Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Multidrug-Resistant Bacterial Infections in Intensive Care Units: A Retrospective Analysis of Pathogen Epidemiology, Antimicrobial Resistance, and Clinical Risk Factors

Nahid Amin
Anwer Khan Modern University
Md Javed Alam
Popular Medical College Hospital
Dr Tufael
Parul University
Md. Abul Kashem Tang.
Islamic University
Nirmal Chandra Mahat
Islamic University
Suhel Ahmed
Daffodil International University
Amena Khatun Manica
University of New Haven
Md Abu Bakar Siddique
St John's University
Papiya Sultana Sharker Sharna
KC Hospital & Diagnostic Centre
Hasibul Hasan
Rajshahi Medical College Hospital
Vijay Jagdish Upadhye
dr.vijaysemilo@gmail.com

Parul University

Research Article

Keywords: Antimicrobial resistance, Intensive care unit (ICU), Multidrug-resistant organisms, Carbapenem resistance, ICU-associated bacterial pathogens

Posted Date: November 1st, 2026

DOI: https://doi.org/10.21203/rs.3.rs-11147843/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Abstract

Background

Adult ICU patients are highly vulnerable to bacterial infections because of critical illness, invasive devices, prolonged hospitalization and antimicrobial exposure. Increasing multidrug resistance, particularly among Gram-negative pathogens, complicates empirical treatment and requires reliable local epidemiological surveillance and effective stewardship planning.

Aims

To characterize ICU-associated bacterial pathogens, antimicrobial-resistance patterns, MDR burden, carbapenem resistance and clinical factors associated with MDR infection in adults.

Methods

A retrospective study analyzed records from ICU patients. Specimens were cultured and isolates identified using routine procedures. Susceptibility was interpreted using recognized breakpoint standards. MDR was defined as non-susceptibility to at least one agent in three or more antimicrobial categories, while carbapenem resistance was assessed among tested Gram-negative isolates. Descriptive statistics and multivariable logistic regression were performed using Python; associations were reported as adjusted odds ratios with 95% confidence intervals.

Results

Among 1,135 specimens, isolates demonstrated a substantial resistance burden. Acinetobacter baumannii showed highest MDR prevalence and carbapenem resistance, followed by Klebsiella pneumoniae and Pseudomonas aeruginosa. Carbapenem resistance occurred in 87.3% of A. baumannii, 51.0% of P. aeruginosa, 42.8% of K. pneumoniae and 9.7% of Escherichia coli. Recent antibiotic exposure was the strongest factor associated with MDR infection (adjusted OR, 3.18; 95% CI, 2.32–4.36; $p < 0.001$), followed by mechanical ventilation and ICU stay exceeding seven days. Diabetes and chronic kidney disease were not independently associated after adjustment.

Conclusion

The findings support continuous ICU surveillance, careful antibiotic use and strengthened infection-prevention practices, while recognizing that this single-cohort study cannot establish causality or national prevalence.

1. Introduction

Intensive care units (ICUs) are among the most complicated healthcare settings, which administer high-level care to patients who have severe infections, organ malfunction, trauma, or the most complex diseases. ICU patients are highly susceptible to HAIs due to bacterial pathogens because they are exposed to invasive procedures, long stays, and are prescribed a high volume of antimicrobials during their time in the hospital. Infections often lead to morbidity, mortality, higher healthcare costs, and longer hospital stays, and they tend to be more prevalent at times of service requirement. Antimicrobial resistance (AMR) is widely recognized as one of the biggest challenges in modern-day critical care medicine, affecting the effectiveness of existing antimicrobial therapy and, therefore, treatment options for critically ill patients [1–3].

Several factors have fueled the spread of AMR worldwide: inappropriate antimicrobial use, selective pressure from broad-spectrum antibiotics, failure to apply infection control measures, and the spread of AMR in healthcare environments. Multiple bacterial pathogens associated with intensive care unit (ICU) infections are listed as priority organisms for urgent action by the World Health Organization [4–6]. They often have multidrug resistance (MDR) and pose a therapeutic challenge because they are not sensitive to many available effective antimicrobial agents.

Geographical patterns, healthcare supply and demand, antimicrobial prescribing, and patient characteristics all affect pathogen patterns and contribute to ICU-associated bacterial infections. Non-fermentative Gram-negative bacteria (e.g., Acinetobacter baumannii and Pseudomonas aeruginosa) that can persist in the hospital environment, develop resistance, and form biofilms on medical devices are the most commonly reported pathogens in the intensive care unit (ICU). Likewise, Klebsiella pneumoniae and Escherichia coli contribute significantly to bloodstream, urinary tract, and respiratory infections through extended-spectrum β-lactamase (ESBL) production and carbapenem resistance [7–9]. Other major causes of ICU infections include clinically important gram-positive organisms such as methicillin-resistant Staphylococcus aureus (MRSA) and vancomycin-resistant enterococci (VRE).

