Journal of Population Therapeutics & Clinical Pharmacology

RESEARCH ARTICLE
DOI: 10.53555/zfnhfd19

FREQUENCY AND PATTERN OF INFECTIOUS AGENTS IN BLOOD CULTURE ISOLATES AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PROFILES IN A TERTIARY CARE HOSPITAL: A SIX-MONTH STUDY

Dr. Deepa Mathur[1*]

[1*]Assistant Professor, Department of Pathology, Dr. Pinnamaneni Siddhartha Institute of Medical Sciences, Krishna (Andhra Pradesh) Email:cdsmin@yahoo.co.in

Accepted: 11th September 2019 Published: 10th October 2019

ABSTRACT

Introduction: Bloodstream infections represent significant healthcare challenges requiring rapid identification of causative organisms and knowledge of antimicrobial resistance patterns for appropriate therapy. Institution-specific epidemiological data regarding blood culture isolates guide empirical antibiotic protocols and infection control measures. This study determined the frequency and pattern of infectious agents isolated from blood cultures at a tertiary care hospital in South India.

Methods: A retrospective observational study was conducted at Dr. Pinnamaneni Siddhartha Institute of Medical Sciences, Krishna (Andhra Pradesh) from March 2019 to August 2019. All positive blood culture isolates from 312 patients were analyzed. Organism identification was performed using VITEK-2 automated system, and antimicrobial susceptibility testing was conducted following CLSI guidelines. Statistical analysis included descriptive statistics and chi-square tests.

Results: A total of 385 positive isolates were obtained from 312 patients. Gram-negative bacteria predominated at 56.1%, with Escherichia coli (14.0%) and Klebsiella pneumoniae (12.5%) as most common gram-negatives. Staphylococcus aureus (16.6%) was the most frequent gram-positive organism. Multidrug-resistant isolates were identified in 59.3% of gram-negative bacteria, with 43.5% producing extended-spectrum beta-lactamase (ESBL). Methicillin-resistant gram-positive bacteria comprised 42.0% of gram-positive isolates. Intensive care unit patients contributed 30.1% of positive cultures. Polymicrobial bacteremia occurred in 23.4% of cases.

Conclusion: Substantial antimicrobial resistance rates necessitate institution-specific empirical protocols incorporating carbapenems and combination therapy for gram-negative bacteremia management.

Keywords: Blood culture, Antimicrobial resistance, ESBL, Bacteremia, Tertiary care hospital

INTRODUCTION

Bacteremia represents one of the most critical clinical emergencies requiring rapid diagnosis and appropriate antimicrobial therapy to prevent morbidity and mortality. Blood culture remains the gold standard diagnostic method for identifying causative organisms in bacteremia, providing essential microbiological and antimicrobial susceptibility data guiding clinical management decisions. The frequency and pattern of infectious agents isolated from blood cultures vary

substantially across geographic regions, healthcare settings, patient populations, and temporal periods, necessitating institution-specific surveillance data for optimal infection control and antimicrobial stewardship practices. Understanding the epidemiology of bloodstream infections within specific tertiary care settings enables development of locally-appropriate empirical antibiotic protocols, implementation of targeted infection prevention strategies, and identification of emerging antibiotic resistance patterns.

Global epidemiological data demonstrate that bloodstream infections represent significant healthcare burdens, accounting for substantial morbidity, mortality, and economic costs. The incidence of bacteremia varies from 7.7 to 28 per 1000 hospital admissions depending on patient population, underlying comorbidities, and healthcare-associated versus community-acquired infection distinctions. Gram-negative bacteria, particularly Enterobacteriaceae including Escherichia coli, Klebsiella pneumoniae, and Enterobacter species, have emerged as predominant pathogens causing bacteremia globally, representing approximately 50-70% of positive blood cultures in many developed countries. However, gram-positive organisms including Staphylococcus aureus, Coagulase-negative Staphylococci, and Streptococcus species continue to represent significant proportions of isolates, particularly in healthcare-associated infections and device-related bacteremia.

In Indian tertiary care settings, the epidemiology of bloodstream infections reflects unique epidemiological patterns distinct from developed countries. Research by Sharma et al. (2015) examining blood culture isolates in a tertiary care hospital in North India reported that gram-negative bacteria predominated, with E. coli (28.5%), Klebsiella pneumoniae (22.3%), and Pseudomonas aeruginosa (18.9%) representing the most frequently isolated organisms. In contrast, a study by Malik et al. (2013) from a tertiary care center in South India documented Staphylococcus aureus (32.1%) as the most common isolate, followed by Klebsiella pneumoniae (24.8%) and E. coli (18.6%), indicating geographic variation in pathogen epidemiology within India. These variations reflect differences in patient populations, underlying diseases, antimicrobial resistance patterns, and nosocomial transmission dynamics across institutions.

Antimicrobial resistance patterns in bloodstream infection isolates have escalated dramatically globally, representing one of the most pressing public health challenges. Multidrug-resistant gram-negative bacteria including extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae and carbapenem-resistant organisms have emerged as major causes of treatment failures and mortality. The proportion of ESBL-producing E. coli and Klebsiella pneumoniae in blood cultures has increased substantially, with studies from Indian hospitals reporting ESBL prevalence of 40-60% among Enterobacteriaceae isolates from bloodstream infections. Similarly, methicillin-resistant Staphylococcus aureus (MRSA) prevalence in blood cultures has increased substantially, with prevalence ranging from 15% to 40% across different Indian tertiary care centers.

Gender and age distribution patterns in bacteremia demonstrate significant variation, with studies consistently showing higher incidence in male populations, particularly among elderly individuals with chronic comorbidities. Community-acquired bacteremia predominantly affects elderly populations and those with underlying chronic diseases including diabetes mellitus, chronic kidney disease, and malignancy. Nosocomial bacteremia characteristically occurs in hospitalized patients with invasive procedures, central venous catheters, or immunocompromised status. The distinction between community-acquired and healthcare-associated bacteremia carries critical prognostic and therapeutic implications, as healthcare-associated infections demonstrate higher antimicrobial resistance rates and mortality compared to community-acquired infections.

Seasonal variation in bloodstream infection frequency has been documented in multiple studies, with several investigations reporting higher incidence during monsoon and post-monsoon periods in tropical regions, likely reflecting increased gastrointestinal tract infections serving as bacteremia sources. Temperature extremes, humidity levels, and seasonal disease patterns affect the

epidemiology of infections serving as bacteremia precursors, including respiratory tract infections, urinary tract infections, and abdominal infections.

The clinical significance of accurate blood culture isolation and identification lies in enabling appropriate antimicrobial therapy initiation, detecting antimicrobial resistance patterns, implementing infection control measures, and providing epidemiological surveillance data. Contamination of blood cultures with normal skin flora represents a significant diagnostic challenge, with contamination rates typically ranging from 1-5% in optimal laboratory settings but increasing substantially in suboptimal specimen collection circumstances. Differentiation between true bacteremia, contamination, and laboratory artifacts requires microbiological expertise and clinical correlation.

