Int.J.Curr.Microbiol.App.Sci (2026) *15*(3): 229-236

EXCELLENT PUBLISHERS

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 15 Number 3 (2026)**
Journal homepage: http://www.ijcmas.com

IJCMAS

Original Research Article https://doi.org/10.20546/ijcmas.2026.1503.024

Bacterial Aetiology and Antibiogram of Bloodstream Infections: A Retrospective Study from a Tertiary Care Centre in Navi Mumbai, India

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Keywords

Bloodstream infection, antibiogram, antimicrobial resistance, MRSA, CoNS

Article Info

Received: 20 January 2026
Accepted: 28 February 2026
Available Online: 10 March 2026

A B S T R A C T

Bloodstream infections (BSIs) are a major cause of morbidity and mortality in hospitalized patients. Early identification of causative organisms and their antimicrobial susceptibility patterns is essential for appropriate empirical therapy and infection control. To evaluate the bacterial aetiology of blood culture isolates and their antimicrobial susceptibility patterns in a tertiary care hospital. This retrospective observational study was conducted over one year (January–December 2022) and included 532 patients with positive blood cultures. Identification of isolates and antimicrobial susceptibility testing were performed using standard microbiological methods in accordance with CLSI guidelines. Out of 532 isolates, Gram-positive cocci (GPC) accounted for 55.1% and Gram-negative bacteria (GNB) for 44.9%. Among GPC, coagulase-negative staphylococci (CoNS) were predominant, with methicillin-resistant CoNS (65.2%). Among GNB, *Klebsiella pneumoniae* (27.2%) and *Pseudomonas aeruginosa* (16.7%) were most common. Methicillin-resistant isolates showed complete resistance to beta-lactam antibiotics but retained high susceptibility to vancomycin and linezolid. Gram-positive cocci were predominant in bloodstream infections, with a significant burden of antimicrobial resistance among both Gram-positive and Gram-negative isolates. Continuous surveillance and antimicrobial stewardship are essential.

Introduction

Bloodstream infections (BSIs) are among the most severe infectious conditions encountered in clinical practice and are associated with high morbidity and mortality worldwide (1, 2). They range from transient bacteremia to life-threatening sepsis and septic shock, particularly in critically ill and immunocompromised patients (3).

The epidemiology of BSIs has evolved significantly over time due to widespread antimicrobial use, invasive procedures, and prolonged hospitalization. A major concern is the increasing prevalence of multidrug-resistant (MDR) organisms, including methicillin-resistant *Staphylococcus aureus* (MRSA), coagulase-negative staphylococci (CoNS), and resistant Gram-negative bacilli such as extended-spectrum beta-lactamase (ESBL) and carbapenem-resistant Enterobacterales (4, 5).

These resistant pathogens complicate empirical therapy and are associated with increased mortality, prolonged hospital stays, and higher healthcare costs (6).

The distribution of causative organisms and their antimicrobial susceptibility patterns varies across regions and healthcare settings. Therefore, institution-specific antibiograms are essential for guiding empirical therapy and developing antimicrobial stewardship policies (7).

While earlier Indian studies have reported a predominance of Gram-negative organisms, recent trends indicate an increasing contribution of Gram-positive cocci, particularly CoNS, in hospital-acquired infections (8–10).

In view of the evolving resistance patterns and the need for updated local data, the present study was undertaken to evaluate the bacterial aetiology and antimicrobial susceptibility patterns of bloodstream infections in a tertiary care hospital in Navi Mumbai.

Materials and Methods

Study Design and Setting

This retrospective descriptive observational study was conducted at a tertiary care hospital in Navi Mumbai over a period of one year (January–December 2022). The objective was to identify bacterial isolates from positive blood cultures and analyze their antimicrobial susceptibility patterns.

Study Population

All patients with clinically suspected bloodstream infections and positive bacterial blood cultures during the study period were included. Relevant laboratory and clinical data were retrieved from the microbiology records.

Inclusion Criteria

- ✓ Patients of all age groups with suspected bloodstream infections
- ✓ Patients with positive bacterial blood culture isolates
- ✓ Patients with complete laboratory records
- ✓ Patients admitted to any department, including ICU and wards

Exclusion Criteria

- ✓ Contaminated blood culture samples
- ✓ Incomplete laboratory records
- ✓ Patients with fungal or viral bloodstream infections

Data Collection

Blood culture reports, antibiotic susceptibility results, and basic patient details (such as MRD number and ward of admission) were collected from laboratory records. Only de-identified data were used for analysis to maintain confidentiality.

