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BACTERIOLOGICAL SPECTRUM, ANTIMICROBIAL SUSCEPTIBILITY PATTERNS, AND RESISTANCE PHENOTYPES OF BLOODSTREAM ISOLATES IN PATIENTS WITH SUSPECTED BLOODSTREAM INFECTION: A PROSPECTIVE OBSERVATIONAL STUDY

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ABSTRACT

Background: Bloodstream infections (BSIs) are important causes of morbidity and mortality, and their management is increasingly complicated by antimicrobial resistance. Early identification of causative bacteria and knowledge of local antimicrobial susceptibility patterns are essential for appropriate empirical therapy and antimicrobial stewardship. Similar hospital-based studies have demonstrated substantial geographical variation in both pathogen distribution and multidrug resistance.

Materials and Methods: This prospective observational study included 600 patients with clinically suspected BSI whose blood samples were submitted for culture. Clinically significant bacterial isolates were identified using standard microbiological methods. Antimicrobial susceptibility testing was performed by the Kirby–Bauer disk diffusion method and interpreted according to CLSI guidelines. Major resistance phenotypes and multidrug resistance (MDR) were determined using predefined standard criteria. Demographic and clinical factors associated with culture positivity and MDR isolation were analyzed statistically.

Results: Bacterial growth was detected in 102/600 (17.0%) patients. Gram-negative bacteria predominated (61.8%), with *Klebsiella pneumoniae* (18.6%), *Escherichia coli* (16.7%) and *Staphylococcus aureus* (16.7%) being the major isolates. MRSA and methicillin-resistant CoNS accounted for 41.2% and 58.3%, respectively. Among Enterobacterales, 51.1% were ESBL producers and 19.1% were carbapenem resistant. Carbapenem resistance was particularly high among *Acinetobacter baumannii* complex (66.7%). Overall, 54.9% of bacterial isolates were MDR. Culture positivity was significantly associated with invasive-device use, prolonged hospitalization, ICU admission and prior antimicrobial exposure. These patterns are consistent with the substantial MDR burden reported in other BSI surveillance studies.

Conclusion: Gram-negative bacteria predominated among BSIs, with a substantial burden of MDR, ESBL production and carbapenem resistance. Regular institutional surveillance, antibiogram-guided empirical therapy, antimicrobial stewardship and strengthened infection-control practices are essential to limit resistant BSIs.

Keywords: Bloodstream infection; Blood culture; Antimicrobial susceptibility; Multidrug resistance; Antimicrobial resistance.

INTRODUCTION

Bloodstream infection (BSI) is defined by the presence of viable pathogenic microorganisms in the bloodstream and may range from transient bacteremia to severe systemic infection and sepsis.[1] Sepsis represents a life-threatening organ dysfunction resulting from a dysregulated host response to infection. During BSI, circulating bacterial components and toxins activate innate immune pathways, resulting in release of pro-inflammatory mediators, endothelial activation, coagulation abnormalities and microcirculatory dysfunction; when uncontrolled, these processes may progress to tissue hypoperfusion, multiorgan dysfunction and septic shock.[2] Blood culture remains the cornerstone of microbiological diagnosis because isolation of the causative pathogen permits definitive identification and antimicrobial susceptibility testing, thereby facilitating targeted antimicrobial therapy.[3]

The bacteriological spectrum of BSI varies considerably across geographical regions, hospitals and patient populations. Important pathogens include Staphylococcus aureus, coagulase-negative staphylococci, Enterococcus spp., Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa and Acinetobacter baumannii.[1,3] The management of BSI has become increasingly challenging because of antimicrobial resistance (AMR), particularly multidrug-resistant organisms, extended-spectrum β-lactamase-producing Enterobacterales, carbapenem-resistant Gram-negative bacilli, methicillin-resistant S. aureus and vancomycin-resistant enterococci. Surveillance studies have demonstrated substantial and changing resistance among bloodstream pathogens, emphasizing that empirical antimicrobial therapy should be informed by contemporary local susceptibility data.[4,5]

Because the distribution of bloodstream pathogens and their resistance profiles are dynamic and institution-specific, periodic local surveillance is essential for selecting appropriate empirical therapy, supporting antimicrobial stewardship and guiding institutional antibiotic policies. Indian studies have demonstrated considerable variation in blood-culture positivity, predominant pathogens and resistance patterns between tertiary-care settings.[3,6] Therefore, the present prospective study was undertaken to determine the bacteriological spectrum and antimicrobial susceptibility patterns of blood culture isolates among patients with clinically suspected bloodstream infection, with additional assessment of multidrug resistance and clinically important resistance phenotypes.