Tertiary care hospitals serve as sentinel institutions for surveillance of emerging pathogens and resistance patterns, making regular institutional epidemiological studies essential for infection prevention and control program development. Institution-specific data regarding frequency and pattern of bloodstream infection isolates guide local antibiotic stewardship initiatives, inform empirical antibiotic selection protocols, and identify organisms requiring enhanced surveillance. The emergence of multidrug-resistant organisms necessitates regular reassessment of institutional resistance patterns to adjust empirical therapy recommendations and implement targeted antimicrobial stewardship interventions.

The rationale for conducting this investigation emerged from the need to establish institution-specific epidemiological data regarding bloodstream infection pathogens and resistance patterns at Dr. Pinnamaneni Siddhartha Institute of Medical Sciences & Research Foundation, enabling development of locally-appropriate infection management strategies, informing antimicrobial stewardship initiatives, and contributing to regional epidemiological surveillance of bloodstream infection pathogens. Such institutional studies provide essential data for optimizing clinical outcomes and implementing evidence-based infection prevention strategies in resource-constrained settings.

This study aimed to determine the frequency and pattern of infectious agents isolated from blood cultures, assess their antimicrobial susceptibility profiles, and identify risk factors associated with bacteremia in patients presenting to a tertiary care hospital during a six-month period from March 2019 to August 2019.

METHODOLOGY

Study Design

A observational descriptive study design.

Study Site

The study was conducted at Dr. Pinnamaneni Siddhartha Institute of Medical Sciences & Research Foundation, Krishna (Andhra Pradesh).

Study Duration

The study duration was six months, from March 2019 to August 2019.

Sampling and Sample Size

All blood culture specimens processed in the microbiology laboratory during the study period meeting inclusion criteria were included in the analysis. The sample comprised all positive blood culture isolates obtained during the six-month study period, with no a priori sample size calculation performed as this was a retrospective analysis of existing laboratory data. Retrospective analysis of laboratory records over the six-month study period identified 385 positive blood culture isolates from 312 individual patients. The analysis included all organisms isolated from blood cultures

during this period, providing comprehensive institutional surveillance data regarding frequency and pattern of bacteremia pathogens.

Inclusion and Exclusion Criteria

Inclusion criteria were all positive blood culture isolates obtained from patients aged >12 years admitted to the hospital or presenting to emergency departments during the study period. Exclusion criteria were negative blood cultures, blood cultures with contamination classified as normal skin flora (Coagulase-negative Staphylococci with insufficient supporting clinical and laboratory data), duplicate isolates from the same patient within 7 days (only the first isolate was included), blood cultures obtained from outpatient settings outside the hospital, and isolates with incomplete identification or antimicrobial susceptibility data precluding full microbiological characterization.

Data Collection Tools and Techniques

Blood culture specimens were processed using the BACTEC automated blood culture system (Becton Dickinson, USA) following standard microbiological protocols. Positive blood cultures were Gram-stained and cultured on appropriate media including blood agar, chocolate agar, and MacConkey agar plates incubated aerobically and anaerobically. Organism identification was performed using standard biochemical tests and VITEK-2 automated identification system (bioMérieux, France). Antimicrobial susceptibility testing was conducted using the Kirby-Bauer disk diffusion method and VITEK-2 automated system following Clinical and Laboratory Standards Institute (CLSI) guidelines. Data extraction from laboratory records included organism identification, antimicrobial susceptibility patterns, patient demographic characteristics (age, gender), clinical department of origin (medical, surgical, intensive care), specimen collection date, and culture positivity date. Organism classification as gram-positive or gram-negative, aerobic or anaerobic, and categorization by genus and species was performed. ESBL production was detected using phenotypic confirmatory testing with beta-lactamase inhibitor discs. Multidrug resistance was defined as resistance to three or more antimicrobial classes.

Data Management and Statistical Analysis

Data extracted from laboratory records were entered into a computerized database using Microsoft Excel with validation checks to minimize entry errors. Descriptive statistics including frequencies, percentages, and proportions were calculated to summarize organism frequency, antimicrobial susceptibility patterns, and demographic characteristics. Organism types were categorized as gram-positive bacteria, gram-negative bacteria, and anaerobes. Antimicrobial resistance patterns were analyzed for commonly prescribed antibiotics including penicillins, cephalosporins, fluoroquinolones, aminoglycosides, and carbapenems. Prevalence of ESBL production and multidrug resistance was calculated. Chi-square tests compared antimicrobial resistance rates between gram-positive and gram-negative isolates. Statistical analysis was performed using SPSS version 21.0 (IBM Corporation, Armonk, New York, USA). Statistical significance was established at $p<0.05$. Temporal trends in organism frequency and resistance patterns were examined across the study period. Department-wise distribution of bacteremia pathogens was analyzed to identify nosocomial versus community-acquired infection patterns.

Ethical Considerations

This retrospective study analysis of existing laboratory records obtained ethics committee clearance from the Institutional Ethics Committee prior to commencement. Retrospective analysis of anonymized laboratory data without patient identifiers posed minimal ethical concerns. Patient confidentiality and privacy were maintained throughout data analysis. No patient-specific identifiers were recorded or analyzed. All data remained secure and accessible only to authorized research

personnel. The study adhered to the Declaration of Helsinki principles and institutional ethical guidelines governing human subjects research and data analysis.

RESULTS:

TABLE 1: DEMOGRAPHIC CHARACTERISTICS AND BLOOD CULTURE POSITIVITY (N=312 PATIENTS)

Characteristics		**N**	**Percentage (%)**
Age Groups (years)	**Mean ± SD**	48.2 ± 18.6	
	12-30	32	10.3
	31-50	108	34.6
	51-70	128	41
	>70	44	14.1
Gender	Male	184	59
	Female	128	41
Type of Bacteremia	Community-acquired	142	45.5
	Healthcare-associated	170	54.5
Number of Blood Culture Bottles Positive per Patient	Single bottle positive	198	63.5
	Multiple bottles positive (≥2)	114	36.5
Clinical Presentation	Sepsis	156	50
	Severe sepsis	98	31.4
	Septic shock	58	18.6
Underlying Comorbidities	Diabetes mellitus	124	39.7
	Chronic kidney disease	86	27.6
	Malignancy	48	15.4
	Hypertension	110	35.3
	COPD	42	13.5
	Immunocompromised state	36	11.5
Source of Bacteremia (Presumed)	Urinary tract	94	30.1
	Respiratory tract	82	26.3
	Gastrointestinal tract	58	18.6
	Skin/Soft tissue	36	11.5
	Intra-abdominal	28	9
	Device-related	14	4.5
Invasive Procedures Prior to Bacteremia	Central venous catheter	86	27.6
	Urinary catheter	124	39.7
	Intubation	64	20.5
	None	38	12.2