Many patient-specific and HA risk factors strongly determine AMR in ICUs. Patients with life-threatening illness often need the placement of urinary catheters, central venous catheters, and mechanical ventilation, which predispose them to a high risk of device-associated infections and enable bacterial growth. Moreover, three factors are resistant to previous antimicrobial exposure: prolonged stays in the intensive care unit (ICU) contribute to the selection, emergence, and maintenance of MDR organisms. Understanding these risk factors is crucial in designing infection prevention programs and tackling antimicrobial selection, in addition to enhancing antimicrobial stewardship [10, 11].

Increasing resistance in IPNs (particularly carbapenem-resistant Gram-negative bacteria) is a growing public health threat, as carbapenems are considered last-line antimicrobials for severe infections. The emergence of carbapenem-resistant A. baumannii, K. pneumoniae, and P. aeruginosa has significantly limited therapeutic options and negatively affected outcomes. The issue is that the majority of CROs are resistant to several antimicrobial classes and have fewer treatment options available than usual;

consequently, they can be more difficult to treat and are becoming resistant more readily to other antimicrobials and/or newer combinations of antimicrobials, including colistin and newer combinations of antimicrobials [12–14].

Despite extensive research on AMR patterns among pathogens isolated from ICU patients, resistance patterns vary significantly across healthcare settings. New pathogens, antimicrobial susceptibilities, and risk factors continue to vary, as do their distribution and susceptibilities across different parts of the country and institutions; local epidemiological surveillance remains necessary. Resource and access limitations, the lack of an effective antimicrobial stewardship system, and antibiotic overuse in many LMIC countries such as Bangladesh could hasten the spread and emergence of resistant organisms. However, surveillance data providing more in-depth information on pathogen distribution, antimicrobial resistance profiles, MDR prevalence, carbapenem resistance, and clinical risk factors are limited, especially in the ICU.

This study aimed to describe the epidemiology and antimicrobial resistance patterns of adult ICU patients with bacterial pathogens associated with admission. We evaluated bacterial distribution in clinical specimens, susceptibility patterns, and MDR prevalence, as well as clinical factors associated with MDR isolates. This study not only presents an integrated assessment of ICU bacterial pathogens and resistance patterns but also offers valuable evidence to enhance antimicrobial stewardship, infection control measures, and the management of critically ill patients.

2. Materials and Methods

2.1 Study Design and Settings

This retrospective observational study included patients with ICU-acquired infections between 1 July 2024 and 29 February 2025 to assess the epidemiology and antimicrobial resistance patterns of ICU-associated bacterial pathogens in adults. This study was conducted in the adult Intensive Care Unit (ICU) and data were collected from the routine clinical and laboratory records of patients attending different tertiary hospitals in Dhaka, Bangladesh. The data included bacterial culture results, pathogen identification, antimicrobial-susceptibility testing, MDR classification, carbapenem resistance, and patient-level risk factors. We systematically reviewed all eligible records from the study period.

2.2 Study Population and Eligibility Criteria

Study subjects were adult patients (age ≥ 18 years) admitted to the ICU with suspected bacterial infection who underwent microbiological studies during the study period. We retrieved and analyzed clinical records and laboratory results to identify clinically significant bacteria and antimicrobial resistance patterns. Patients were eligible if clinical information and culture data were available. We excluded incomplete microbiological data, contaminated cultures, duplicate clinical isolates not clinically relevant, and very young patients to ensure accurate epidemiological and resistance analysis.

2.3 Clinical Data Collection

A structured data collection form was used to obtain clinical and demographic data from ICU medical records and laboratory databases. The table included patient age, sex, primary diagnosis at ICU admission, exposure factors associated with ICU admission, prior antimicrobial use, presence or use of invasive devices, underlying comorbidities, and clinical outcomes. Information regarding mechanical ventilation (MV), central venous catheter (CVC), urinary catheter (UC), intensive care unit (ICU) length of stay (LOS), and mortality was captured. These variables were analyzed to describe the cohort's clinical characteristics and identify potential factors associated with MDR infections.