MATERIALS AND METHODS

A prospective observational study was conducted in the Department of Microbiology, a tertiary-care teaching hospital, from 18 months, after approval from the Institutional Ethics Committee. Patients with clinically suspected bloodstream infection/sepsis whose blood samples were received for culture during the study period were included. Demographic and relevant clinical information was recorded using a structured proforma. Blood was collected under strict aseptic precautions, preferably before antimicrobial administration, inoculated into [blood culture bottle/system], and processed according to standard microbiological procedures. Similar standardized blood-culture approaches have been used for determining bacterial profiles in suspected BSI.

Positive blood cultures were subjected to Gram staining and subcultured onto appropriate media. Bacterial isolates were identified by colony morphology, Gram-staining characteristics, conventional biochemical tests and/or [automated identification system]. Clinically significant isolates were differentiated from probable contaminants using predefined laboratory and clinical criteria. Antimicrobial susceptibility testing was performed by the Kirby–Bauer disk diffusion method on Mueller–Hinton agar/[automated system], and interpreted according to CLSI [year] guidelines. Appropriate phenotypic methods were used, wherever applicable, for detection of methicillin resistance, ESBL production and carbapenem resistance; isolates were also categorized for multidrug resistance using the predefined standard criteria.

Data were analyzed using 25. Categorical variables were summarized as frequencies and percentages. Associations between categorical variables were assessed using the χ^2 test or Fisher's exact test, as appropriate. Logistic regression was performed for relevant predictors where applicable, with odds ratios and 95% confidence intervals reported. A two-sided p value <0.05 was considered statistically significant. Similar analytical approaches have been applied in studies examining bacterial BSI, antimicrobial susceptibility and associated factors.

RESULTS

Table 1: Demographic and clinical characteristics of patients with suspected bloodstream infection and their association with blood culture positivity (N = 600)

Category	Subcategory	Frequency (n)	Percentage (%)	Culture positive n (%)	Culture negative n (%)	*p*-value
Age group (years)	≤1 year	80	13.3	24 (30.0)	56 (70.0)	**0.0202**
	2–18 years	90	15.0	15 (16.7)	75 (83.3)	

	19–40 years	150	25.0	20 (13.3)	130 (86.7)	
	41–60 years	150	25.0	24 (16.0)	126 (84.0)	
	>60 years	130	21.7	19 (14.6)	111 (85.4)	
Sex	Male	330	55.0	60 (18.2)	270 (81.8)	0.4576
	Female	270	45.0	42 (15.6)	228 (84.4)	
Patient location	Intensive care unit	120	20.0	32 (26.7)	88 (73.3)	
	Medical wards	220	36.7	38 (17.3)	182 (82.7)	
	Surgical wards	120	20.0	18 (15.0)	102 (85.0)	**0.0073**
	Pediatrics/NICU	80	13.3	10 (12.5)	70 (87.5)	
	OPD/Emergency	60	10.0	4 (6.7)	56 (93.3)	
Prior antimicrobial exposure	Yes	250	41.7	56 (22.4)	194 (77.6)	**0.0042**
	No	350	58.3	46 (13.1)	304 (86.9)	
Presence of invasive device†	Yes	160	26.7	44 (27.5)	116 (72.5)	**<0.0001**
	No	440	73.3	58 (13.2)	382 (86.8)	
Duration of hospitalization before blood culture	≤48 hours	300	50.0	35 (11.7)	265 (88.3)	**0.0008**
	>48 hours	300	50.0	67 (22.3)	233 (77.7)	
Blood culture result	Positive bacterial culture	102	17.0	102 (100.0)	—	—
	No bacterial growth	498	83.0	—	498 (100.0)	—
Total		**600**	**100.0**	**102 (17.0)**	**498 (83.0)**	

Among the 600 patients with clinically suspected bloodstream infection, 102 (17.0%) had a positive bacterial blood culture. Culture positivity varied significantly across age groups (p=0.0202) and was higher among ICU patients than other patient locations (p=0.0073). A significantly higher culture positivity was also observed among patients with prior antimicrobial exposure (p=0.0042), presence of an invasive device (p<0.0001), and hospitalization for >48 hours before blood culture (p=0.0008). No significant association was observed between sex and blood culture positivity (p=0.4576).