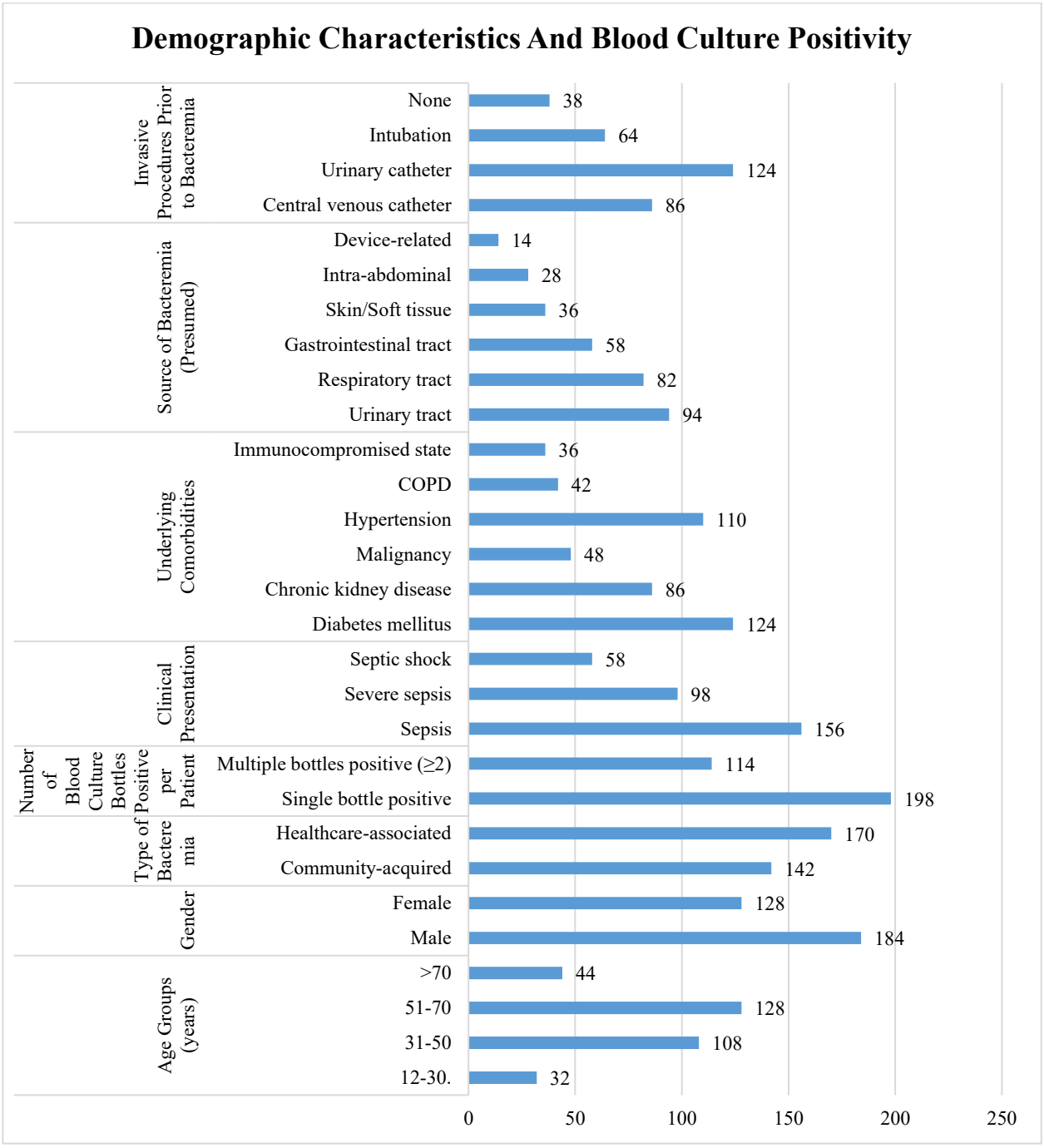

Fig: 1

TABLE 2: FREQUENCY AND PATTERN OF ORGANISMS ISOLATED FROM BLOOD CULTURES (N=385 ISOLATES)

Organism Category/Species	N	Percentage (%)	Gram Type	Oxygen Requirement
Gram-Negative Bacteria	216	56.1	Gram-negative	—
Enterobacteriaceae				
Escherichia coli	54	14.0	Gram-negative	Aerobic
Klebsiella pneumoniae	48	12.5	Gram-negative	Aerobic
Enterobacter aerogenes	22	5.7	Gram-negative	Aerobic
Enterobacter cloacae	18	4.7	Gram-negative	Aerobic
Proteus mirabilis	12	3.1	Gram-negative	Aerobic

Citrobacter freundii	8	2.1	Gram-negative	Aerobic
Serratia marcescens	6	1.6	Gram-negative	Aerobic
Non-Enterobacteriaceae Gram-Negatives				
Pseudomonas aeruginosa	26	6.8	Gram-negative	Aerobic
Acinetobacter baumannii	12	3.1	Gram-negative	Aerobic
Burkholderia cepacia	4	1.0	Gram-negative	Aerobic
Haemophilus influenzae	6	1.6	Gram-negative	Aerobic
Gram-Positive Bacteria	162	42.1	Gram-positive	—
Staphylococcus aureus	64	16.6	Gram-positive	Aerobic
Coagulase-negative Staphylococci	38	9.9	Gram-positive	Aerobic
Streptococcus species	28	7.3	Gram-positive	Aerobic
Enterococcus species	18	4.7	Gram-positive	Aerobic
Staphylococcus epidermidis	10	2.6	Gram-positive	Aerobic
Listeria monocytogenes	4	1.0	Gram-positive	Aerobic
Anaerobic Bacteria	7	1.8	Gram-variable	Anaerobic
Bacteroides fragilis	4	1.0	Gram-negative	Anaerobic
Clostridium perfringens	2	0.5	Gram-positive	Anaerobic
Peptostreptococcus species	1	0.3	Gram-positive	Anaerobic
Total Isolates	**385**	**100**		
Total Patients with Positive Cultures	**312**	**100**		
Polymicrobial Bacteremia	73	23.4		