2.4 Clinical Specimen Collection and Bacterial Identification

Standard clinical laboratory techniques were used to process clinical samples from adult ICU patients with suspected bacterial infection. Respiratory samples (endotracheal aspirate and bronchoalveolar lavage), blood, urine, pus/wound specimens, catheter tips, and cerebrospinal fluid were the specimen types. We used diagnostic procedures to identify bacterial isolates, followed by standard laboratory procedures. We recorded the specimen location and pathogen type for each recovered bacterium. We considered more than one isolate from two specimens collected at different times, or from two different outbreaks of an infection, as an independent clinical finding when assessing bacterial distribution and antimicrobial susceptibility.

2.5 Antimicrobial Susceptibility Testing

We performed antimicrobial susceptibility testing (AST) on clinically significant bacterial isolates using standard microbiological laboratory techniques. We selected antibiotic panels based on bacterial species and clinical relevance, including commonly used antibiotics for ICU-associated infections. The antimicrobial groups that were tested were carbapenems, cephalosporins, β-lactam/β-lactamase inhibitor combinations, fluoroquinolones, aminoglycosides, glycopeptides, oxazolidinones, and polymyxins (where present). Susceptibility results were assessed using known CLSI/EUCAST breakpoints. Resistance ratios were determined as the percentage of resistant isolates of the available tested isolates for each antimicrobial agent. These data enabled assessment of resistance patterns in all tested pathogens and the overall burden of antimicrobial resistance.

2.6 Definition of Multidrug Resistance (MDR) and Carbapenem Resistance

According to internationally accepted definitions, we defined multidrug-resistant (MDR) organisms as bacterial isolates resistant to at least one antimicrobial agent from three or more antimicrobial categories. We evaluated MDR prevalence among predominant bacterial pathogens associated with ICU (*Acinetobacter baumannii, Klebsiella pneumoniae, Pseudomonas aeruginosa, Escherichia coli*, *Staphylococcus aureus, and Enterococcus spp.*). We defined carbapenem resistance as resistance to at least one tested carbapenem (meropenem or imipenem). We estimated the burden of critical AMR phenotypes in bacterial isolates from the ICU using MDR and carbapenem resistance proportions.

2.7 Risk Factor Analysis for MDR Infections

We assessed two sets of clinical risk factors for MDR infections to determine their independent association with antimicrobial resistance in ICU patients. We analyzed the following variables: antimicrobial exposure in the previous 90 days, previous ICU admission, advanced age (≥ 65 y), central venous catheterization, urinary catheterization, diabetes mellitus, chronic kidney disease, mechanical ventilation, and prolonged ICU stay (> 7 days). We estimated univariate associations of each risk factor with MDR infection status, followed by multivariable logistic regression analysis. We expressed the effect of each factor as an adjusted odds ratio (aOR) with a 95% confidence interval (CI) to assess its independent contribution. A p-value < 0.05 was considered significant.

2.8 Statistical Analysis

We carried out statistical analyses using Python statistical tools. We used descriptive statistics to summaries patients' characteristics, pathogen distribution, and antimicrobial resistance patterns. We summarized categorical data as frequencies and percentages. We derived adjusted odds ratios (aORs) and 95% confidence intervals (CIs) using logistic regression to identify risk factors for MDR. A significant p-value of < 0.05 was considered.

3. Results

3.1 Demographic and Clinical Characteristics of ICU Patients

We included 1135 adult ICU patients, predominantly older (50.0% aged > 60 years) and male (60.0%). The top diagnosis on admission to the ICU was septic shock or septicemia (31.4%), followed by pneumonia/VAP (21.8%). Urinary catheterization (72.5%), antimicrobial exposure (61.9%), and mechanical ventilation (55.0%) were the most commonly instituted interventions in the ICU (Table 1). At least one comorbidity was seen in most patients (65.7%), with the most common conditions being hypertension and diabetes mellitus. The median ICU stay was 9 days (IQR 5–16), with an overall survival rate of 2%, and the mortality rate was 8%. These observations paint a picture of a high-risk, highly burdened, highly exposed, and highly complex population of patients in ICUs, calling for targeted ICU-based approaches to preventing infection – and approaches to managing it across care settings.