Blood Culture Processing

Blood samples were aseptically collected from suspected cases of bloodstream infection. For adults, 10–20 mL of blood was collected, while for pediatric patients, 1–5 mL was collected. Samples were inoculated into aerobic and anaerobic blood culture bottles and processed using an automated blood culture system (e.g., BACTEC/BacT-Alert) at 37°C for up to 5–7 days.

Positive samples were subcultured onto appropriate media such as blood agar and MacConkey agar for isolation of organisms.

Identification of Isolates

Isolates were identified based on colony morphology, Gram staining, and standard biochemical tests such as catalase, coagulase, oxidase, and sugar fermentation tests. Automated identification systems (e.g., VITEK 2) were used where required.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the modified Kirby–Bauer disk diffusion method on Mueller–Hinton agar. The bacterial inoculum was

adjusted to 0.5 McFarland standard and incubated at 35–37°C for 16–18 hours.
The results were interpreted as sensitive, intermediate, or resistant according to Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI 2023).

Statistical Analysis

Data were entered and analyzed using Microsoft Excel. Categorical variables were expressed as frequencies and percentages.

Results and Discussion

A total of 532 bacterial isolates obtained from blood cultures during the study period were analyzed.

Overall Distribution of Isolates

Out of the total isolates, Gram-positive cocci (GPC) accounted for 293 isolates (55.1%), while Gram-negative bacteria (GNB) accounted for 239 isolates (44.9%), indicating a slight predominance of Gram-positive organisms in bloodstream infections in the present study.

Distribution of Gram-Positive Cocci

Among the Gram-positive isolates, coagulase-negative staphylococci (CoNS) constituted the majority.

Methicillin-resistant CoNS (MRCoNS): 191 isolates (65.2%)
Methicillin-sensitive CoNS (MSCoNS): 60 isolates (20.5%)

Together, CoNS accounted for a significant proportion of bloodstream infections.

Staphylococcus aureus was isolated in 20 cases, of which:

MRSA: 13 isolates (4.4%)
MSSA: 7 isolates (2.4%)

Other Gram-positive organisms included:

Enterococcus spp.: 16 isolates
- *E. faecalis*: 5
- *E. faecium*: 5
- Unspecified: 6

Streptococcus spp.: 5 isolates (1.7%)

The graphical representation clearly demonstrates the predominance of MRCoNS among Gram-positive isolates, followed by MSCoNS. *Staphylococcus aureus* contributed a relatively smaller proportion. The high proportion of methicillin-resistant isolates suggests a significant burden of antimicrobial resistance among staphylococci.

Distribution of Gram-Negative Bacteria

Among Gram-negative isolates, members of Enterobacterales and non-fermenters were identified.

Klebsiella pneumoniae: 65 isolates (27.2%)
Escherichia coli: 31 isolates (12.9%)
Pseudomonas aeruginosa: 40 isolates (16.7%)
Acinetobacter spp.: 30 isolates (12.6%)

Other organisms included:

Salmonella spp.: 13 isolates (5.4%)
Enterobacter spp.: 4 isolates (1.7%)
Citrobacter spp.: 2 isolates (0.8%)
Serratia marcescens and *Shigella* spp.: 1 isolate each

The graphical analysis highlights *Klebsiella pneumoniae* as the most frequent Gram-negative isolate, followed by *Pseudomonas aeruginosa*. The presence of non-fermenters such as *Acinetobacter* spp. reflects the contribution of hospital-acquired infections.

Antimicrobial Susceptibility Pattern – Gram-Positive Cocci

The antimicrobial susceptibility testing of Gram-positive isolates revealed distinct resistance patterns:

MRCoNS and MRSA showed **complete resistance (100%) to beta-lactam antibiotics** such as penicillin and oxacillin.
Both groups demonstrated **high susceptibility (~99–100%) to vancomycin and linezolid**, indicating their continued effectiveness.
MSCoNS showed:
Moderate resistance to penicillin (75%)
Moderate resistance to ampicillin (~51.6%)
High susceptibility to oxacillin, vancomycin, and

linezolid

MSSA isolates were:
Fully susceptible to cefoxitin and vancomycin
Completely resistant to ciprofloxacin
Showed high resistance to erythromycin

The graph demonstrates that glycopeptides and oxazolidinones remain highly effective against methicillin-resistant isolates, while resistance to commonly used antibiotics such as penicillin and fluoroquinolones is widespread.

