Microbiological Surveillance in the Intensive Care Unit of a Tertiary Care Center, Mahabodhi Medical College, Gaya, Bihar

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Abstract

Background: Intensive care units are major reservoirs of healthcare-associated infections and antimicrobial-resistant organisms. Local surveillance is essential for guiding empirical therapy and antimicrobial stewardship.

Methods: A prospective observational study was conducted over 12 months among 428 ICU patients at Mahabodhi Medical College and Hospital, Gaya, Bihar. Clinical specimens were processed using standard microbiological methods, and antimicrobial susceptibility was interpreted according to CLSI guidelines. Multidrug resistance was defined as non-susceptibility to at least one agent in three or more antimicrobial categories.

Results: Of 633 suitable specimens, 234 (37.0%) yielded clinically significant growth; 204 patients (47.7%) had at least one positive culture. Among 251 primary isolates, Gram-negative bacilli predominated (72.1%). The most frequent organisms were *Klebsiella pneumoniae* (23.1%), *Pseudomonas aeruginosa* (16.3%), *Acinetobacter baumannii* complex (14.7%), and *Escherichia coli* (12.4%). Multidrug resistance occurred in 69.3% of bacterial isolates. Carbapenem resistance was highest in *A. baumannii* complex (78.4%) and *P. aeruginosa* (56.1%). MRSA and VRE accounted for 44.8% and 5.6%, respectively.

Conclusion: ICU infections were predominantly caused by multidrug-resistant Gram-negative bacilli, highlighting the need for regular antibiogram updates and strengthened antimicrobial-stewardship and infection-control measures.

Keywords: Intensive care unit; antimicrobial resistance; multidrug resistance; antibiogram; Gram-negative bacilli

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Introduction

Infections are a major cause of morbidity and mortality among critically ill patients. Intensive care unit (ICU) patients are particularly vulnerable because of severe underlying illness, impaired host defenses, prolonged hospitalization, frequent exposure to broad-spectrum antimicrobials, and the use of invasive devices. In the international EPIC III study, more than half of ICU patients had suspected or proven infection, and infection—particularly when acquired in the ICU—was associated with increased mortality.[1] The ICU therefore represents an important setting for both the emergence and transmission of antimicrobial-resistant pathogens.

Antimicrobial resistance has become a major global health concern. A systematic analysis of data from 2019 estimated that bacterial antimicrobial resistance was associated with 4.95 million deaths and directly attributable to 1.27 million deaths worldwide.[2] The principal pathogens contributing to this burden included Escherichia coli, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, and Pseudomonas aeruginosa, several of which are also prominent causes of healthcare-associated infection.[2] These organisms overlap substantially with the ESKAPE group of pathogens, which are characterized by their capacity to persist in healthcare environments, acquire multiple resistance mechanisms, and evade commonly used antimicrobial agents.[3]

The burden of severe infection and antimicrobial resistance is especially important in India. A multicentre point-prevalence study reported a high prevalence of sepsis among adults admitted to Indian ICUs, with substantial antimicrobial exposure and mortality.[4] More recent prospective registry data have further demonstrated the considerable clinical burden of sepsis in Indian critical-care settings.[5] Factors such as

unrestricted antimicrobial availability, empirical use of broad-spectrum agents, variation in infection-control practices, and limited access to timely microbiological diagnosis contribute to the selection and dissemination of resistant organisms.[6] A multicentre study of ICU isolates from different regions of India also documented extensive resistance among Gram-negative pathogens, emphasizing the need for institution-specific surveillance rather than reliance on aggregated regional susceptibility data.[7]

Although bacterial pathogens predominate in most ICU surveillance studies, invasive fungal infections are also clinically important. Indian multicentre data have shown that ICU-acquired candidemia may occur relatively early during critical illness and is associated with considerable mortality.[8] The changing distribution of Candida species and the emergence of antifungal resistance further support the inclusion of clinically significant yeasts in ICU surveillance programmes.

Microbial distribution and antimicrobial susceptibility vary between hospitals, individual ICUs, specimen sources, patient populations, and time periods. Consequently, local cumulative antibiograms are essential for selecting appropriate empirical therapy, monitoring resistance trends, supporting antimicrobial-stewardship programmes, and identifying priorities for infection prevention and control.[9] Periodic unit-specific surveillance is particularly important in ICUs, where delayed effective therapy can adversely affect outcomes, whereas unnecessary use of broad-spectrum agents may further promote resistance.

