72) | 7 (28) |
| Piperacillin–Tazobactam | 15 (60) | 10 (40) |

Table.4 Antibiotic Susceptibility Pattern of *Klebsiella pneumoniae* Isolates (n = 8)

| Antibiotic | Sensitive n (%) | Resistant n (%) |
|-------------|-----------------|-----------------|
| Amikacin | 3 (37.5) | 5 (62.5) |
| Tigecycline | 4 (50.0) | 4 (50.0) |
| Imipenem | 0 (0) | 8 (100) |
| Meropenem | 0 (0) | 8 (100) |
| Ertapenem | 0 (0) | 8 (100) |

Table.5 Antibiotic Susceptibility Pattern of *Staphylococcus aureus* Isolates (n = 96)

| Antibiotic | Sensitive n (%) | Resistant n (%) |
|-----------------|-----------------|-----------------|
| Vancomycin | 94 (97.9) | 2 (2.1) |
| Linezolid | 94 (97.9) | 2 (2.1) |
| Daptomycin | 94 (97.9) | 2 (2.1) |
| Doxycycline | 77 (80.2) | 19 (19.8) |
| Chloramphenicol | 82 (85.4) | 14 (14.6) |
| Oxacillin | 26 (27.1) | 70 (72.9) |

MRSA prevalence: 72.9%

The use of automated blood culture systems facilitated rapid detection and identification of pathogens, enabling timely initiation of targeted antimicrobial therapy and improved patient management.

In conclusion, Bloodstream infections remain a significant cause of morbidity and mortality and require prompt diagnosis and appropriate antimicrobial therapy. In the present study, *Staphylococcus aureus* was the most frequently isolated organism, with a high prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA). Gram-negative organisms, particularly *Escherichia coli* and *Klebsiella pneumoniae*, exhibited considerable resistance to commonly used antibiotics.

The emergence of multidrug-resistant organisms, including carbapenem-resistant *Klebsiella pneumoniae*, represents a major clinical challenge because of limited therapeutic options. Aminoglycosides, glycopeptides, linezolid, and tigecycline retained good activity against several isolates.

Regular surveillance of antimicrobial susceptibility patterns and implementation of robust antimicrobial stewardship programs are essential to control the spread of resistant organisms and to guide empirical therapy. Automated blood culture systems play an important role in facilitating early detection and timely management of bloodstream infections.

Author Contributions

Poonam Slathia: Investigation, formal analysis, writing—original draft. Shivani Raina: Validation, methodology, writing—reviewing.

Data Availability

The datasets generated during and/or analyzed during the

current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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How to cite this article:

Poonam Slathia and Shivani Raina. 2026. Bacteriological Profile and Antibiogram of Blood Culture Isolates Using an Automated Blood Culture System in a Tertiary Care Hospital in Jammu, Jammu and Kashmir, India. *Int.J.Curr.Microbiol.App.Sci.* 15(5): 160-166. doi: <https://doi.org/10.20546/ijcmas.2026.1505.021>