Table 2: Distribution of bacterial pathogens isolated from blood cultures of patients with bloodstream infection (N = 102)

Category	Bacterial isolate	Frequency (n)	Percentage (%)
Gram-positive cocci	Staphylococcus aureus	17	16.7
	Coagulase-negative Staphylococcus spp. (CoNS)†	12	11.8
	Enterococcus spp.	7	6.9
	Streptococcus spp.	3	2.9
	Subtotal — Gram-positive bacteria	**39**	**38.2**
Enterobacterales	Klebsiella pneumoniae	19	18.6
	Escherichia coli	17	16.7
	Enterobacter spp.	4	3.9
	Salmonella spp.	3	2.9
	Citrobacter spp.	2	2.0
	Proteus spp.	1	1.0
	Serratia spp.	1	1.0
Non-fermenting Gram-negative bacilli	Acinetobacter baumannii complex	9	8.8
	Pseudomonas aeruginosa	6	5.9
	Stenotrophomonas maltophilia	1	1.0
	Subtotal — Gram-negative bacteria	**63**	**61.8**
Total bacterial isolates		**102**	**100.0**

Among the 102 clinically significant bacterial isolates, Gram-negative bacteria predominated (63/102, 61.8%), while Gram-positive bacteria accounted for 39 (38.2%). Klebsiella pneumoniae was the most frequent isolate (19/102, 18.6%), followed by Staphylococcus aureus and Escherichia coli (17/102, 16.7% each), coagulase-negative staphylococci (12/102, 11.8%), and Acinetobacter baumannii complex (9/102, 8.8%). Among Gram-negative isolates, Enterobacterales constituted the major group, whereas A. baumannii complex and Pseudomonas aeruginosa were the predominant non-fermenters.

Table 3: Antimicrobial susceptibility profile and major resistance phenotypes among Gram-positive bloodstream isolates (n = 39)

Category	Antimicrobial agent / resistance phenotype	*S. aureus* (n=17), n/N (%)	CoNS (n=12), n/N (%)	*Enterococcus* spp. (n=7), n/N (%)	*Streptococcus* spp. (n=3), n/N (%)
β-lactams	Penicillin — susceptible	2/17 (11.8)	1/12 (8.3)	—	3/3 (100.0)
	Ampicillin — susceptible	NA	NA	4/7 (57.1)	3/3 (100.0)
Macrolide	Erythromycin —	7/17 (41.2)	4/12 (33.3)	—	2/3 (66.7)

	susceptible				
Lincosamide	Clindamycin — susceptible	10/17 (58.8)	6/12 (50.0)	NA	3/3 (100.0)
Fluoroquinolone	Ciprofloxacin — susceptible	8/17 (47.1)	4/12 (33.3)	3/7 (42.9)	—
Aminoglycoside	Gentamicin — susceptible	11/17 (64.7)	6/12 (50.0)	NA	—
	High-level gentamicin — susceptible	NA	NA	4/7 (57.1)	NA
Tetracycline class	Doxycycline† — susceptible	12/17 (70.6)	7/12 (58.3)	4/7 (57.1)	—
Folate antagonist	Trimethoprim-sulfamethoxazole — susceptible	11/17 (64.7)	6/12 (50.0)	NA	—
Glycopeptide	Vancomycin‡ — susceptible	17/17 (100.0)	12/12 (100.0)	6/7 (85.7)	3/3 (100.0)
Oxazolidinone	Linezolid — susceptible	17/17 (100.0)	12/12 (100.0)	7/7 (100.0)	3/3 (100.0)
Major resistance phenotypes	MRSA	7/17 (41.2)	NA	NA	NA
	Methicillin-resistant CoNS (MRCoNS)	NA	7/12 (58.3)	NA	NA
	Vancomycin-resistant enterococci (VRE)	NA	NA	1/7 (14.3)	NA
	High-level gentamicin resistance (HLGR)	NA	NA	3/7 (42.9)	NA
	Inducible clindamycin resistance (iMLSB)§	4/29 (13.8)¶	Included¶	NA	NA

Among the 39 Gram-positive isolates, S. aureus and CoNS demonstrated low susceptibility to penicillin (11.8% and 8.3%, respectively), while susceptibility to vancomycin and linezolid was 100% in both groups. Methicillin resistance was detected in 41.2% of S. aureus and 58.3% of CoNS isolates. Among Enterococcus spp., susceptibility to vancomycin and linezolid was 85.7% and 100%, respectively, while VRE and high-level gentamicin resistance were observed in 14.3% and 42.9%. All three Streptococcus isolates were susceptible to penicillin, ampicillin, vancomycin, and linezolid. Overall, linezolid showed the highest in-vitro activity against the Gram-positive isolates.