Antimicrobial Susceptibility Pattern – Gram-Negative Bacteria

The antimicrobial susceptibility patterns among Gram-negative bacteria showed variability across different species:

Enterobacterales such as *Klebsiella pneumoniae* and *E. coli* exhibited moderate to high resistance to commonly used antibiotics, including cephalosporins and fluoroquinolones.
Non-fermenters such as *Acinetobacter baumannii* showed higher resistance rates, reflecting their multidrug-resistant nature.
Pseudomonas aeruginosa demonstrated variable susceptibility, indicating the need for targeted therapy based on culture reports.

The graph illustrates the heterogeneity in susceptibility patterns among Gram-negative organisms, with non-fermenters showing relatively higher resistance compared to Enterobacterales.

The present study provides important insights into the bacterial profile and antimicrobial resistance patterns of bloodstream infections in a tertiary care setting. Gram-positive cocci were found to be more prevalent than Gram-negative bacteria, which contrasts with earlier Indian studies that reported Gram-negative predominance (8, 10). This shift may be attributed to increased use of invasive devices, prolonged hospitalization, and improved detection of Gram-positive organisms.

Coagulase-negative staphylococci (CoNS), particularly methicillin-resistant CoNS (MRCoNS), were the most common isolates. Although CoNS are often considered contaminants, they are increasingly recognized as significant pathogens in patients with indwelling devices and immunocompromised states (11, 13). The high proportion of MRCoNS in this study suggests a substantial burden of methicillin resistance, necessitating careful clinical correlation to distinguish true infection from contamination.

The prevalence of methicillin resistance among staphylococci is a major concern. In this study, both MRCoNS and MRSA exhibited complete resistance to beta-lactam antibiotics but retained high susceptibility to vancomycin and linezolid. These findings are consistent with previous studies, which have reported preserved efficacy of glycopeptides and oxazolidinones against resistant Gram-positive organisms (12, 14). This highlights the continued importance of these agents in the treatment of resistant infections.

Among Gram-negative bacteria, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* were the predominant pathogens, consistent with other Indian studies (14, 15). The presence of non-fermenters such as *Acinetobacter baumannii* is particularly concerning due to their intrinsic resistance mechanisms and association with hospital-acquired infections.

The antimicrobial susceptibility patterns observed in this study indicate increasing resistance among Gram-negative organisms, particularly non-fermenters. This trend may be attributed to selective antibiotic pressure, inappropriate antibiotic use, and cross-transmission within hospital settings. Similar findings have been reported in previous studies, emphasizing the growing challenge of multidrug-resistant Gram-negative infections (15, 16).

The variability in susceptibility patterns across different organisms underscores the importance of institution-specific antibiograms. Empirical therapy based on outdated or generalized data may lead to inappropriate treatment and adverse outcomes. Therefore, continuous surveillance and periodic updating of antibiograms are essential.

Overall, the findings of this study highlight the urgent need for effective antimicrobial stewardship programs, strict infection control measures, and rational use of antibiotics to curb the emergence and spread of antimicrobial resistance (6, 16).

Figure.1 Distribution of Gram-positive cocci isolates.