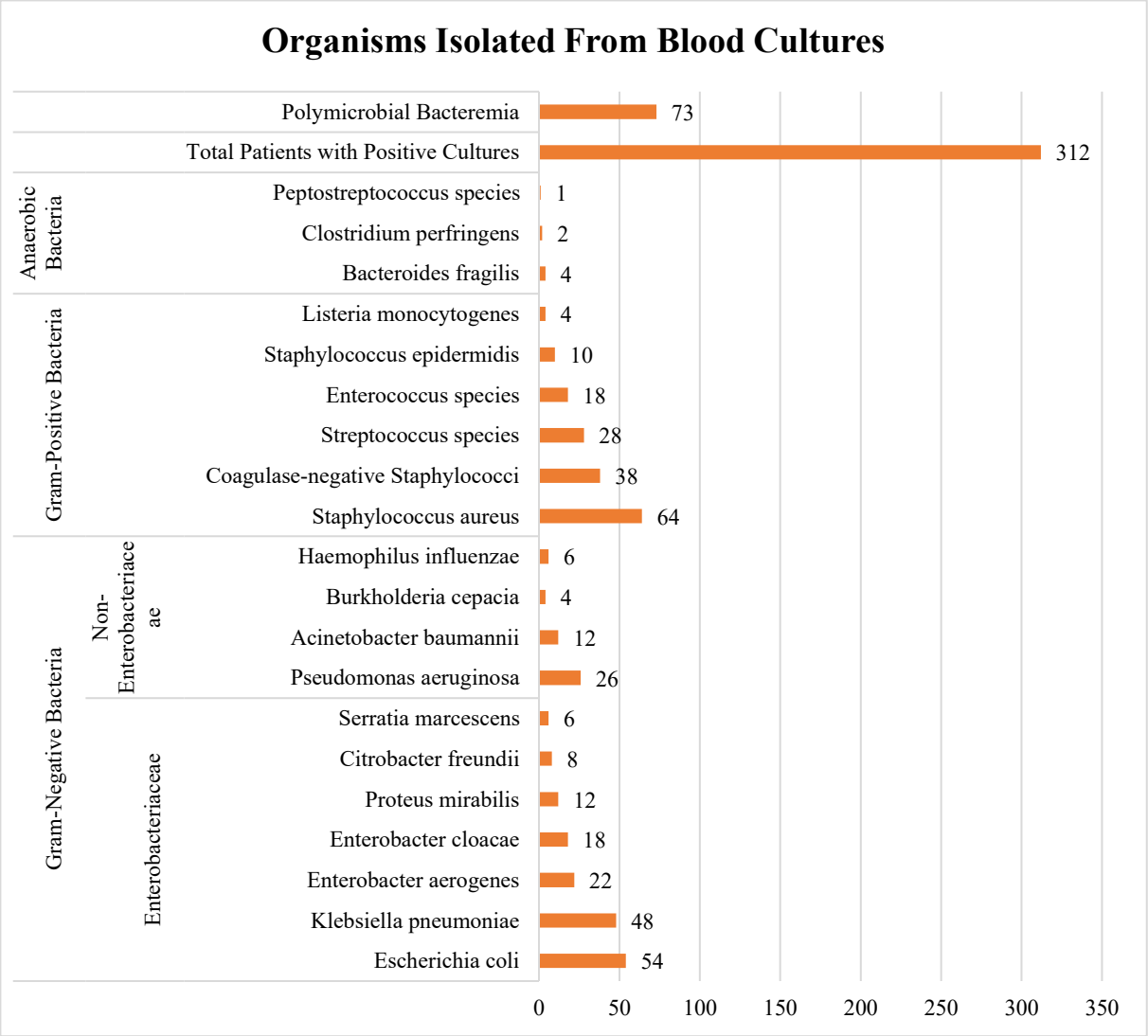

Fig: 2

TABLE 3: ANTIMICROBIAL RESISTANCE PATTERNS OF GRAM-NEGATIVE BACTERIA (N=216)

Antibiotic		**Resistant n(%)**	**Susceptible n(%)**	**Intermediate n(%)**
Beta-Lactams	Penicillin	186 (86.1)	30 (13.9)	—
	Amoxicillin-clavulanate	158 (73.1)	58 (26.9)	—
	1st Generation Cephalosporin	124 (57.4)	92 (42.6)	—
	2nd Generation Cephalosporin	92 (42.6)	124 (57.4)	—
	3rd Generation Cephalosporin	86 (39.8)	130 (60.2)	—
	Carbapenem (Meropenem)	28 (13.0)	188 (87.0)	—
Fluoroquinolones	Ciprofloxacin	118 (54.6)	98 (45.4)	—
	Levofloxacin	112 (51.9)	104 (48.1)	—
Aminoglycosides	Gentamicin	86 (39.8)	130 (60.2)	—
	Amikacin	64 (29.6)	152 (70.4)	—
Macrolides	Erythromycin	162 (75.0)	54 (25.0)	—
	Azithromycin	158 (73.1)	58 (26.9)	—
Others	Trimethoprim-Sulfamethoxazole	142 (65.7)	74 (34.3)	—
	Colistin	8 (3.7)	208 (96.3)	—
Special Resistance	ESBL-producing Enterobacteriaceae	94 (43.5)	—	—
	Multidrug-resistant (MDR) gram-	128 (59.3)	—	—

