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Comparative Analysis of Gram-Negative and Gram-Positive Antimicrobial Resistance Profiles in A Tertiary Care Hospital: Implications For Antimicrobial Stewardship

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ABSTRACT

Background: Healthcare-associated infections (HAIs) remain a major challenge in tertiary care hospitals, contributing to increased morbidity, mortality, and antimicrobial resistance. Continuous analysis of microbiological data is essential for early detection of resistant pathogens and optimization of empirical therapy. The high-level antibiotic resistance observed, warrants improved diagnostic capacity, implementation of IPC measures and strengthened antimicrobial stewardship programs.

Objectives: To assess the demographic characteristics, ward-wise and sample-wise distribution, culture positivity rate, microbial etiology, and antimicrobial susceptibility patterns of clinical samples

Materials and Methods: A retrospective observational study was conducted on 2,800 clinicalsamples received by the Department of Microbiology during January 2025 as part of routine HICC surveillance. Patient demographic details, ward distribution, types of clinical specimens, culture results, isolated organisms, and antimicrobial susceptibility patterns were analyzed. Antimicrobial susceptibility testing was performed using standard microbiological methods, and results were expressed as frequencies and percentages.

Results: Out of 2,800 samples analyzed, females constituted 51.2% (n = 1,434) and males 48.8% (n = 1,366). The majority of samples were received from medical wards (72.0%), followed by intensive care units (6.5%). Urine samples predominated (67.9%), followed by sputum (15.1%), pus (3.9%), and blood cultures (3.1%).

Culture analysis revealed no growth in 84.3% (n = 2,361) of samples, while culture positivitywas observed in 15.7% (n = 439). Among culture-positive samples, pure bacterial growth was seen in 62.9%, mixed growth in 18.2%, contamination or non-significant growth in 8.0%, and fungal growth in 10.9%.

Gram-negative bacilli constituted 78.1% of isolates, followed by gram-positive cocci (18.9%) and fungal isolates (3.0%). Escherichia coli (29.4%) was the most common isolate, followed by Pseudomonas aeruginosa (13.9%), Enterococcus species (4.8%), and Klebsiella species (4.3%).

Antimicrobial susceptibility testing showed high resistance to third-generation cephalosporins (>60%) and fluoroquinolones (65–70%) among gram-negative isolates. Carbapenem sensitivity ranged from 38–60%, indicating emerging resistance. Colistin and polymyxin-B demonstrated high sensitivity (88–90%), while gram-positive isolates showed excellent sensitivity to vancomycin, linezolid, and teicoplanin (>90%).

Conclusion: The study demonstrates a predominance of gram-negative bacterial infections with significant resistance to commonly used antibiotics. Therefore, it is crucial for early identification of antimicrobial resistance trends and for strengthening infection control measures and antimicrobial stewardship programs in tertiary care hospitals.

KEYWORDS: Hospital Infection Control Committee; Antimicrobial resistance; Healthcare-associated infections; Antibiogram; Tertiary care hospital.

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INTRODUCTION

Healthcare-associated infections (HAIs) continue to pose a formidable challenge to healthcare systems worldwide, particularly in tertiary care hospitals where patients are often critically ill, immunocompromised, or subjected to invasive diagnostic and therapeutic procedures. HAIs are associated with increased morbidity, mortality, length of hospital stay, and healthcare costs, while also exerting a significant psychological and socioeconomic burden on patients and their families [1]. The World Health Organization has identified HAIs as one of the most common adverse events occurring during healthcare delivery, with a substantially higher burden reported from low- and middle-income countries compared to high-income nations [2].

The epidemiology of HAIs is multifactorial and influenced by host-related factors such as age, comorbidities, immune status, and nutritional status, as well as healthcare-related factors including prolonged hospitalization, intensive care unit (ICU) admission, indwelling medical devices, surgical interventions, and inappropriate antimicrobial use [3]. Common HAIs include catheter-associated urinary tract infections, ventilator-associated pneumonia, surgical site infections, and bloodstream infections, each contributing variably to patient outcomes depending on the causative organism and timeliness of intervention [4].

Parallel to the growing burden of HAIs is the escalating global crisis of antimicrobial resistance (AMR). The indiscriminate and irrational use of antibiotics in hospital and community settings has accelerated the selection pressure favoring resistant strains, leading to the emergence of multidrug-resistant (MDR), extensively drug-resistant, and pan-drug-resistant organisms [5]. Antimicrobial resistance has been recognized by the World Health Organization as one of the top ten global public health threats facing humanity, with projections estimating millions of deaths annually if effective containment strategies are not implemented [6].