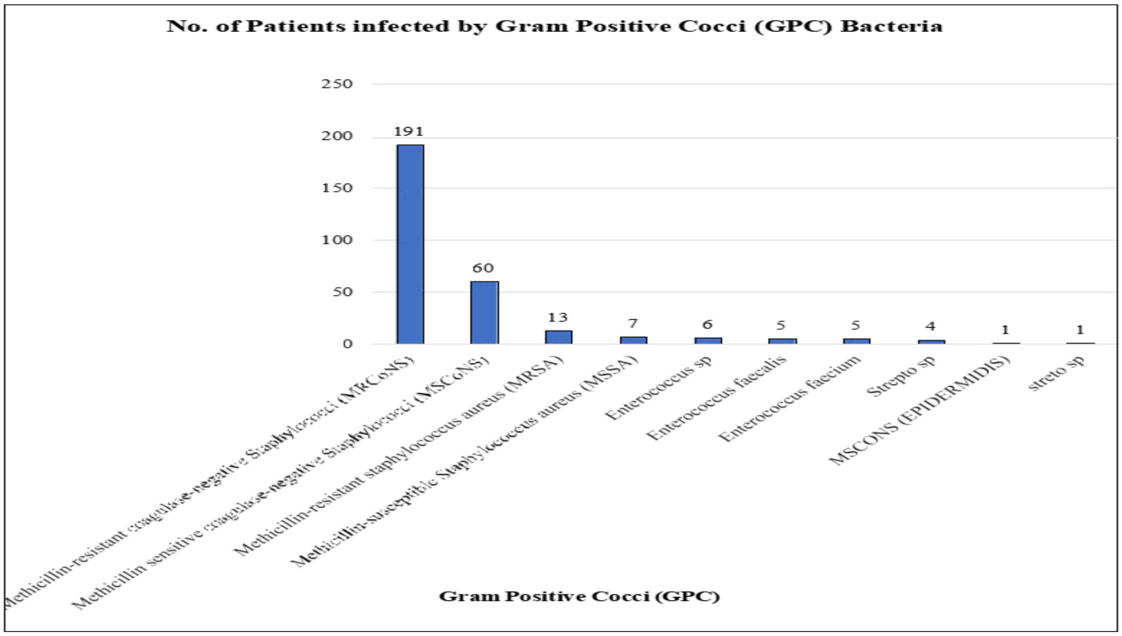


Figure.2 Distribution of Gram-negative bacterial isolates

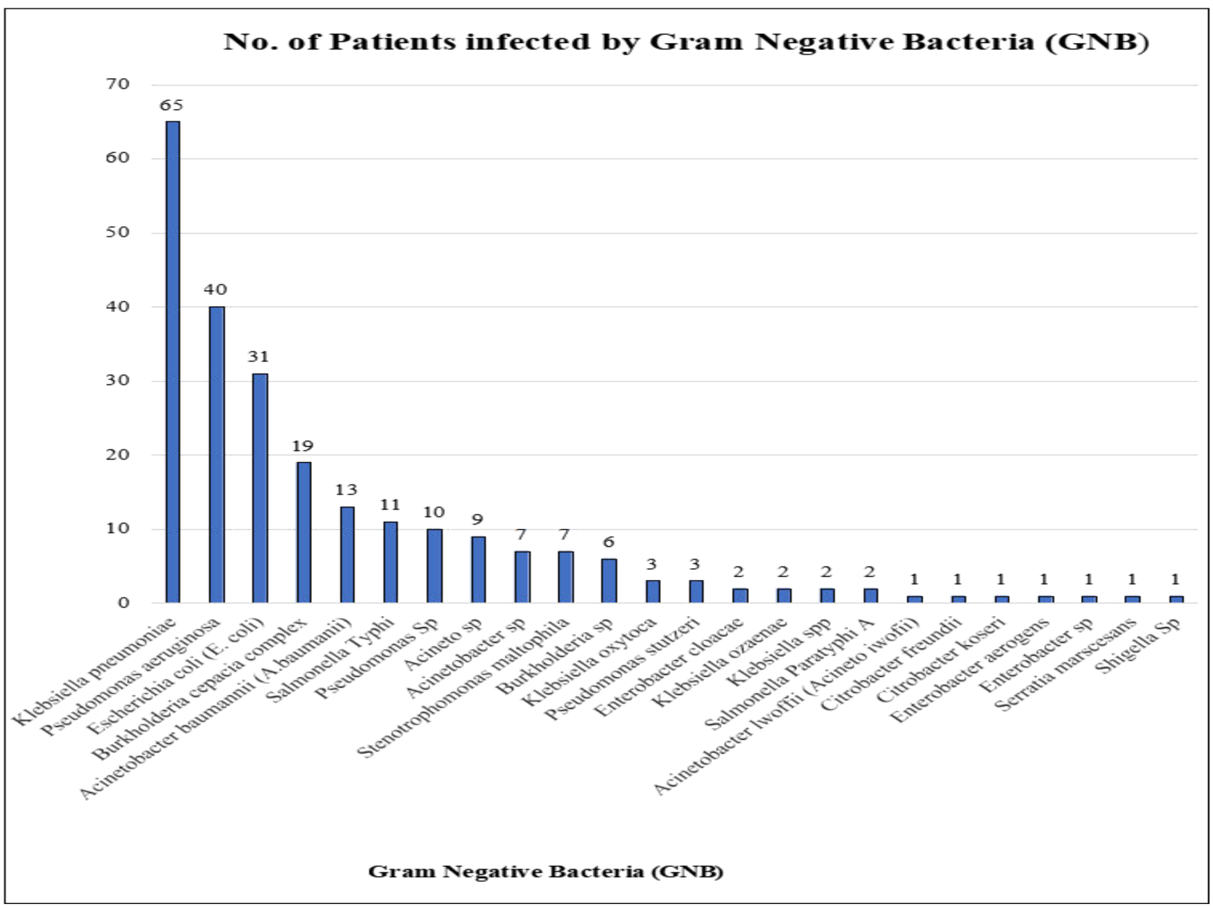