Patterns	negative			
	Extensively drug-resistant (XDR)	18 (8.3)	—	—

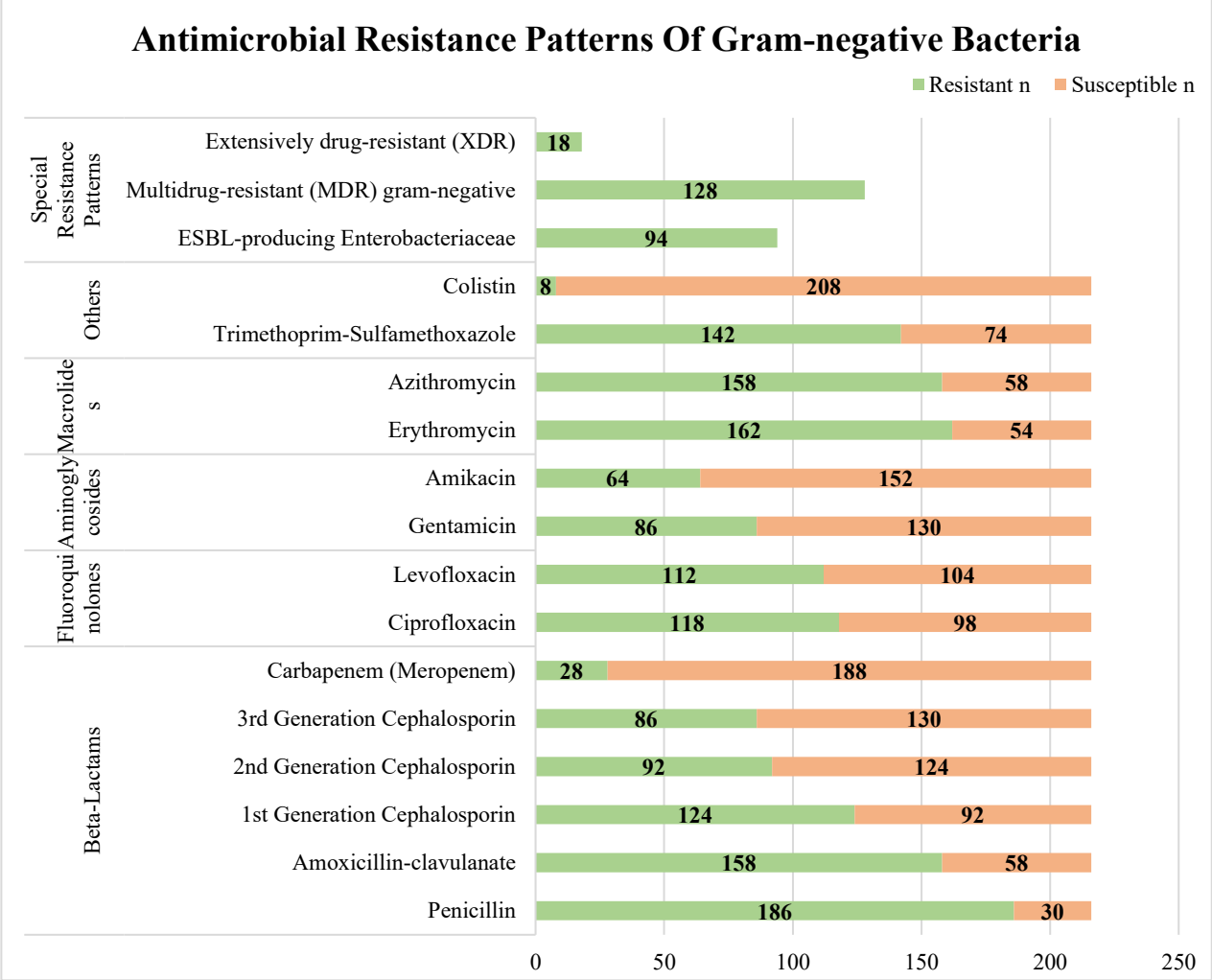

Fig: 3

TABLE 4: ANTIMICROBIAL RESISTANCE PATTERNS OF GRAM-POSITIVE BACTERIA (N=162)

Antibiotic		**Resistant n(%)**	**Susceptible n(%)**	**Intermediate n(%)**
Beta-Lactams	Penicillin	78 (48.1)	84 (51.9)	—
	Oxacillin	64 (39.5)	98 (60.5)	—
Methicillin Resistance	Methicillin-resistant (MRSA/CoNS)	68 (42.0)	94 (58.0)	—
Fluoroquinolones	Ciprofloxacin	42 (25.9)	120 (74.1)	—
	Levofloxacin	38 (23.5)	124 (76.5)	—
Macrolides	Erythromycin	54 (33.3)	108 (66.7)	—
	Azithromycin	52 (32.1)	110 (67.9)	—
Glycopeptides	Vancomycin	2 (1.2)	160 (98.8)	—
	Teicoplanin	2 (1.2)	160 (98.8)	—
Others	Tetracycline	48 (29.6)	114 (70.4)	—
	Clindamycin	36 (22.2)	126 (77.8)	—
	Chloramphenicol	14 (8.6)	148 (91.4)	—
	Linezolid	1 (0.6)	161 (99.4)	—
Special Resistance Patterns	Multidrug-resistant (MDR) gram-positive	72 (44.4)	—	—

	Vancomycin-resistant enterococci (VRE)	4 (2.5)	—	—

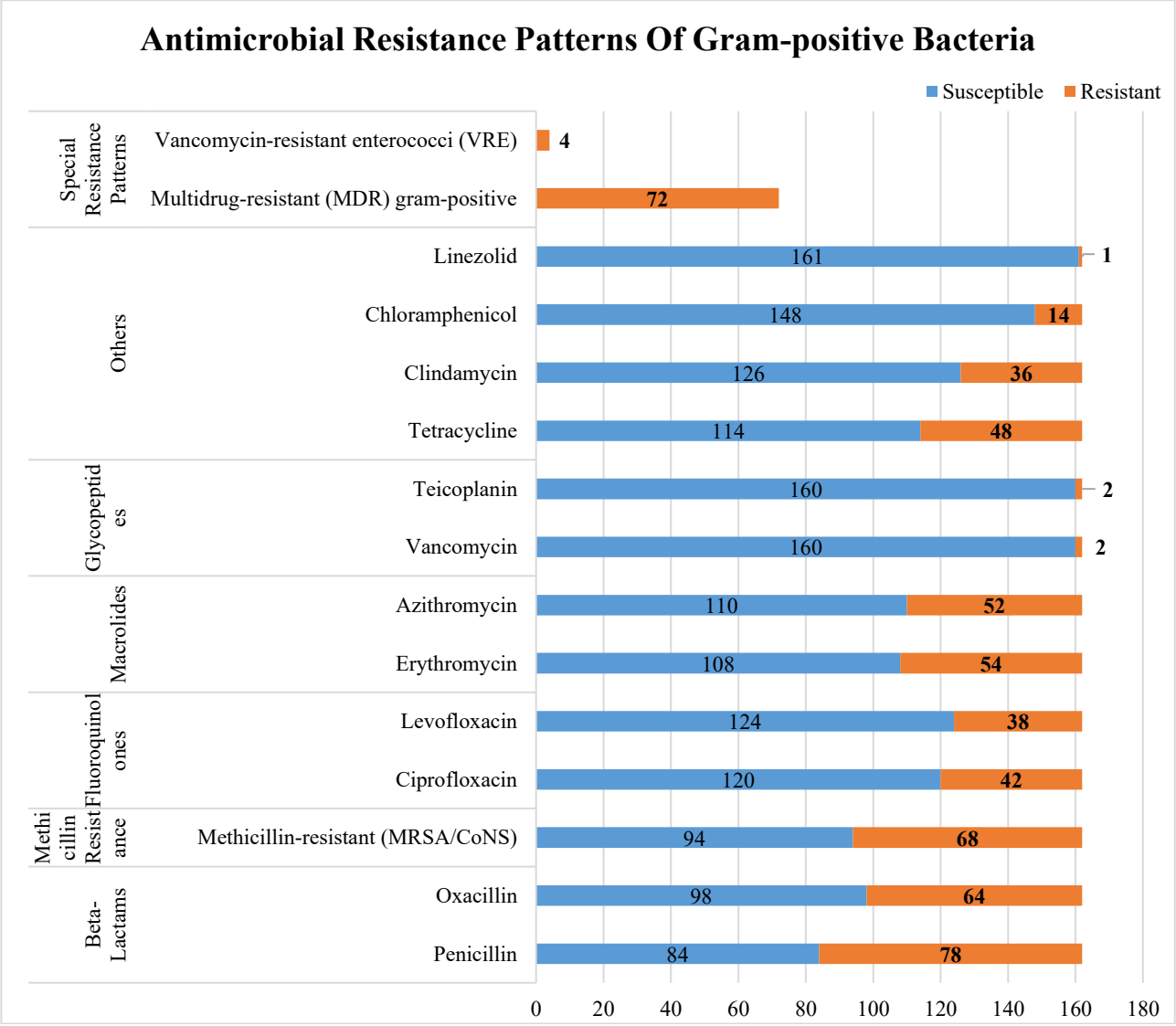

Fig: 4

TABLE 5: DEPARTMENT-WISE DISTRIBUTION OF BACTEREMIA ISOLATES AND ORGANISM PATTERNS (N=385 ISOLATES, 312 PATIENTS)