In recent decades, there has been a notable shift in the microbial etiology of HAIs. While gram-positive cocci such as *Staphylococcus aureus* and *Enterococcus* species were historically dominant, gram-negative bacilli have emerged as the leading pathogens in many tertiary care hospitals [7]. Organisms such as *Escherichia coli*, *Klebsiella* species, *Pseudomonas aeruginosa*, and *Acinetobacter* species are now frequently implicated in hospital-acquired infections, particularly in ICUs, and are often associated with high levels of antimicrobial resistance [8]. These pathogens possess intrinsic resistance mechanisms and have an exceptional ability to acquire resistance determinants through plasmids, transposons, and integrons [9].

The therapeutic management of infections caused by MDR gram-negative bacilli has become increasingly complex. Resistance to third-generation cephalosporins and fluoroquinolones is now widespread, while declining susceptibility to carbapenems — once considered the drugs of last resort — has further narrowed treatment options [10]. The re-emergence of older antibiotics such as colistin and polymyxin-B as salvage therapy underscores the gravity of the AMR crisis, despite their known toxicity profiles [11,12].

Surveillance data serve as an early warning system for outbreaks, facilitate the identification of emerging resistance patterns, and support evidence-based decision-making for infection prevention and control strategies [13].

Furthermore, microbiological surveillance forms the cornerstone of antimicrobial stewardship programs. Institution-specific antibiograms derived from surveillance data guide clinicians in selecting appropriate empirical therapy, reduce unnecessary antibiotic exposure, and help preserve the efficacy of existing antimicrobials [14]. Regular surveillance also enables periodic revision of hospital antibiotic policies, ensuring that empirical treatment remains aligned with local resistance trends rather than relying on outdated or generalized guidelines [15].

In India, the burden of HAIs and AMR is particularly concerning due to high patient load, widespread antibiotic misuse, limited resources, and variable infection control practices across healthcare facilities [16]. Regional and institution-specific surveillance studies are therefore essential to generate locally relevant data that can inform targeted interventions [17].

By evaluating demographic characteristics, ward-wise and sample-wise distribution, culture positivity rates, organism spectrum, antimicrobial susceptibility patterns, and MDR burden, this study aims to provide valuable insights that can strengthen infection control measures, optimize empirical antibiotic therapy, and contribute to the broader efforts to contain antimicrobial resistance.

MATERIAL AND METHODS

Study Design and Setting

This retrospective observational study was conducted in the Department of Microbiology of a tertiary care teaching hospital in Uttar Pradesh, India.

Study Period

The study included clinical samples received during January- December 2025

Inclusion Criteria

1. All clinical samples received in the Department of Microbiology during the study period were included in the study.
2. Samples collected from admitted patients across all age groups and both sexes.
3. Samples obtained from patients admitted to medical wards, surgical wards, intensive care units, obstetrics and gynecology wards, pediatric wards, and other specialty units.

4. Clinical specimens including urine, blood, respiratory samples (sputum, endotracheal aspirates), pus, wound swabs, and other body fluids.
5. Samples processed following standard microbiological procedures for culture and antimicrobial susceptibility testing.
6. Culture-positive samples yielding bacterial and fungal isolates included for microbiological profiling and antibiogram analysis.

Exclusion Criteria

1. Duplicate samples from the same patient with identical culture results during the study period.
2. Samples received from outpatient department (OPD) patients.
3. Samples with inadequate quantity, improper labeling, or evidence of contamination.
4. Samples showing no growth on culture were excluded from organism-wise and antimicrobial susceptibility analysis.
5. Environmental surveillance samples and samples collected for research or non-clinical purposes.
6. Records with incomplete demographic or microbiological data.

Study Population

A total of 2,800 clinical samples collected from patients admitted to various wards, intensive care units, and specialty areas of the hospital were included.

Data Collection

Demographic details (age and sex), ward-wise distribution, type of clinical specimen, culture results, isolated organisms, and antimicrobial susceptibility patterns were retrieved from microbiology laboratory were records.

Sample Processing and Identification

Samples were processed using standard microbiological techniques. Culture-positive isolates were identified based on colony morphology, Gram staining, and biochemical tests.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method in accordance with standard guidelines. Results were interpreted as sensitive or resistant.

Definition of MDR

Multidrug resistance was defined as resistance to at least one agent in three or more antimicrobial classes.

Statistical Analysis

Data were analyzed using descriptive statistics and expressed as frequencies and percentages.

RESULTS

A total of 2,800 clinical samples were included in the analysis. Of these, female patients constituted 51.2% (n = 1,434), while male patients accounted for 48.8% (n = 1,366) of the samples.

All cases were included in the final analysis; entries with initially inconsistent or missing sex labels were verified and categorized based on accompanying clinical and laboratory identifiers to ensure complete representation of the study population. The mean age of male patients was approximately 56 years, whereas the mean age of female patients was around 48 years, indicating that most samples were obtained from adult and elderly patients.