Data describing the microbiological and antimicrobial-resistance profile of ICU patients at Mahabodhi Medical College and Hospital, Gaya, Bihar, are required to guide local therapeutic and infection-control policies. Therefore, the present study was undertaken to determine the distribution of clinically significant microbial isolates and their antimicrobial susceptibility patterns among ICU patients and to develop an institution-specific ICU antibiogram.

Materials and Methods

Study design and setting

A prospective observational study was conducted over 12 months in the intensive care unit and Department of Microbiology of Mahabodhi Medical College and Hospital, Gaya, Bihar. All consecutive ICU patients from whom one or more clinical specimens were submitted for microbiological investigation because of suspected infection were considered for inclusion.

Sample size and study population

The sample size was calculated using the single-population-proportion formula:

[n=]

where (Z) is 1.96 at a 95% confidence level, (p) is the expected prevalence, and (d) is the absolute precision.

As reliable institution-specific prevalence data are unavailable, an expected prevalence of 50% was be used to provide the maximum sample size. With a 5% absolute precision:

[n==384.16]

The minimum required sample size was calculated to be 385 patients. After accounting for approximately 10% incomplete or unusable data, the final sample size was calculated to be be 428 patients. Consecutive eligible patients were enrolled until the required sample size was achieved. All eligible patients were included .

Data and specimen collection

Demographic and clinical information, including age, sex, comorbidities, primary ICU diagnosis, referral status, prior antimicrobial exposure within 30 days, use of mechanical ventilation, central venous catheterization, urinary catheterization, duration of ICU stay, and hospital outcome, was recorded using a structured data-collection form.

Clinical specimens included blood, urine, respiratory samples, pus or wound specimens, sterile body fluids, catheter tips, and other clinically relevant samples. Specimens were collected using standard aseptic precautions and transported promptly to the microbiology laboratory. Specimen suitability was assessed before processing.

Microbiological processing

Specimens were processed using standard microbiological methods. Depending on the specimen type, samples were inoculated onto appropriate culture media and incubated under recommended conditions. Organisms were identified by colony morphology, Gram staining, conventional biochemical tests, and the VITEK 2 Compact automated identification system using appropriate GN, GP, and YST identification cards (bioMérieux, Marcy-l'Étoile, France).

Culture results were classified as clinically significant growth, non-significant growth, or no growth on the basis of specimen quality, organism identity, colony count where applicable, repeated isolation, and available clinical information. Polymicrobial growth was recorded when more than one clinically significant organism was recovered from the same specimen.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed by the Kirby–Bauer disc-diffusion method, minimum inhibitory concentration testing, and/or an automated susceptibility system, as appropriate. Results were

interpreted according to the Clinical and Laboratory Standards Institute guidelines applicable during the study period.

Extended-spectrum β-lactamase production, carbapenem resistance, methicillin resistance in *Staphylococcus aureus*, and vancomycin resistance in enterococci were identified using standard phenotypic methods. Antifungal susceptibility testing of clinically significant *Candida* isolates was performed using the VITEK 2 Compact automated system with AST-YS08 yeast susceptibility cards (bioMérieux, Marcy-l'Étoile, France). Minimum inhibitory concentrations were determined for fluconazole, voriconazole, amphotericin B, caspofungin, and micafungin and interpreted according to the CLSI criteria applicable during the study period.Multidrug resistance was defined as acquired non-susceptibility to at least one antimicrobial agent in three or more antimicrobial categories.

Outcome measures

The primary outcomes were culture positivity, distribution of clinically significant microbial isolates, and antimicrobial susceptibility patterns. Secondary outcomes included the prevalence of multidrug resistance, extended-spectrum β-lactamase production, carbapenem resistance, methicillin-resistant *S. aureus*, and vancomycin-resistant enterococci.

An ICU-specific cumulative antibiogram was prepared using the first eligible isolate of each species from each patient. Repeat isolates were excluded to avoid overrepresentation of patients with prolonged ICU stays or repeated sampling.

Statistical analysis

Data were analyzed using SPSS version 26. Continuous variables were expressed as median with interquartile range and categorical variables as frequencies and percentages; group differences were assessed using Pearson's chi-square or Fisher's exact test, with two-sided $P<0.05$ considered statistically significant. Proportions were calculated using appropriate denominators and presented with 95% Wilson confidence intervals where applicable.