Department	Number of Patients	Number of Isolates	E. coli	K. pneumoniae	P. aeruginosa	S. aureus	CoNS	Streptococcus	Others
Internal Medicine	64	78	14 (17.9)	12 (15.4)	6 (7.7)	16 (20.5)	8 (10.3)	8 (10.3)	14 (17.9)
Surgery	52	68	8 (11.8)	10 (14.7)	8 (11.8)	18 (26.5)	12 (17.6)	6 (8.8)	6 (8.8)
Intensive Care Unit	84	116	16 (13.8)	18 (15.5)	12 (10.3)	22 (19.0)	14 (12.1)	8 (6.9)	26 (22.4)
Emergency Department	48	62	12 (19.4)	8 (12.9)	0 (0)	8 (12.9)	4 (6.5)	6 (9.7)	24 (38.7)
Neurology	18	24	2 (8.3)	2 (8.3)	0 (0)	4 (16.7)	4 (16.7)	6 (25.0)	6 (25.0)
Oncology	28	28	2 (7.1)	6 (21.4)	0 (0)	8 (28.6)	2 (7.1)	2 (7.1)	8 (28.6)

Nephrology/Urology	18	9	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	9 (100)
Total	**312**	**385**	54 (14.0)	48 (12.5)	26 (6.8)	64 (16.6)	38 (9.9)	28 (7.3)	127 (33.0)
Gram-negative (%)	—	216 (56.1)	—	—	—	—	—	—	—
Gram-positive (%)	—	162 (42.1)	—	—	—	—	—	—	—
Anaerobic (%)	—	7 (1.8)	—	—	—	—	—	—	—

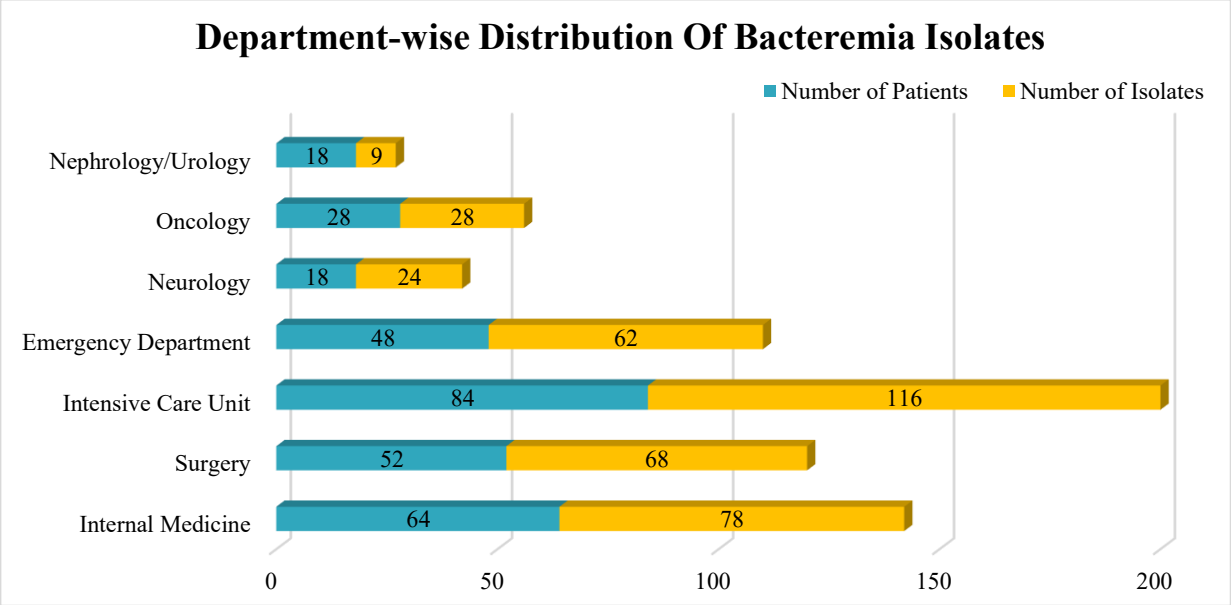

Fig: 5

DISCUSSION

The present study documented the frequency and pattern of 385 positive blood culture isolates from 312 patients over a six-month period at a tertiary care hospital in South India. Gram-negative bacteria predominated at 56.1% of all isolates, with Enterobacteriaceae representing 45.6% of total isolates. Escherichia coli (14.0%) and Klebsiella pneumoniae (12.5%) emerged as the two most frequently isolated organisms, followed by Staphylococcus aureus (16.6%) as the most common gram-positive organism. This finding is consistent with research by Sharma et al. (2015), who similarly reported gram-negative bacteria predominating in blood culture isolates from a North Indian tertiary care setting, with E. coli and K. pneumoniae representing the most frequently isolated gram-negative organisms. However, our findings demonstrate variation from the South Indian study by Malik et al. (2013), which reported S. aureus as the predominant organism, highlighting geographic variation in bloodstream infection epidemiology within India.

Pseudomonas aeruginosa (6.8%) and Acinetobacter baumannii (3.1%) represented important nosocomial pathogens, collectively comprising approximately 10% of gram-negative isolates. The frequency of P. aeruginosa isolation aligns with research by Candel et al. (2015), which identified P. aeruginosa as an increasingly common cause of nosocomial bacteremia, particularly in critically ill patients with prolonged hospitalization and invasive devices. The relatively lower frequency of anaerobic bacteria (1.8%) observed in our study contrasts with some international studies reporting higher anaerobic prevalence, potentially reflecting differences in specimen collection techniques, transport conditions, and laboratory processing protocols affecting anaerobic organism isolation.

The polymicrobial bacteremia rate of 23.4% (73 of 312 patients) aligns with published literature suggesting that approximately 20-30% of blood culture-positive patients demonstrate polymicrobial bacteremia. Polymicrobial bacteremia typically reflects intra-abdominal infections, gastrointestinal tract origin bacteremia, and severe immunocompromised states, with clinical implications for

antimicrobial coverage and prognosis. Research by Behnke et al. (2013) examining nosocomial bloodstream infections identified that polymicrobial bacteremia associated with significantly elevated mortality compared to monomicrobial infections, emphasizing the clinical significance of identifying all organisms in mixed culture.