Figure.3 Antibiotic susceptibility pattern of Gram-positive cocci

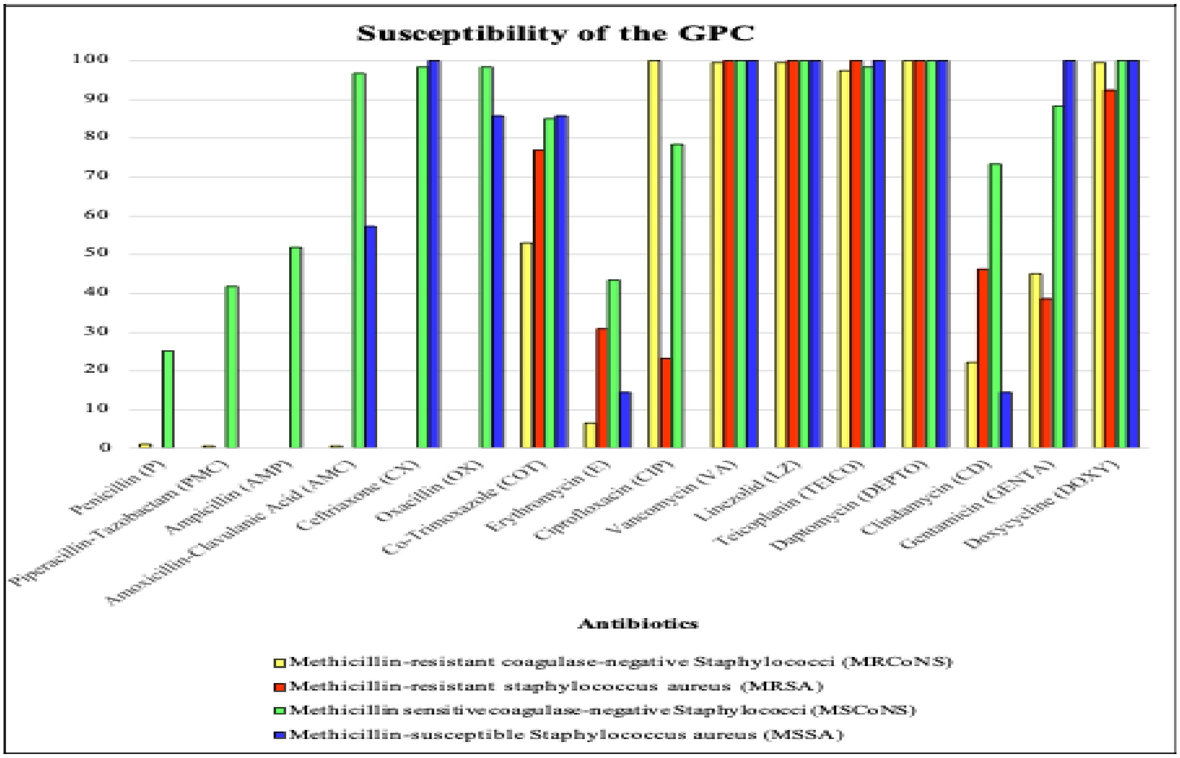
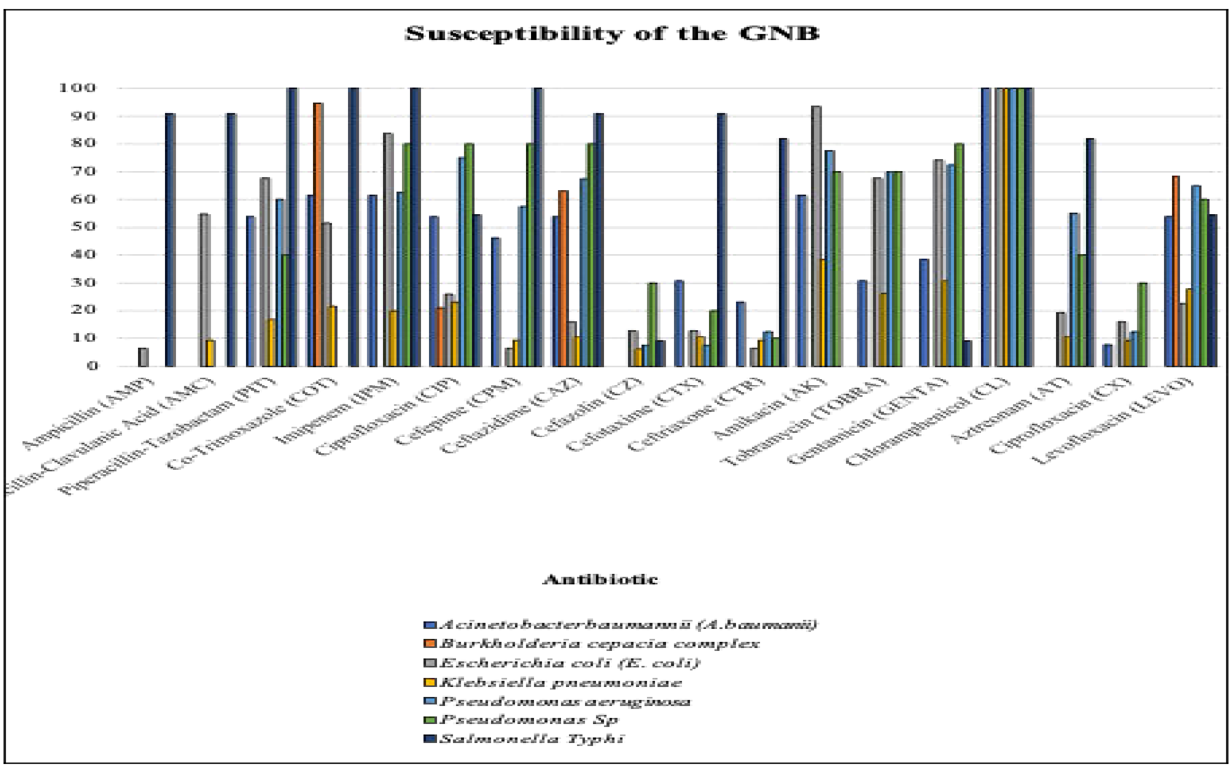