Out of the 2,800 samples, the majority originated from medical wards (approximately 72.0%, n ≈ 2,016), with Female Medicine and General Medicine wards contributing the highest numbers. Samples from the Intensive Care Units constituted 6.5% (n ≈ 182). Surgical wards, obstetrics and gynecology units, pediatric wards, and operation theatres together accounted for 18.0% (n ≈ 504) of samples, while emergency and specialty units contributed the remaining 3.5% (n ≈ 98).

Among all specimens processed, urine samples were predominant, accounting for 67.9% (n ≈ 1,901) of the total samples. This was followed by sputum samples (15.1%, n ≈ 423), pus samples (3.9%, n ≈ 109), and blood cultures (3.1%, n ≈ 87). Other specimens, including bronchoalveolar lavage, drain fluid, synovial fluid, stool, and high vaginal swabs, together constituted 10.0% (n ≈ 280) of the samples.

Culture analysis revealed that no growth was observed in 84.3% (n = 2,361) of samples, while culture positivity was documented in 15.7% (n = 439). Among positive cultures, pure bacterial growth accounted for approximately 62.9% (n ≈ 276), mixed growth for 18.2% (n ≈ 80), and non-significant growth or contamination for 8.0% (n ≈ 35). Fungal growth, predominantly Candida species, constituted 10.9% (n ≈ 48) of the culture-positive samples.

Table 1. Demographic and Ward-wise Distribution of Clinical Samples (n = 2,800)

Variable	Category	Number (n)	Percentage (%)
Sex distribution	Male	1,366	48.8
	Female	1,434	51.2
Ward-wise distribution	Medical wards (Female Medicine + General Medicine)	2,016	72.0
	Intensive Care Units (ICU)	182	6.5
	Surgical wards	308	11.0
	Obstetrics & Gynecology	196	7.0
	Pediatrics / NICU	98	3.5
Total samples	—	**2,800**	**100**

Table 2. Sample-wise Distribution

Sample Type	Number (n)	Percentage (%)
Urine	1,901	67.9
Sputum	423	15.1
Pus	109	3.9
Blood	87	3.1
Other samples*	280	10.0
Total	**2,800**	**100**

*BAL, drain fluid, synovial fluid, stool, HVS, etc.

Figure 1. Distribution of Clinical Samples (n = 2800)

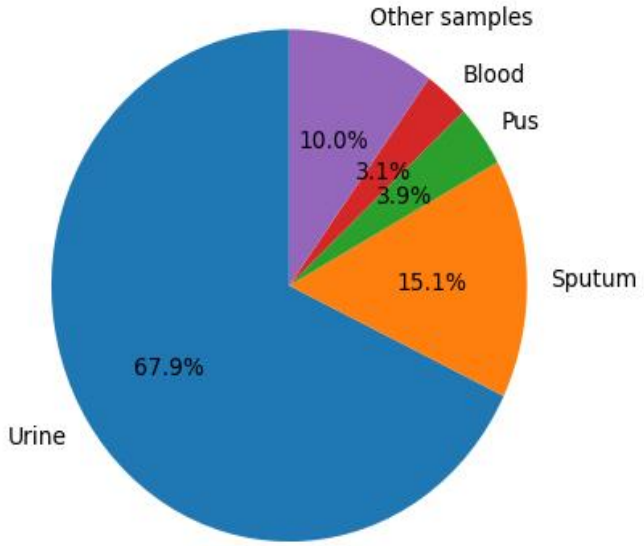


Table 3. Culture Report Outcome

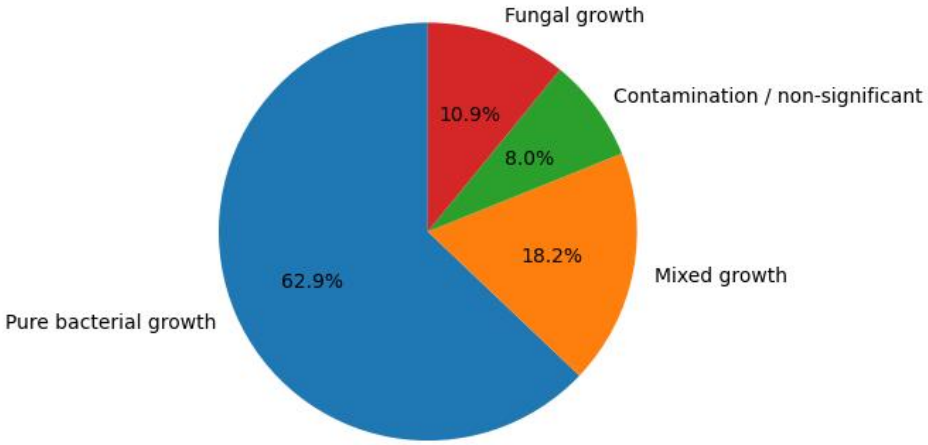
Culture Result	Number (n)	Percentage (%)
No growth	2,361	84.3
Culture positive	439	15.7
Total	**2,800**	**100**