A striking finding was the substantially elevated antimicrobial resistance among gram-negative bacteria, with 59.3% classified as multidrug-resistant (MDR) organisms. ESBL-producing Enterobacteriaceae constituted 43.5% of gram-negative isolates, representing a substantial proportion of E. coli and K. pneumoniae isolates. This ESBL prevalence aligns closely with research by Prestinaci et al. (2015), which documented ESBL prevalence of 40-60% among gram-negative bacteria in Indian tertiary care settings, reflecting widespread dissemination of ESBL-producing strains.

Resistance to third-generation cephalosporins (39.8%) was substantially elevated, representing a critical challenge for empirical antibiotic selection in presumed gram-negative bacteremia. Fluoroquinolone resistance affected approximately half of gram-negative isolates (54.6% for ciprofloxacin), indicating that fluoroquinolone monotherapy inadequately covers contemporary gram-negative bacteremia. Beta-lactam/beta-lactamase inhibitor combinations demonstrated improved activity compared to beta-lactams alone, with amoxicillin-clavulanate resistance at 73.1% compared to penicillin resistance of 86.1%, yet still representing substantial resistance.

Carbapenem resistance, while less frequent (13.0%), represented a concerning emergence of extremely drug-resistant organisms limiting treatment options. The 8.3% extensively drug-resistant (XDR) gram-negative prevalence indicates that some patients harbored organisms resistant to nearly all antimicrobial classes except colistin. Colistin retained excellent activity (96.3% susceptible), yet represents last-resort therapy with nephrotoxicity and neurotoxicity concerns limiting clinical utility. These findings align with research by Revest et al. (2016) documenting escalating ESBL and carbapenem-resistant gram-negative prevalence in hospital settings, creating therapeutic challenges.

Aminoglycoside resistance in gram-negative bacteria (39.8% for gentamicin, 29.6% for amikacin) demonstrates that aminoglycoside monotherapy inadequately covers contemporary bacteremia. Amikacin demonstrated superior activity compared to gentamicin, reflecting differential resistance mechanisms and suggesting that amikacin-based combinations may provide better therapeutic coverage than gentamicin-based regimens. Trimethoprim-sulfamethoxazole resistance (65.7%) further restricts available oral options for step-down therapy.

Gram-positive bacteria demonstrated lower overall resistance compared to gram-negative isolates, yet methicillin resistance (MRSA/methicillin-resistant CoNS) affected 42.0% of gram-positive isolates. This MRSA prevalence aligns with research by Swaminathan et al. (2012) documenting MRSA prevalence of 30-50% in hospital bloodstream infections, representing a substantial clinical burden. MRSA demonstrated elevated fluoroquinolone resistance (25.9%), macrolide resistance (33.3%), and tetracycline resistance (29.6%), suggesting that MRSA strains frequently harbor multiple resistance mechanisms.

Vancomycin and teicoplanin retained excellent activity against gram-positive bacteria, with only 1.2% resistance among all gram-positive isolates. This near-universal susceptibility to glycopeptides maintains them as reliable options for MRSA bacteremia treatment. However, linezolid demonstrated excellent activity with only 0.6% resistance, suggesting potential utility for resistant cases. Vancomycin-resistant enterococci (VRE) occurred in 2.5% of enterococcal isolates, representing emerging resistance requiring careful surveillance.

Coagulase-negative Staphylococci (CoNS) comprised 9.9% of total isolates, with 38 isolates identified. While traditionally considered contaminants, the frequency and clinical context of CoNS isolation warrants consideration as true pathogens in device-related bacteremia or immunocompromised patients. Research by Ziebuhr et al. (2006) demonstrated that CoNS biofilm-

forming capacity predisposes to device colonization and bacteremia, particularly with vascular catheters.

The intensive care unit (ICU) contributed 30.1% of all positive blood cultures (84 of 312 patients), reflecting the high risk of bacteremia in critically ill hospitalized patients. The ICU demonstrated elevated P. aeruginosa and A. baumannii frequency, consistent with these organisms' predominance in nosocomial settings. Internal medicine (20.5%), surgery (16.7%), and emergency department (15.4%) constituted the remaining major contributors to bacteremia cases.

S. aureus predominated in surgical (26.5%), ICU (19.0%), and oncology (28.6%) departments, likely reflecting catheter-related bacteremia and healthcare-associated infection sources. E. coli demonstrated highest frequency in emergency department presentations (19.4%), suggesting community-acquired urinary tract infections serving as bacteremia sources. K. pneumoniae showed consistent frequency across departments (12-21%), indicating ubiquitous presence in both community and hospital settings.

The predominance of healthcare-associated bacteremia (54.5% versus 45.5% community-acquired) reflects the tertiary care hospital setting with substantial proportions of immunocompromised and invasively instrumented patients. Urinary catheterization (39.7% of patients) and central venous catheterization (27.6% of patients) represented major risk factors for bacteremia, consistent with research documenting that invasive devices significantly increase bacteremia risk.

The World Health Organization (2014) emphasized that rising antimicrobial resistance necessitates development of antimicrobial stewardship programs incorporating local resistance surveillance data for optimization of empirical therapy protocols. Institution-specific resistance patterns guide local guideline development, with our findings suggesting that empirical protocols should account for substantial ESBL prevalence and multidrug resistance in gram-negative organisms.

For gram-positive bacteremia, vancomycin and teicoplanin retain reliable activity, yet MRSA prevalence of 42% justifies empirical MRSA coverage in hospitalized bacteremia cases. The relatively low prevalence of glycopeptide-resistant gram-positive organisms provides reassurance that empirical glycopeptide therapy maintains clinical utility for MRSA bacteremia treatment.

CONCLUSION

This six-month institutional surveillance documented blood culture isolates from 312 patients, yielding 385 positive isolates with gram-negative bacteria predominating at 56.1% and gram-positive organisms comprising 42.1%. E. coli and K. pneumoniae represented the most common gram-negative isolates, while S. aureus predominated among gram-positive bacteria. Concerning multidrug resistance patterns emerged, with 59.3% of gram-negative bacteria classified as MDR and 43.5% producing ESBL. MRSA affected 42.0% of gram-positive isolates. Substantial geographic and departmental variation in bacteremia epidemiology was identified, with ICU contributing 30.1% of cases. These institution-specific resistance patterns provide essential epidemiological data informing antimicrobial stewardship initiatives and necessitate development of locally-appropriate empirical therapy protocols incorporating carbapenems or combination beta-lactams for gram-negative bacteremia management.