Ethical considerations

The study was approved by the Institutional Ethics Committee of Mahabodhi Medical College and Hospital, Gaya, Bihar . The requirement for informed consent was waived because the study used specimens and data generated during routine clinical care.

Results

Study population and specimen profile

During the 12-month study period, 428 ICU patients were included. The median age was 61 years (IQR, 46–72), and 267 (62.4%) patients were male. Prior antimicrobial exposure within 30 days was recorded in 258 (60.3%) patients; 174 (40.7%) received mechanical ventilation, 220 (51.4%) had a central venous catheter, and 285 (66.6%) had a urinary catheter. The median ICU stay was 9 days (IQR, 6–12) (Table 1).

A total of 662 specimens were submitted; 29 (4.4%) were unsuitable, leaving 633 specimens for analysis. Clinically significant growth was detected in 234 (37.0%) specimens, while 31 (4.9%) yielded non-significant growth and 368 (58.1%) showed no growth. At the patient level, 204 (47.7%) patients had at least one clinically significant culture.

Culture positivity by specimen type

Culture positivity differed across specimen types (χ^2 = 43.77, df = 6, $p < 0.001$). The highest yields were observed for pus/wound specimens [34/57 (59.6%)], catheter tips [16/34 (47.1%)], and respiratory specimens [92/201 (45.8%)]. Blood cultures were positive in 35/158 (22.2%) suitable submissions (Table 2; Figure 1).

Microbial profile

Among the 234 clinically significant cultures, 24 (10.3%) were polymicrobial. A total of 258 clinically significant isolates were recovered; after exclusion of 7 repeat isolates, 251 primary isolates were analyzed. Gram-negative bacilli accounted for 181 (72.1%) isolates, Gram-positive bacteria for 50 (19.9%), and yeasts for 20 (8.0%). The leading organisms were *Klebsiella pneumoniae [58 (23.1%)]*, *Pseudomonas aeruginosa [41 (16.3%)]*, *Acinetobacter baumannii complex [37 (14.7%)]*, *Escherichia coli [31 (12.4%)]*, and *Staphylococcus aureus [29 (11.6%)]* (Table 3).

The broad microbial profile varied by specimen source (χ^2 = 13.56, df = 4, p = 0.009). Respiratory isolates were dominated by *P. aeruginosa* and *A. baumannii* complex [24/97 (24.7%) each], whereas *E. coli* was most frequent in urine [18/49 (36.7%)], and *K. pneumoniae* was the leading bloodstream isolate [11/36 (30.6%)].

Antimicrobial resistance

Of 231 bacterial isolates, 160 (69.3%) were multidrug resistant. MDR was present in 138/181 (76.2%) Gram-negative bacilli and 22/50 (44.0%) Gram-positive isolates. MDR prevalence differed by organism group (χ^2 = 37.93, df = 3, $p < 0.001$), reaching 66/78 (84.6%) among non-fermenting Gram-negative bacilli and 72/103 (69.9%) among Enterobacterales.

ESBL production was detected in 58/103 (56.3%) Enterobacterales, and carbapenem resistance in 83/181 (45.9%) Gram-negative bacilli. Carbapenem resistance differed across the major Gram-negative species (χ^2 = 25.10, df = 3, $p < 0.001$), with the highest prevalence in *A. baumannii* complex [29/37 (78.4%)], followed by *P. aeruginosa [23/41 (56.1%)]*. MRSA accounted for 13/29 (44.8%) *S. aureus* isolates, and VRE for 1/18 (5.6%) enterococci (Table 4; Figure 2).

Antimicrobial susceptibility patterns and ICU antibiogram

Among the four leading Gram-negative pathogens, colistin susceptibility ranged from 32/37 (86.5%) in *A. baumannii* complex to 30/31 (96.8%) in *E. coli*. Amikacin susceptibility was highest in *E. coli [26/31 (83.9%)]* and lowest in *A. baumannii* complex [12/37 (32.4%)]. Meropenem susceptibility was 23/31 (74.2%) in *E. coli*, 37/58 (63.8%) in *K. pneumoniae*, 17/41 (41.5%) in *P. aeruginosa*, and 9/37 (24.3%) in *A. baumannii* complex (Table 5).

All 29/29 (100.0%) *S. aureus* isolates were susceptible to vancomycin; susceptibility to teicoplanin and linezolid was 28/29 (96.6%) and 25/29 (86.2%), respectively. Among Candida isolates, susceptibility was 20/20 (100.0%) to micafungin, 19/20 (95.0%) to amphotericin B and caspofungin, and 18/20 (90.0%) to fluconazole (Table 6).