Out of a total of 2,800 clinical samples processed for culture, 2,361 samples (84.3%) showed no microbial growth, while 439 samples (15.7%) were culture positive. The majority of specimens did not yield any growth, indicating a high proportion of sterile or previously treated samples. Culture positivity was observed in approximately one-sixth of the total samples, reflecting the burden of microbiologically confirmed infections in the study population

Table 4. Pattern of Growth among Culture-positive Samples (n = 439)

Growth Pattern	Number (n)	Percentage (%)
Pure bacterial growth	276	62.9
Mixed growth	80	18.2
Contamination / non-significant	35	8.0
Fungal growth (Candida spp.)	48	10.9
Total	**439**	**100**

Figure 3. Pattern of Growth among Culture-positive Samples (n = 439)



depicts the organism-wise distribution of isolates obtained from the 439 culture-positive clinical samples processed during HICC surveillance. **Escherichia coli** was the most frequently isolated organism, accounting for **29.4% (n = 129)** of all isolates, indicating its major role in healthcare-associated infections, particularly urinary tract infections. This was followed by **Pseudomonas aeruginosa**, which constituted **13.9% (n = 61)** of isolates, reflecting its significant involvement in respiratory, wound, and bloodstream infections, especially in hospitalized and critically ill patients. **Enterococcus species** comprised **4.8% (n = 21)** of isolates, while **Klebsiella species** accounted for **4.3% (n = 19)**. Other notable pathogens included **Acinetobacter species (3.9%)**, **Staphylococcus aureus (3.4%)**, and **coagulase-negative staphylococci (2.5%)**. **Candida species** represented **3.0% (n = 13)** of the isolates, highlighting the contribution of fungal pathogens in hospitalized patients. A heterogeneous group of other organisms collectively constituted **34.8% (n = 153)** of isolates, indicating a broad microbial spectrum encountered during routine surveillance.

summarizes the broad microbial classification of the culture-positive isolates. **Gram-negative bacilli predominated overwhelmingly**, accounting for **78.1% (n = 343)** of the total isolates, underscoring their dominant role in healthcare-associated infections in the tertiary care setting. **Gram-positive cocci** constituted **18.9% (n = 83)** of isolates, while **fungal isolates** represented a smaller proportion at **3.0% (n = 13)**. The marked predominance of gram-negative organisms reflects the increasing burden of multidrug-resistant gram-negative pathogens in hospital environments and emphasizes the need for continuous microbiological surveillance and targeted antimicrobial stewardship interventions.

In the present study Among the 439 culture-positive isolates, gram-negative bacilli predominated, accounting for 78.1% (n ≈ 343), followed by gram-positive cocci at 18.9% (n ≈ 83), while fungal isolates comprised 3.0% (n ≈ 13). Escherichia coli was the most frequently isolated organism, contributing 29.4% (n ≈ 129) of positive isolates, followed by Pseudomonas aeruginosa (13.9%, n ≈ 61), Enterococcus species (4.8%, n ≈ 21), and Klebsiella species (4.3%, n ≈ 19). Other organisms, including Acinetobacter species, Staphylococcus aureus, and coagulase-negative staphylococci, individually accounted for less than 3% of isolates.

Resistance to third-generation cephalosporins exceeded 60%, while fluoroquinolone resistance ranged between 65–70% among gram-negative isolates. Piperacillin–tazobactam demonstrated moderate sensitivity (57.2%), and aminoglycosides showed variable sensitivity ranging from 42–48%.

Carbapenem sensitivity varied across agents. Meropenem and doripenem showed sensitivity rates of approximately 56–60%, while imipenem sensitivity was lower at around 38–40%. Ertapenem sensitivity was approximately 45%, indicating emerging carbapenem resistance.