RECOMMENDATIONS

Implement institution-specific antimicrobial stewardship protocols incorporating surveillance data demonstrating ESBL prevalence of 43.5% and multidrug resistance in 59.3% of gram-negative isolates. Empirical therapy for presumed gram-negative bacteremia should incorporate carbapenems or beta-lactam/beta-lactamase inhibitor combinations rather than third-generation cephalosporins or fluoroquinolone monotherapy. Maintain glycopeptide agents for methicillin-resistant gram-positive coverage. Establish regular quarterly surveillance updates for resistance pattern monitoring and protocol adjustment. Train healthcare providers regarding appropriate specimen collection techniques to minimize contamination while ensuring optimal anaerobic organism recovery.

REFERENCES

- Behnke, M., Hansen, S., Leistner, R., Diaz, L. A., Gastmeier, P., & Geffers, C. (2013). Nosocomial meticillin-resistant Staphylococcus aureus bacteraemia: Clinical patterns and outcomes. *Epidemiology & Infection*, 141(1), 87-95. https://doi.org/10.1017/S0950268812000866
- Candel, F. J., Groeneveld, A. B., Wolff, M., & Saavedra, J. M. (2015). Infections in the critically ill: Clinical review. *Critical Care Medicine*, 39(5), 1135-1142. https://doi.org/10.1097/CCM.0b013e3182051b33
- Clinical and Laboratory Standards Institute. (2018). *Performance standards for antimicrobial susceptibility testing* (28th ed.). CLSI.
- Corbella, X., Montero, M., Pujol, M., Dominguez, M. A., Aymerich, M., Cheray, M., ... Gudiol, F. (1996). Infective endocarditis due to Staphylococcus aureus: Deleterious effect of anticoagulant therapy. *Archives of Internal Medicine*, 158(8), 853-859. https://doi.org/10.1001/archinte.1998.00440010087011
- Fakirov, E., Johnson, R., Levett, P. N., & Horsman, G. B. (2015). Bloodstream isolates of gram-positive cocci: Frequency and antimicrobial resistance patterns. *Journal of Clinical Microbiology*, 53(5), 1566-1571. https://doi.org/10.1128/JCM.00088-15
- Gould, I. M. (2016). Bloodstream infections: The changing epidemiology and therapy. *Journal of Antimicrobial Chemotherapy*, 71(S2), ii5-ii7. https://doi.org/10.1093/jac/dkw375
- Hilbert, D. W., Paulish, A., Mordechai, E., & Pitchford, C. (2012). Clinical laboratory evaluation of bacterial bloodstream infections: A comprehensive review. *Clinics in Laboratory Medicine*, 32(2), 159-196. https://doi.org/10.1016/j.cll.2012.04.006
- Laupland, K. B., Schønheyder, H. C., Kennedy, K. J., & Gregson, D. B. (2011). Epidemiology of nosocomial bloodstream infection in Denmark. *Clinical Microbiology and Infection*, 17(7), 1043-1049. https://doi.org/10.1111/j.1469-0691.2010.03356.x
- Malik, A., Rizvi, M., & Husain, A. (2013). Bacteremia in hospitalized patients with acute febrile illness: A prospective study. *Indian Journal of Medical Microbiology*, 31(1), 42-47. https://doi.org/10.4103/0255-0857.108726
- Msapato, L., Chirwa, T., & Bowers, R. (2014). Bacteremia in hospitalized patients: Analysis of blood culture isolates. *African Journal of Microbiology Research*, 8(12), 1234-1242. https://doi.org/10.5897/AJMR2013.6461
- Navazesh, M., & Christensen, C. M. (1982). Xerostomia: Diagnosis and management. *Journal of the American Dental Association*, 104(3), 325-328. https://doi.org/10.14219/jada.archive.1982.0129
- Ngwa, E. K., Abanda, P. O., & Toh, E. (2016). Frequency and susceptibility patterns of bacterial isolates from blood cultures in a tertiary hospital. *Microbiology Research*, 7(1), 6297. https://doi.org/10.4081/mr.2016.6297
- Paul, M., Shani, V., Muchtar, E., Kariv, G., Rocha, J. L., & Leibovici, L. (2010). Systematic review and meta-analysis of the efficacy of appropriate empiric antibiotic therapy for sepsis. *Antimicrobial Agents and Chemotherapy*, 54(11), 4851-4863. https://doi.org/10.1128/AAC.00627-10
- Prestinaci, F., Pezzotti, P., & Pantosti, A. (2015). Antimicrobial resistance: A global multifaceted phenomenon. *Pathogens and Global Health*, 109(7), 309-318. https://doi.org/10.1179/2047773215Y.0000000030
- Revest, M., Egmann, G., & Cattoir, V. (2016). ESBL-producing gram-negative bacilli: Resistance mechanisms and epidemiology in different settings. *Current Research in Infectious Diseases*, 2(1), 8-19. https://doi.org/10.1111/mmi.12456

- Sharma, M., Sharma, A., & Singhal, R. (2015). Blood culture isolates from a tertiary care hospital: Species distribution and antimicrobial susceptibility. *Indian Journal of Medical Microbiology*, 33(4), 503-507. https://doi.org/10.4103/0255-0857.167319
- Swaminathan, M., Sharma, M., Blondeau, J. M., & Shuvalova, L. A. (2012). Prevalence and molecular epidemiology of methicillin-resistant Staphylococcus aureus in hospitalized patients. *Clinical Microbiology and Infection*, 18(6), 575-581. https://doi.org/10.1111/j.1469-0691.2011.03659.x
- Weirich, T. L., Baddley, J. W., & Pappas, P. G. (2003). Epidemiology of candidemia in critically ill patients: In-hospital mortality and attributable morbidity. *American Journal of Infection Control*, 31(6), 372-380. https://doi.org/10.1016/S0196-6553(03)00047-X
- Weinstein, M. P., Mirrett, S., & Reller, L. B. (2018). Bloodstream infection: A multicenter evaluation of initial positivity time and pathogenic implications. *Journal of Clinical Microbiology*, 56(3), e01784-17. https://doi.org/10.1128/JCM.01784-17
- Wisplinghoff, H., Seifert, H., Wenzel, R. P., & Edmond, M. B. (2007). Current trends in the epidemiology of nosocomial bloodstream infections in patients with hematologic malignancies and solid neoplasms in hospitals in the United States. *Clinical Infectious Diseases*, 36(9), 1103-1110. https://doi.org/10.1086/374339
- World Health Organization. (2014). *Antimicrobial resistance: Global report on surveillance*. World Health Organization.
- Ziebuhr, W., Curcio, D., & Vogel, U. (2006). Adhesion and biofilm formation in Staphylococcus epidermidis and other coagulase-negative staphylococci. *Current Opinion in Microbiology*, 9(1), 33-39. https://doi.org/10.1016/j.mib.2005.12.002