Table 1. Demographic and clinical characteristics of the ICU cohort (N = 428)

Characteristic	Value
Age, years	61 (46–72)
Age group: 18-39 years	59 (13.8%)
Age group: 40-59 years	143 (33.4%)
Age group: 60-79 years	171 (40.0%)
Age group: 80+ years	55 (12.9%)
Sex: Male	267 (62.4%)
Sex: Female	161 (37.6%)
Diabetes mellitus	132 (30.8%)
Hypertension	155 (36.2%)
Chronic kidney disease	42 (9.8%)
COPD/chronic lung disease	44 (10.3%)
Malignancy/immunosuppression	28 (6.5%)
No recorded comorbidity	163 (38.1%)
Referral from another facility	257 (60.0%)
Prior antimicrobial exposure (30 days)	258 (60.3%)
Mechanical ventilation	174 (40.7%)
Central venous catheter	220 (51.4%)
Urinary catheter	285 (66.6%)
ICU stay, days	9 (6–12)
Hospital outcome: transferred to ward	96 (22.4%)
Hospital outcome: discharged	253 (59.1%)
Hospital outcome: died	79 (18.5%)
Primary ICU admission diagnosis	
Sepsis or septic shock	122 (28.5%)
Severe pneumonia / ARDS	113 (26.4%)
Postoperative critical care	57 (13.3%)
Major trauma	40 (9.3%)
Stroke / neurological emergency	32 (7.5%)
Intra-abdominal sepsis / pancreatitis	28 (6.5%)
Acute kidney injury	16 (3.7%)
Acute cardiac emergency	14 (3.3%)
Diabetic ketoacidosis / metabolic emergency	6 (1.4%)

Data are n (%) unless otherwise indicated. IQR, interquartile range; ICU, intensive care unit; COPD, chronic obstructive pulmonary disease; ARDS, acute respiratory distress syndrome.

Table 2. Culture outcomes according to specimen type

Specimen type	Submitted, n	Unsuitable, n	Suitable, n	Clinically significant positive, n (%)	Non-significant growth, n (%)	No growth, n (%)
Blood	164	6	158	35 (22.2%)	10 (6.3%)	113 (71.5%)
Urine	132	7	125	46 (36.8%)	3 (2.4%)	76 (60.8%)
Respiratory	212	11	201	92 (45.8%)	13 (6.5%)	96 (47.8%)
Pus / wound	57	0	57	34 (59.6%)	3 (5.3%)	20 (35.1%)
Sterile body fluid	40	0	40	8 (20.0%)	0 (0.0%)	32 (80.0%)
Catheter tip	37	3	34	16 (47.1%)	1 (2.9%)	17 (50.0%)
Other	20	2	18	3 (16.7%)	1 (5.6%)	14 (77.8%)
Overall	662	29	633	234 (37.0%)	31 (4.9%)	368 (58.1%)

Percentages for culture outcomes use suitable specimens as the denominator. Culture positivity differed by specimen type: Pearson $\chi^2 = 43.77$, df = 6, $p < 0.001$.

Table 3. Distribution of primary clinically significant isolates according to specimen source

Organism	Respiratory, n	Blood, n	Urine, n	Pus/wound, n	Other, n	Total, n (%)
Klebsiella pneumoniae	23	11	10	9	5	58 (23.1%)
Pseudomonas aeruginosa	24	6	2	7	2	41 (16.3%)
Acinetobacter baumannii complex	24	4	1	3	5	37 (14.7%)
Escherichia coli	2	5	18	5	1	31 (12.4%)
Staphylococcus aureus	11	5	0	8	5	29 (11.6%)
Enterococcus faecalis	0	2	5	1	2	10 (4.0%)
Enterococcus faecium	0	0	4	3	1	8 (3.2%)
Enterobacter cloacae complex	4	1	1	1	1	8 (3.2%)
Candida albicans	3	0	2	0	2	7 (2.8%)
Proteus mirabilis	2	0	3	1	0	6 (2.4%)
Candida tropicalis	3	1	0	1	1	6 (2.4%)
Candida parapsilosis	1	0	2	1	2	6 (2.4%)
Coagulase-negative staphylococci	0	1	0	0	2	3 (1.2%)
Candida glabrata	0	0	1	0	0	1 (0.4%)
Total	97	36	49	40	29	251 (100.0%)

Other includes catheter tips, sterile body fluids, and other specimen types. The proportion of Gram-negative versus non-Gram-negative isolates differed across the five source categories: Pearson $\chi^2 = 13.56$, df = 4, $p = 0.009$.