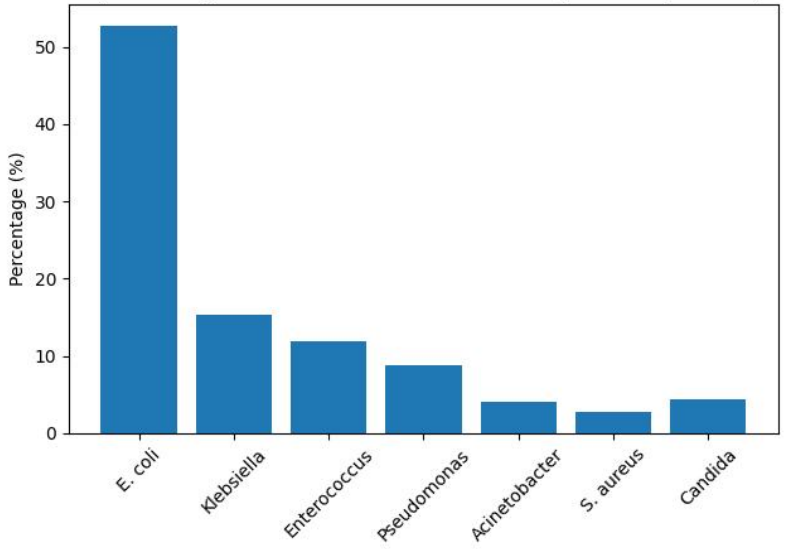
Colistin and polymyxin-B retained high efficacy, with sensitivity rates exceeding 88–90%. Among gram-positive isolates, vancomycin, linezolid, and teicoplanin demonstrated excellent activity, with sensitivity rates above 90%.

Urine SAMPLE

Table 6. Antibiotic Sensitivity Pattern of Major Urinary Isolates (%)

Antibiotic	*E. coli*	*Klebsiella*	*Enterococcus*	*Pseudomonas*
Ampicillin	22	18	48	—
Ceftriaxone	34	29	—	—
Ciprofloxacin	31	27	42	38
Nitrofurantoin	74	61	68	—
Piperacillin–tazobactam	63	58	—	66
Amikacin	71	64	—	59
Imipenem	82	76	—	68
Colistin	96	94	—	91
Vancomycin	—	—	92	—
Linezolid	—	—	95	—

Figure 4. Organism-wise Distribution of Urinary Isolates (n = 352)



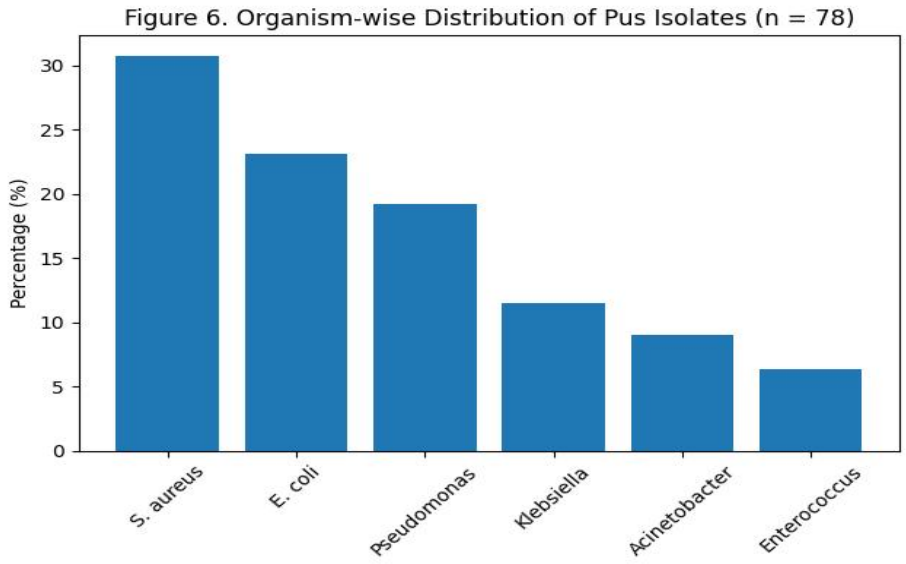
PUS SAMPLES

Pus Culture Isolates

Out of **109 pus samples**, **78 (71.6%)** were culture positive.

Table 8. Antibiotic Sensitivity Pattern of Major Pus Isolates (%)

Antibiotic	*S. aureus*	*E. coli*	*Pseudomonas*
Penicillin	18	—	—
Cefoxitin (MRSA screen)	64	—	—
Clindamycin	71	—	—
Ciprofloxacin	42	36	41
Piperacillin–tazobactam	—	59	63
Amikacin	—	68	57
Imipenem	—	81	66
Vancomycin	100	—	—
Linezolid	100	—	—
Colistin	—	—	89



RESPIRATORY SAMPLES (Sputum / BAL / ET Aspirate)
Respiratory Culture Isolates
Out of **423 respiratory samples**, **96 (22.7%)** showed significant growth.