Figure.4 Antibiotic susceptibility pattern of Gram-negative bacteria



In conclusion, this study demonstrates that Gram-positive cocci, particularly methicillin-resistant coagulase-negative staphylococci, are the predominant pathogens causing bloodstream infections in the study setting. Gram-negative bacteria, including *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*, also contribute significantly.

The high prevalence of antimicrobial resistance among both Gram-positive and Gram-negative isolates emphasizes the need for continuous surveillance, institution-specific antibiograms, and antimicrobial stewardship programs. Strengthening infection control practices and promoting rational antibiotic use are essential to improve patient outcomes and limit the spread of resistant organisms (6, 7, 16).

Author Contributions

Rita Swaminathan: Investigation, formal analysis, writing—original draft. Aparna Khedkar: Validation, methodology, writing—reviewing. Ranjana Santra:—Formal analysis, writing—review and editing. Shrikrishna A. Joshi: Investigation, 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:

Rita Swaminathan, Aparna Khedkar, Ranjana Santra and Shrikrishna A. Joshi. 2026. Bacterial Aetiology and Antibiogram of Bloodstream Infections: A Retrospective Study from a Tertiary Care Centre in Navi Mumbai, India. *Int.J.Curr.Microbiol.App.Sci.* 15(3): 229-236. **doi:** https://doi.org/10.20546/ijcmas.2026.1503.024