Table 4. Prevalence of major antimicrobial-resistance phenotypes

Resistance phenotype or organism group	Resistant, n/N (%)	Comparison	Test statistic	p-value
MDR among all bacterial isolates	160/231 (69.3%)			
MDR among Gram-negative bacilli	138/181 (76.2%)			
Enterobacterales	72/103 (69.9%)	MDR by organism group	$\chi^2 = 37.93$ (df = 3)	<0.001
Non-fermenting Gram-negative bacillus	66/78 (84.6%)			
Staphylococci	20/32 (62.5%)			
Enterococci	2/18 (11.1%)			
ESBL-producing Enterobacterales	58/103 (56.3%)			
Klebsiella pneumoniae	35/58 (60.3%)	ESBL: K. pneumoniae vs E. coli	$\chi^2 = 1.88$ (df = 1)	0.170
Escherichia coli	14/31 (45.2%)			
Carbapenem-resistant Gram-negative bacilli	83/181 (45.9%)			
Klebsiella pneumoniae	22/58 (37.9%)	Carbapenem resistance across major species	$\chi^2 = 25.10$ (df = 3)	<0.001
Escherichia coli	7/31 (22.6%)			
Pseudomonas aeruginosa	23/41 (56.1%)			
Acinetobacter baumannii complex	29/37 (78.4%)			
Methicillin-resistant Staphylococcus aureus	13/29 (44.8%)			
Vancomycin-resistant enterococci	1/18 (5.6%)			

MDR was defined as acquired non-susceptibility to at least one agent in three or more antimicrobial categories. ESBL, extended-spectrum β-lactamase; GNB, Gram-negative bacilli; MRSA, methicillin-resistant Staphylococcus aureus; VRE, vancomycin-resistant enterococci. Pearson χ^2 tests were used for group comparisons.

Table 5. ICU antibiogram for the four most frequent Gram-negative pathogens

Antimicrobial	K. pneumoniae (n = 58)	E. coli (n = 31)	P. aeruginosa (n = 41)	A. baumannii complex (n = 37)
Piperacillin-tazobactam	27/58 (46.6%)	18/31 (58.1%)	17/41 (41.5%)	5/37 (13.5%)
Ceftriaxone	10/58 (17.2%)	11/31 (35.5%)	—	—
Cefepime	17/58 (29.3%)	13/31 (41.9%)	15/41 (36.6%)	4/37 (10.8%)
Ceftazidime	—	—	16/41 (39.0%)	4/37 (10.8%)
Amikacin	40/58 (69.0%)	26/31 (83.9%)	24/41 (58.5%)	12/37 (32.4%)
Gentamicin	36/58 (62.1%)	23/31 (74.2%)	15/41 (36.6%)	4/37 (10.8%)
Ciprofloxacin	26/58 (44.8%)	19/31 (61.3%)	16/41 (39.0%)	5/37 (13.5%)
Imipenem	38/58 (65.5%)	25/31 (80.6%)	18/41 (43.9%)	12/37 (32.4%)
Meropenem	37/58 (63.8%)	23/31 (74.2%)	17/41 (41.5%)	9/37 (24.3%)
Colistin	53/58 (91.4%)	30/31 (96.8%)	38/41 (92.7%)	32/37 (86.5%)
Trimethoprim-sulfamethoxazole	29/58 (50.0%)	16/31 (51.6%)	—	—

Antimicrobial	K. pneumoniae (n = 58)	E. coli (n = 31)	P. aeruginosa (n = 41)	A. baumannii complex (n = 37)
Nitrofurantoin	7/10 (70.0%)	15/18 (83.3%)	—	—
Fosfomycin	8/10 (80.0%)	16/18 (88.9%)	—	—
Minocycline	—	—	—	27/37 (73.0%)
Aztreonam	—	—	12/41 (29.3%)	—