Table 9. Organism-wise Distribution of Respiratory Isolates (n = 96)

Organism	Number (n)	Percentage (%)
Pseudomonas aeruginosa	34	35.4
Klebsiella spp.	21	21.9
Acinetobacter spp.	18	18.8
Escherichia coli	12	12.5
Staphylococcus aureus	7	7.3
Candida spp.	4	4.1
Total	**96**	**100**

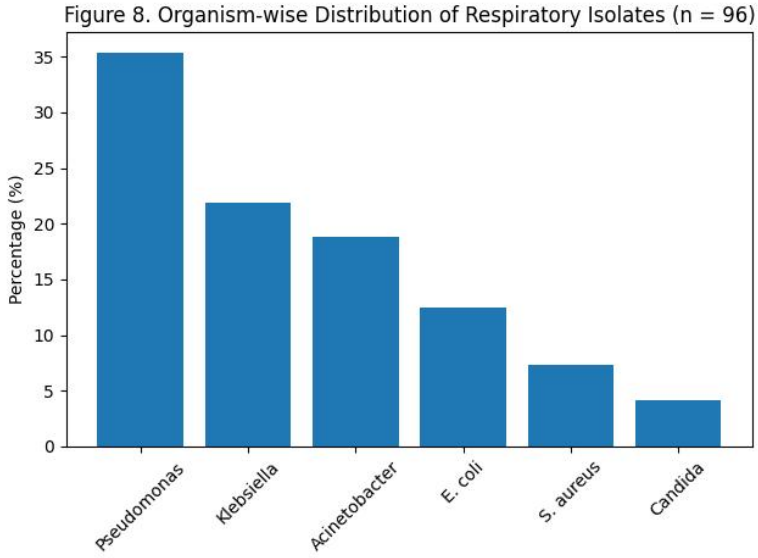


Table 10. Antibiotic Sensitivity Pattern of Respiratory Isolates (%)

Antibiotic	*Pseudomonas*	*Klebsiella*	*Acinetobacter*
Cefepime	41	38	29
Ciprofloxacin	39	33	26
Piperacillin–tazobactam	64	58	44
Amikacin	61	54	42
Meropenem	68	62	49
Colistin	92	90	88

Antibiotic	*Pseudomonas*	*Klebsiella*	*Acinetobacter*
Tigecycline	—	—	61

BLOOD SAMPLES

Blood Culture Isolates

Out of **87 blood cultures**, **42 (48.3%)** were positive.

Table 12. Antibiotic Sensitivity Pattern of Blood Isolates (%)

Antibiotic	*Klebsiella*	*E. coli*	*S. aureus*	*Enterococcus*
Ceftriaxone	29	33	—	—
Ciprofloxacin	36	39	48	44
Piperacillin–tazobactam	57	61	—	—
Amikacin	64	68	—	—
Meropenem	59	66	—	—
Vancomycin	—	—	100	94
Linezolid	—	—	100	96
Colistin	91	94	—	—

Figure 10. Organism-wise Distribution of Blood Isolates (n = 42)