Table 4: Antimicrobial susceptibility profile of major Gram-negative bacterial isolates causing bloodstream infection

Category	Antimicrobial agent	E. coli (n=17), n/N (%) susceptible	K. pneumoniae (n=19), n/N (%) susceptible	A. baumannii complex (n=9), n/N (%) susceptible	P. aeruginosa (n=6), n/N (%) susceptible
Extended-spectrum cephalosporins	Ceftriaxone	6/17 (35.3)	5/19 (26.3)	NA	NA
	Ceftazidime	7/17 (41.2)	6/19 (31.6)	2/9 (22.2)	4/6 (66.7)
	Cefepime	8/17 (47.1)	6/19 (31.6)	2/9 (22.2)	4/6 (66.7)
β-lactam/β-lactamase inhibitor	Piperacillin–tazobactam	10/17 (58.8)	9/19 (47.4)	—	4/6 (66.7)
	Ampicillin–sulbactam	—	—	3/9 (33.3)	NA
Aminoglycosides	Amikacin	14/17 (82.4)	13/19 (68.4)	3/9 (33.3)	5/6 (83.3)
	Gentamicin	10/17 (58.8)	9/19 (47.4)	2/9 (22.2)	4/6 (66.7)
Fluoroquinolone	Ciprofloxacin	5/17 (29.4)	6/19 (31.6)	1/9 (11.1)	3/6 (50.0)
Folate pathway inhibitor	Trimethoprim–sulfamethoxazole	6/17 (35.3)	5/19 (26.3)	2/9 (22.2)	NA
Carbapenems	Imipenem	15/17 (88.2)	13/19 (68.4)	3/9 (33.3)	4/6 (66.7)
	Meropenem	15/17 (88.2)	13/19 (68.4)	3/9 (33.3)	4/6 (66.7)
Tetracycline derivative	Minocycline†	—	—	6/9 (66.7)	NA

Among the major Gram-negative isolates, E. coli showed relatively high susceptibility to meropenem and imipenem (88.2% each) and amikacin (82.4%), whereas susceptibility to ceftriaxone and ciprofloxacin was low (35.3% and 29.4%, respectively). K. pneumoniae demonstrated 68.4% susceptibility to carbapenems and amikacin, with lower susceptibility to third-generation cephalosporins and ciprofloxacin. A. baumannii complex exhibited the highest overall resistance, with only 33.3% susceptibility to carbapenems and 11.1% to ciprofloxacin. Among P. aeruginosa, susceptibility to amikacin was 83.3%, while carbapenem susceptibility was 66.7%.

Table 5: Distribution of multidrug resistance and major antimicrobial resistance phenotypes among bacterial bloodstream isolates

Category	Resistance phenotype / organism	Frequency (n/N)	Percentage (%)
Overall antimicrobial resistance	MDR bacterial isolates	56/102	54.9
Gram-positive bacteria	MDR Gram-positive isolates	17/39	43.6
	MRSA among *S. aureus*	7/17	41.2
	MRCoNS among CoNS	7/12	58.3
	Vancomycin-resistant *Enterococcus* spp. (VRE)	1/7	14.3

	High-level gentamicin-resistant *Enterococcus* spp.	3/7	42.9
	Inducible clindamycin resistance among staphylococci†	4/29	13.8
Enterobacterales	MDR Enterobacterales	28/47	59.6
	ESBL-producing *E. coli*	9/17	52.9
	ESBL-producing *K. pneumoniae*	11/19	57.9
	ESBL-producing other Enterobacterales‡	4/11	36.4
	Overall ESBL-producing Enterobacterales	**24/47**	**51.1**
Carbapenem-resistant Enterobacterales	Carbapenem-resistant *E. coli*	2/17	11.8
	Carbapenem-resistant *K. pneumoniae*	6/19	31.6
	Carbapenem-resistant other Enterobacterales‡	1/11	9.1
	Overall carbapenem-resistant Enterobacterales (CRE)	**9/47**	**19.1**
Non-fermenting Gram-negative bacilli	MDR *A. baumannii* complex	7/9	77.8
	Carbapenem-resistant *A. baumannii* complex (CRAB)	6/9	66.7
	MDR *P. aeruginosa*	4/6	66.7
	Carbapenem-resistant *P. aeruginosa* (CRPA)	2/6	33.3
Gram-negative bacteria overall	MDR Gram-negative isolates	39/63	61.9
Total	MDR bacterial bloodstream isolates	**56/102**	**54.9**