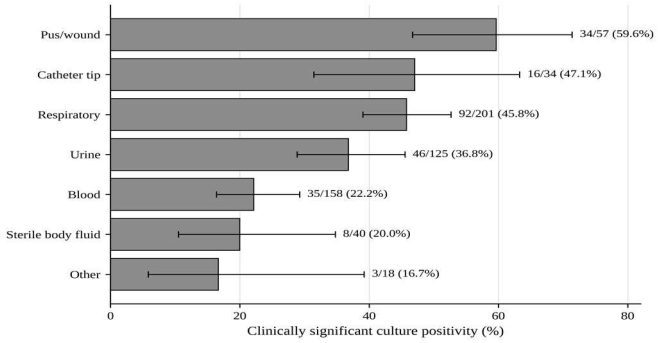
Values are susceptible isolates/tested isolates (% susceptible). Nitrofurantoin and fosfomycin results represent urinary isolates. A dash indicates that the antimicrobial was not tested for that organism.

Table 6. Selected antimicrobial susceptibility patterns of Gram-positive bacteria and Candida species

Antimicrobial	S. aureus (n = 29)	E. faecalis (n = 10)	E. faecium (n = 8)	Candida spp. (n = 20)
Cefoxitin	14/29 (48.3%)	—	—	—
Ampicillin	—	9/10 (90.0%)	3/8 (37.5%)	—
High-level gentamicin	—	7/10 (70.0%)	3/8 (37.5%)	—
Gentamicin	21/29 (72.4%)	—	—	—
Ciprofloxacin	13/29 (44.8%)	—	—	—
Erythromycin	16/29 (55.2%)	—	—	—
Clindamycin	17/29 (58.6%)	—	—	—
Doxycycline	21/29 (72.4%)	—	—	—
Trimethoprim-sulfamethoxazole	21/29 (72.4%)	—	—	—
Vancomycin	29/29 (100.0%)	8/10 (80.0%)	8/8 (100.0%)	—
Teicoplanin	28/29 (96.6%)	9/10 (90.0%)	7/8 (87.5%)	—
Linezolid	25/29 (86.2%)	9/10 (90.0%)	8/8 (100.0%)	—
Nitrofurantoin	—	3/5 (60.0%)	3/4 (75.0%)	—
Fluconazole	—	—	—	18/20 (90.0%)
Voriconazole	—	—	—	17/20 (85.0%)
Amphotericin B	—	—	—	19/20 (95.0%)
Caspofungin	—	—	—	19/20 (95.0%)
Micafungin	—	—	—	20/20 (100.0%)

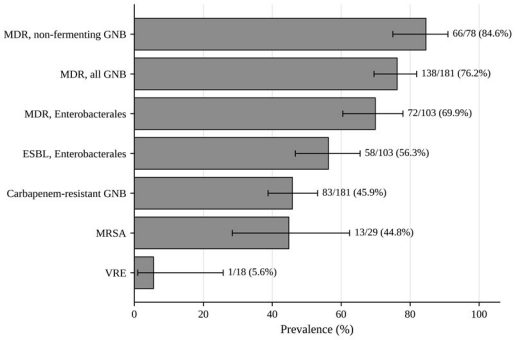
Values are susceptible isolates/tested isolates (% susceptible). Nitrofurantoin results represent urinary enterococcal isolates. A dash indicates that the antimicrobial was not tested for that organism.

Figure 1. Clinically significant culture positivity according to specimen type



Bars show the percentage of suitable specimens with clinically significant growth; error bars indicate 95% Wilson confidence intervals. Labels show n/N (%). Overall comparison: Pearson $\chi^2 = 43.77$, df = 6, $p < 0.001$.

Figure 2. Prevalence of major antimicrobial-resistance phenotypes



Bars show prevalence within the specified organism denominator; error bars indicate 95% Wilson confidence intervals. Labels show n/N (%). ESBL, extended-spectrum β-lactamase; GNB, Gram-negative bacilli; MDR, multidrug resistant; MRSA, methicillin-resistant Staphylococcus aureus; VRE, vancomycin-resistant enterococci.

Discussion

The present study provides a unit-specific assessment of the microbial spectrum and antimicrobial-resistance patterns among patients admitted to the ICU of a tertiary-care centre in Bihar. Clinically significant microbial growth was detected in 37.0% of suitable specimens, and nearly half of the patients had at least one positive culture. Gram-negative bacilli accounted for 72.1% of primary isolates, with Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter baumannii complex, and Escherichia coli comprising the majority. Of particular concern, 69.3% of bacterial isolates were multidrug resistant, including 76.2% of Gram-negative bacilli, and almost half of all Gram-negative isolates were resistant to carbapenems.