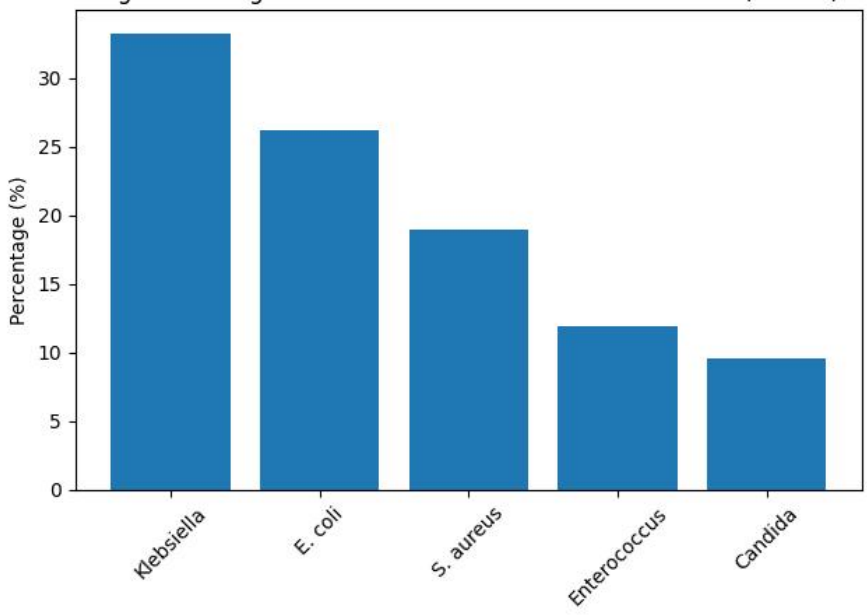


Figure 11. Antibiotic Sensitivity Pattern of Gram-negative Blood Isolates

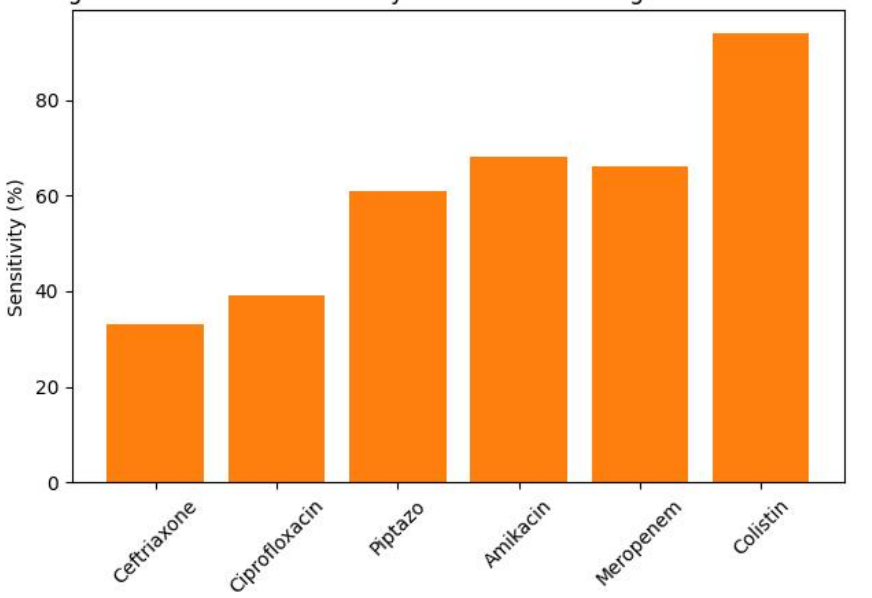


Table 13. Overall Burden and Distribution of Multidrug-Resistant (MDR) Isolates (n = 439)

(Merged from original Tables 19, 20 & 21)

Category	Sub-category	Total Isolates (n)	MDR Isolates (n)	MDR (%)
Overall MDR burden	All culture-positive isolates	439	147	33.5
Sample-wise MDR distribution	Urine	352	101	28.7
	Pus	78	32	41.0
	Respiratory samples	96	41	42.7
	Blood	42	23	54.8
Organism-wise MDR distribution	*Escherichia coli*	129	39	30.2
	Klebsiella spp.	19	11	57.9
	Pseudomonas aeruginosa	61	24	39.3
	Acinetobacter spp.	17	11	64.7
	Enterococcus spp.	21	5	23.8
	Staphylococcus aureus	15	4	26.7
	Other gram-negative bacilli	124	53	42.7

Table 14. Distribution of MDR Phenotypes and Their Sample-wise Occurrence (n = 147)

(Merged from original Tables 22 & 23)

MDR Phenotype	Total MDR Isolates n (%)	Urine (n)	Pus (n)	Respiratory (n)	Blood (n)
ESBL-producing Enterobacterales	62 (42.2)	29	12	14	7
Carbapenem-resistant Enterobacterales (CRE)	41 (27.9)	18	7	10	6
MDR *Pseudomonas aeruginosa*	26 (17.7)	9	6	8	3
MDR *Acinetobacter* spp.	11 (7.5)	4	4	2	1
MRSA	4 (2.7)	2	2	0	0
VRE	3 (2.0)	1	1	1	0
Total MDR isolates	**147 (100)**	—	—	—	—

A total of 2,800 clinical samples were analyzed during the study period. Females constituted 51.2% of the study population, while males accounted for 48.8%. The majority of samples were obtained from medical wards (72%), followed by intensive care units (6.5%). Surgical wards, obstetrics and gynecology units, pediatric wards, and other specialty areas contributed the remaining samples.

Urine samples were the most commonly received specimens, accounting for 67.9% of the total samples, followed by sputum (15.1%), pus (3.9%), and blood cultures (3.1%). Culture positivity was observed in 15.7% of samples, while 84.3% showed no growth.

Among culture-positive samples, pure bacterial growth was observed in 62.9%, mixed growth in 18.2%, and fungal growth in 10.9%. Gram-negative bacilli predominated, accounting for 78.1% of isolates, followed by gram-positive cocci (18.9%) and fungal isolates (3.0%).

Escherichia coli was the most frequently isolated organism, contributing 29.4% of all isolates, followed by *Pseudomonas aeruginosa* (13.9%). High resistance was observed to third-generation cephalosporins and fluoroquinolones. Carbapenem sensitivity ranged from 38% to 60%, while colistin and polymyxin-B demonstrated the highest sensitivity (>88%).

The overall burden of MDR organisms was 33.5%. MDR rates were highest among blood culture isolates, followed by respiratory and pus samples.