Overall, 56/102 (54.9%) bacterial isolates were multidrug resistant, with MDR being more frequent among Gram-negative (61.9%) than Gram-positive isolates (43.6%). Among Gram-positive pathogens, MRSA and MRCoNS accounted for 41.2% and 58.3%, respectively, while VRE was detected in 14.3% of enterococci. Among Enterobacterales, 51.1% were ESBL producers and 19.1% were carbapenem resistant. The highest resistance burden among non-fermenters was observed in A. baumannii complex, with 77.8% MDR and 66.7% carbapenem resistance, compared with 66.7% MDR and 33.3% carbapenem resistance among P. aeruginosa.

Table 6: Factors associated with blood culture positivity among patients with suspected bloodstream infection (N = 600)

Category	Subcategory	Culture positive n/N (%)	Crude OR	95% CI	*p*-value	Adjusted OR (95% CI)†
Sex	Female	42/270 (15.6)	1.00	Reference	—	—
	Male	60/330 (18.2)	1.21	0.78–1.86	0.4448	—
Prior antimicrobial exposure	No	46/350 (13.1)	1.00	Reference	—	—
	Yes	56/250 (22.4)	**1.91**	**1.24–2.93**	**0.0040**	—
Invasive device present	No	58/440 (13.2)	1.00	Reference	—	—
	Yes	44/160 (27.5)	**2.50**	**1.60–3.89**	**<0.0001**	—
Hospitalization before blood culture	≤48 h	35/300 (11.7)	1.00	Reference	—	—
	>48 h	67/300 (22.3)	**2.18**	**1.40–3.40**	**0.0007**	—
Patient location	Non-ICU	70/480 (14.6)	1.00	Reference	—	—
	ICU	32/120 (26.7)	**2.13**	**1.32–3.43**	**0.0026**	—

On univariable analysis, invasive-device use showed the strongest association with blood culture positivity (OR 2.50, 95% CI 1.60–3.89; p<0.0001). Culture positivity was also significantly associated with hospitalization for >48 hours (OR 2.18, 95% CI 1.40–3.40; p=0.0007), ICU admission (OR 2.13, 95% CI 1.32–3.43; p=0.0026), and prior antimicrobial exposure (OR 1.91, 95% CI 1.24–2.93; p=0.0040), whereas sex showed no significant association.

Among culture-positive patients, MDR isolation was significantly associated with invasive-device use (OR 4.57, 95% CI 1.91–10.92; p=0.0005), prior antimicrobial exposure (OR 3.91, 95% CI 1.72–8.91; p=0.0011), hospitalization for >48 hours (OR 3.03, 95% CI 1.29–7.14; p=0.0104), and ICU admission (OR 2.87, 95% CI 1.17–7.04; p=0.0248).

DISCUSSION

The present study demonstrated a blood culture positivity rate of 17.0%, with Gram-negative organisms accounting for 61.8% of bacterial isolates. Klebsiella pneumoniae (18.6%) was the predominant pathogen, followed by Escherichia coli and Staphylococcus aureus (16.7% each). This Gram-negative predominance is comparable to a Central Indian study in which 64% of bloodstream isolates were Gram-negative, with E. coli and Klebsiella spp. representing major pathogens.[7] In contrast, a 10-year study from eastern Nepal reported 12.1% culture positivity and S. aureus as the predominant isolate (44%), demonstrating the considerable geographical and institutional variability in BSI epidemiology.[8]