The overall culture-positivity rate in the present study was comparable to that reported by Chakraborty et al. in Kolkata, where 38% of 1,251 ICU specimens yielded bacterial or Candida growth. Positivity rates were 37% in adult ICUs and 40% in paediatric ICUs. Their study also demonstrated a predominance of Enterobacterales and non-fermenting Gram-negative bacilli. However, the distribution of positive cultures according to specimen type differed from that observed in the present study. In their cohort, blood accounted for 56% of positive cultures, respiratory specimens for 27%, and urine for 17%, whereas respiratory and pus or wound specimens showed the highest positivity rates in our cohort. Chakraborty et al. also reported markedly high carbapenem-resistance rates among adult ICU isolates, including 88% in Klebsiella spp. and 89% in Pseudomonas spp., compared with 37.9% and 56.1%, respectively, in the present study.[10] These differences highlight the considerable variation in microbial ecology and antimicrobial selection pressure across healthcare institutions.

The predominance of Gram-negative organisms was also consistent with the findings of Savanur and Gururaj. In their ICU cohort, E. coli was the most frequently isolated bacterium, accounting for 18.6% of isolates, followed by Acinetobacter spp. at 14.5%, Klebsiella spp. at 11.6%, and Pseudomonas spp. at 9.8%. In contrast, K. pneumoniae was the most common organism in the present study, whereas E. coli ranked fourth overall but remained the predominant urinary isolate. Their study also reported fungal growth in approximately 15% of positive specimens and considerable resistance to commonly used β-lactams and fluoroquinolones. The lower proportion of yeasts in the present study, accounting for 8.0% of primary isolates, may be related to differences in patient characteristics, specimen-submission practices, previous antifungal exposure, and the criteria used to distinguish colonization from clinically significant infection.[11]

The burden of resistant Enterobacterales was substantial in the present cohort. Overall, 56.3% were extended-spectrum β-lactamase producers, 69.9% were multidrug resistant, and carbapenem resistance was identified in 37.9% of K. pneumoniae isolates and 22.6% of E. coli isolates. Parajuli et al., in a study of Gram-negative healthcare-associated infections in a critical-care unit in Nepal, similarly reported a high burden of resistance among Klebsiella, E. coli, Acinetobacter, and Pseudomonas. Their isolates showed extensive non-susceptibility to third-generation cephalosporins and fluoroquinolones, frequent extended-spectrum β-lactamase production among Enterobacterales, and limited susceptibility to commonly used empirical antimicrobial agents. Resistance was particularly prominent among isolates obtained from respiratory, urinary, and bloodstream infections. Considered together, these findings suggest that cephalosporin-based empirical regimens may provide inadequate coverage in many South Asian ICUs unless treatment decisions are informed by current local susceptibility data.[12]

Non-fermenting Gram-negative bacilli were the most resistant group of organisms identified in the present study, with multidrug resistance detected in 84.6% of isolates. Carbapenem resistance was observed in 78.4% of A. baumannii complex isolates and 56.1% of P. aeruginosa isolates. Susceptibility to colistin remained relatively high at 86.5% and 92.7%, respectively. Yadav et al. recovered 402 non-fermenting Gram-negative bacilli from 6,216 clinical specimens in Nepal, of which 43.0% were obtained from the lower respiratory tract. A. baumannii and P. aeruginosa accounted for 44.0% and 40.1% of isolates, respectively. The overall prevalence of multidrug resistance was 78.1% and increased to 91.0% among A. baumannii isolates. All tested A. baumannii and P. aeruginosa isolates remained susceptible to colistin and polymyxin B.[13] The similarities in organism distribution and resistance burden between the two studies emphasize the role of mechanically ventilated and device-exposed ICU patients as important reservoirs of highly resistant non-fermenting organisms.