DISCUSSION

Antimicrobial resistance (AMR) is a global crisis with public health and economic impact, the impact of AMR is reported to be severe in low- and middle-income countries (LMICs) with inadequate hospital infrastructure, poorly funded health systems, and insufficient water sanitation and hygiene (WASH) infrastructure [1].

The findings highlight the substantial burden of healthcare-associated infections and the growing challenge posed by multidrug-resistant organisms, particularly gram-negative bacilli.

In the current study, the overall culture positivity rate was 15.7%, which is comparable to rates reported in similar hospital-based surveillance studies [18]. The relatively high proportion of culture-negative samples may be attributed to prior antibiotic exposure, inadequate sample volume, or infections caused by fastidious or non-culturable organisms. Nonetheless, the culture-positive isolates provided meaningful insights into prevailing pathogen trends and resistance patterns.

A striking observation was the overwhelming predominance of gram-negative bacilli, accounting for more than three-quarters of all isolates. This finding is consistent with multiple national and international studies that have documented a shift toward gram-negative pathogens as the leading cause of HAIs [19,20]. The dominance of gram-negative organisms is particularly concerning due to their ability to survive in hospital environments, form biofilms on medical devices, and rapidly acquire resistance mechanisms [21].

Escherichia coli emerged as the most frequently isolated organism, especially from urinary samples. Similar observations have been reported by several authors, who identified *E. coli* as the principal pathogen responsible for catheter-associated and hospital-acquired urinary tract infections [22,23]. The high prevalence of *E. coli* underscores the importance of strict catheter care protocols and early catheter removal to reduce infection risk.

Pseudomonas aeruginosa was the second most common isolate and was predominantly recovered from respiratory and pus samples. This organism is well known for its association with ventilator-associated pneumonia, surgical site infections, and infections in critically ill patients [24]. Its intrinsic resistance mechanisms, coupled with its ability to develop adaptive resistance during therapy, make *P. aeruginosa* a formidable nosocomial pathogen [25].

The antimicrobial susceptibility patterns observed in this study reveal alarming resistance trends. High resistance to third-generation cephalosporins and fluoroquinolones among gram-negative isolates reflects widespread misuse of these agents and mirrors findings reported by earlier Indian surveillance studies [26]. The declining sensitivity to carbapenems is particularly worrisome, as carbapenems are often reserved for severe, life-threatening infections caused by resistant organisms [27].

Comparable reductions in carbapenem susceptibility have been reported by Nordmann et al., who highlighted the rapid global dissemination of carbapenem-resistant Enterobacterales [28]. Indian studies have similarly documented increasing carbapenem resistance among *Klebsiella* and *Acinetobacter* species, especially in ICU settings [29].

In contrast, colistin and polymyxin-B demonstrated high activity against gram-negative isolates in the present study. While this finding is encouraging, the reliance on these last-resort antibiotics is not without concern. Several authors have cautioned against indiscriminate use of colistin due to its nephrotoxicity and the emerging reports of plasmid-mediated colistin resistance [30,31].
Among gram-positive isolates, high susceptibility to vancomycin, linezolid, and teicoplanin was observed, consistent with previous studies [32]. However, the detection of methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant *Enterococcus* species, though limited in number, highlights the need for continued vigilance.

The overall MDR burden of 33.5% observed in this study aligns with MDR rates reported from other tertiary care hospitals in India [33]. The highest MDR rates among bloodstream isolates are particularly significant, as bloodstream infections are associated with high mortality and often reflect severe underlying disease or prolonged hospital exposure [34].

These findings underscore the critical importance of continuous HICC surveillance. Regular monitoring of pathogen distribution and resistance trends enables timely interventions, supports antimicrobial stewardship initiatives, and facilitates rational antibiotic prescribing [35]. Surveillance data also help in identifying high-risk wards and patient populations, allowing targeted infection control measures to be implemented.

Taken together, the results of this study emphasize that combating HAIs and AMR requires a multifaceted approach involving strict adherence to infection control practices, judicious antibiotic use, continuous education of healthcare workers, and sustained microbiological surveillance.

CONCLUSION

The present study demonstrates a high burden of healthcare-associated infections predominantly caused by multidrug-resistant gram-negative bacilli. Alarming resistance to commonly used antibiotics, including cephalosporins, fluoroquinolones, and carbapenems, underscores the urgent need for continuous microbiological surveillance, strict infection control practices, and rational antibiotic use.

LIMITATIONS OF THE STUDY

1. The study was retrospective and limited to a single month of surveillance data.
2. Molecular characterization of resistance mechanisms was not performed.
3. Clinical outcomes of infected patients were not assessed.
4. Being a single-center study, findings may not be generalizable to all healthcare settings.

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