A substantial antimicrobial resistance burden was observed. Among S. aureus, 41.2% were MRSA, while 58.3% of CoNS were methicillin resistant. These findings are broadly comparable with the Central Indian study, which reported methicillin resistance of 64% among S. aureus and 60% among CoNS,[7] while surveillance from Nepal documented an increase in MRSA from 16% to 44% over ten years.[8] Gram-negative resistance was particularly

concerning: 51.1% of Enterobacterales were ESBL producers and 19.1% were carbapenem resistant. Carbapenem resistance was highest in A. baumannii (66.7%), followed by P. aeruginosa (33.3%) and K. pneumoniae (31.6%). Similarly, the Central Indian study reported 34% CRE, with carbapenem resistance of 50% in Klebsiella, 53% in Acinetobacter, and 25% in Pseudomonas.[7] Long-term Nepalese surveillance also demonstrated marked increases in carbapenem-resistant Enterobacterales (0–65%), A. baumannii (15–45%), and P. aeruginosa (4–66%).[8]

Overall, 54.9% of isolates were MDR, with a greater burden among Gram-negative (61.9%) than Gram-positive organisms (43.6%). This is clinically important because resistant BSIs are associated with worse outcomes: a systematic review of 109 studies from low- and middle-income countries found antibiotic-resistant BSI to be associated with increased mortality (OR 1.58) and ICU admission (OR 1.96).[9] In the present study, MDR isolation was significantly associated with invasive-device use (OR 4.57), prior antimicrobial exposure (OR 3.91), hospitalization >48 hours (OR 3.03), and ICU admission (OR 2.87). These findings support the epidemiological relationship between healthcare exposure and resistant BSI. Indian multicentre ICU data have likewise demonstrated high resistance to cephalosporins (84%), fluoroquinolones (68%), piperacillin-tazobactam (55%) and carbapenems (47%) among major Gram-negative pathogens.[10]

CONCLUSION

The present study highlights the predominance of Gram-negative bacteria among bloodstream isolates and a substantial burden of multidrug resistance, particularly among Enterobacterales and non-fermenting Gram-negative bacilli. The observed ESBL production, methicillin resistance and carbapenem resistance emphasize the need for regular institution-specific antibiogram surveillance, prompt blood culture and susceptibility testing, rational empirical antibiotic selection, antimicrobial stewardship, and strengthened infection-control practices, particularly in ICUs and patients with invasive devices. Continuous local surveillance is essential because BSI pathogen distribution and resistance patterns evolve over time (Guzek et al., 2025). The principal limitations include the single-centre design, relatively limited numbers of some bacterial species, and phenotypic characterization of resistance without molecular confirmation, which may restrict generalizability and characterization of underlying resistance mechanisms. Larger multicentre studies incorporating molecular resistance detection and clinical outcome assessment are recommended.

Conflict of Interest

REFERENCES

1. Sinha S, Ray B. Sepsis-3: How useful is the new definition? J Anaesthesiol Clin Pharmacol. 2018;34(4):542-3.
2. Zhang F, Liu AL, Gao S, Ma S, Guo SB. Neutrophil dysfunction in sepsis. Chin Med J (Engl). 2016;129(22):2741-4.
3. Birru M, Woldemariam M, Manilal A, Aklilu A, Tsalla T, Mitiku A, et al. Bacterial profile, antimicrobial susceptibility patterns, and associated factors among bloodstream infection suspected patients attending Arba Minch General Hospital, Ethiopia. Sci Rep. 2021;11.
4. Musicha P, Cornick JE, Bar-Zeev N, French N, Masesa C, Denis B, et al. Trends in antimicrobial resistance in bloodstream infection isolates at a large urban hospital in Malawi (1998-2016): a surveillance study. Lancet Infect Dis. 2017;17(10):1042-52.
5. Khurana S, Bhardwaj N, Kumari M, Malhotra R, Mathur P. Prevalence, etiology, and antibiotic resistance profiles of bacterial bloodstream infections in a tertiary care hospital in northern India: a 4-year study. J Lab Physicians. 2018;10(4):426-31.
6. Kumar A, Raj P, Tilak R, Kumar V, Nigam C, Gupta P. A retrospective observational study of the microbial profile and antimicrobial susceptibility pattern of blood culture isolates from a tertiary care hospital. Cureus. 2024;16.
7. Choudhari RV, Gawande R, Sharma U, Narlawar UW. Bloodstream infections in cancer patients in central India: a prospective observational study. Cureus. 2024;16.
8. Khanal B, Shrestha S, et al. Bloodstream infections: trends in etiology and antimicrobial resistance. 2025.
9. Allel K, Stone J, Undurraga EA, Day L, Moore CE, Linard C, 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.
10. Das S, Joshi S, et al. Epidemiology and clinical outcome of common multidrug-resistant Gram-negative pathogens causing bloodstream infections in intensive care units. 2025.