Similar concerns have also been reported outside South Asia. Uc-Cachón et al. evaluated Gram-negative bacilli isolated from adult, paediatric, and neonatal ICUs in Mexico and observed extensive resistance among A. baumannii, P. aeruginosa, K. pneumoniae, and E. coli. Resistance was particularly high to cephalosporins, fluoroquinolones, and several β-lactam/β-lactamase-inhibitor combinations, whereas carbapenem resistance was concentrated primarily among non-fermenting organisms. The study further demonstrated that susceptibility patterns varied across ICU populations and specimen sources, supporting the use of unit-specific rather than hospital-wide antibiograms. Despite differences in geographical setting and antimicrobial-prescribing practices, both the Mexican study and the present investigation identified A. baumannii as a major therapeutic challenge and demonstrated the limitations of applying uniform empirical-treatment protocols across different ICU settings.[14]

The ICU antibiogram reported by Negm et al. in Egypt provides a useful comparison with the susceptibility patterns observed in the present study. Among 45,221 first isolates, 74.4% were Gram-negative organisms. K. pneumoniae accounted for 33.5% of isolates and E. coli for 19.3%. Colistin susceptibility remained high among K. pneumoniae, E. coli, and Acinetobacter spp., at 96.2%, 94.7%, and 89.9%, respectively. These values were broadly comparable to the susceptibility range of 86.5%–96.8% observed among the leading Gram-negative pathogens in the present study. However, carbapenem susceptibility was considerably lower in the Egyptian cohort. Meropenem susceptibility was reported in 19.0% of K. pneumoniae isolates, 52.7% of E. coli isolates, 20.3% of Acinetobacter isolates, and 15.2% of P. aeruginosa isolates. The corresponding values in the present study were 63.8%, 74.2%, 24.3%, and 41.5%, respectively. These findings demonstrate that even when the predominant pathogens are similar, the magnitude of resistance may differ substantially between institutions, reinforcing the importance of regularly updated local antibiograms.[15]

Gram-positive organisms accounted for a smaller proportion of isolates in the present study. Nevertheless, methicillin resistance was identified in 44.8% of S. aureus isolates. All S. aureus isolates remained susceptible to vancomycin, while only one vancomycin-resistant Enterococcus isolate was detected. Yeasts accounted for 8.0% of all isolates, with Candida albicans being the most frequently identified species, followed by C. tropicalis and C. parapsilosis. In a prospective ICU study of candidemia, Ahmad et al. reported a predominance of non-albicans Candida species, identified associations with invasive devices and exposure to broad-spectrum antimicrobial agents, and demonstrated species-dependent differences in azole susceptibility. Their study also showed an association between higher Candida scores and candidemia, while echinocandins retained comparatively reliable activity.[16] In the present study, susceptibility to micafungin, caspofungin, amphotericin B, and fluconazole remained high. However, the relatively small number of yeast isolates limits the precision of species-specific resistance estimates.

The findings of the present study have several clinical implications. First, the predominance of K. pneumoniae, P. aeruginosa, and A. baumannii complex, together with the high prevalence of multidrug resistance, suggests that third-generation cephalosporins and fluoroquinolones may not provide reliable empirical coverage for severe ICU-acquired infections. Second, carbapenem susceptibility was better preserved among E. coli and K. pneumoniae than among non-fermenting Gram-negative bacilli. Empirical antimicrobial selection should therefore take into account the probable source of infection and the likely causative pathogen rather than adopting a uniform approach to all Gram-negative infections. Third, although colistin demonstrated the highest in-vitro activity against several resistant Gram-negative organisms, its use should be restricted to carefully selected cases. Susceptibility was not universal, and indiscriminate use could contribute to the further emergence of resistance. Finally, the preserved activity of vancomycin against S. aureus and echinocandins against Candida provides useful guidance for local treatment protocols, although continued surveillance remains necessary.

The study has several strengths. These include prospective consecutive enrolment, the inclusion of multiple specimen categories, analysis at both patient and isolate levels, exclusion of repeat isolates, and the development of an ICU-specific antibiogram. Nevertheless, several limitations should be considered. The study was conducted at a single centre, and the number of isolates available for certain organisms was limited. Molecular characterization of antimicrobial-resistance mechanisms was not performed. In addition, infection could not always be conclusively distinguished from colonization, particularly in respiratory specimens and catheter-tip cultures. The study also did not assess the appropriateness of empirical antimicrobial therapy or determine the independent effect of antimicrobial resistance on patient mortality.

Conclusion

Infections among ICU patients at this tertiary-care centre were predominantly caused by Gram-negative bacilli and were characterized by a high prevalence of multidrug and carbapenem resistance, particularly among A. baumannii complex and P. aeruginosa. These findings support the regular updating of the ICU antibiogram, microbiology-guided antimicrobial de-escalation, restriction of reserve antimicrobial agents, and strengthening of device-care and infection-prevention practices. Continued surveillance is required to identify temporal changes in microbial distribution and susceptibility patterns and to evaluate the effect of antimicrobial-stewardship interventions.

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