Table 1
Baseline Demographic and Clinical Characteristics of Adult ICU Patients Included in the Study (n = 1135)

Variables	Categories	n (%)
Age (years)	Mean ± SD	58.4 ± 17.6
	Median age (IQR)	61 (45–72)
	Age range	18–96
	18–40 years	188 (16.6)
	41–60 years	372 (32.8)
	> 60 years	575 (50.7)
Gender	Male	681 (60.0)
	Female	454 (40.0)
Primary ICU admission diagnosis	Sepsis/septic shock	356 (31.4)
	Pneumonia/Ventilator-associated pneumonia (VAP)	247 (21.8)
	Bloodstream infection (BSI)	132 (11.6)
	Urinary tract infection (UTI)	96 (8.5)
	Trauma-related admission	118 (10.4)
	Post-operative complications	103 (9.1)
	Other medical conditions	83 (7.3)
ICU-related exposure factors	Invasive mechanical ventilation during ICU stays	624 (55.0)
	Central venous catheterization during ICU stays	438 (38.6)
	Urinary catheterization during ICU stays	823 (72.5)
	Previous antimicrobial exposure within 90 days before ICU admission	703 (61.9)

Variables	Categories	n (%)
Underlying comorbidities	At least one comorbidity	746 (65.7)
	Diabetes mellitus	356 (31.4)
	Hypertension	419 (36.9)
	Chronic kidney disease	171 (15.1)
	Chronic respiratory disease	156 (13.7)
	Cardiovascular disease	231 (20.4)
	Immunosuppression	104 (9.2)
Clinical outcomes	ICU length of stay, median (IQR), days	9 (5–16)
	ICU survivors	842 (74.2)
	ICU mortality	293 (25.8)

Data are presented as mean ± SD, median (IQR), or n (%) as appropriate. Continuous variables were summarized using descriptive statistics, and categorical variables were presented as frequencies and percentages.

3.2 Distribution of Clinical Specimens and Recovery of Bacterial Isolates

From these 1135 clinical specimens, we recovered 808 bacterial isolates after microbiological analysis. Respiratory specimens were the largest group collected (412/1135, 36.3%), and bacterial culture from these specimens had the highest positivity rate (338/808, 41.8%), with an 82.0% culture positivity rate (Table 2). Blood specimens accounted for 25.2% of submitted specimens and yielded 142 (17.6%) bacterial isolates, whereas urine specimens accounted for 19.5% of samples and yielded 156 (19.3%) bacterial isolates.

Pus or wound samples had a high recovery rate (81.4%), while fewer isolates were obtained from BAL samples (67.4%) and catheter tip samples (75.9%). CSF samples comprised only 2.0% of sample types but had a perfect recovery rate (73.9%). The prevalence of bacterial isolates in respiratory specimens showed that these are the most important source of bacteria causing infections in the Intensive Care Units.

Table 2
Distribution of Clinical Specimens Submitted for Microbiological Analysis and Recovery of Bacterial Isolates Among Adult ICU Patients.

Clinical Specimen	Samples Submitted n (%)	Bacterial Isolates Recovered n (%)	Culture Positivity Rate (%)
Endotracheal aspirate / Respiratory specimen	412 (36.3)	338 (41.8)	82
Blood	286 (25.2)	142 (17.6)	49.7
Urine	221 (19.5)	156 (19.3)	70.6
Pus/Wound specimen	118 (10.4)	96 (11.9)	81.4
Bronchoalveolar lavage (BAL)	46 (4.1)	31 (3.8)	67.4
Catheter tip	29 (2.6)	22 (2.7)	75.9
Cerebrospinal fluid (CSF)	23 (2.0)	23 (2.1)	73.9
Total	**1135 (100)**	**808 (100)**	—

3.3 Distribution of Gram-Negative Bacterial Pathogens

Non-fermenting Gram-negative bacilli and Enterobacterales were the most prevalent Gram-negative pathogen groups isolated from adult ICU patients. The most frequently isolated Gram-negative pathogen was Acinetobacter baumannii (220 isolates, 35.5%), followed by Klebsiella pneumoniae (145 isolates, 23.4%). The third most common organism was Pseudomonas aeruginosa, accounting for 98 isolates (15.8%) of Gram-negative bacteria found (Fig. 1).

Other Enterobacterales, such as Escherichia coli (72 strains, 11.6%) and Enterobacter spp. Proteus spp. (7.3%) and Proteus spp. (28 isolates, 4.5%) were also commonly found. A total of 12 organisms (1.9%) were Gram-negative. Multidrug-resistant Gram-negative bacteria associated with the ICUs consistently included A. baumannii, K. pneumoniae, and P. aeruginosa, with non-fermenters and resistant Enterobacterales playing an important role in the bacterial burden of critically ill patients.

3.4 Distribution of Gram-Positive Bacterial Pathogens

The most common Gram-positive pathogen among adult ICU patient samples was Staphylococcus aureus (82 isolates, 41.0%). Enterococcus faecium (54 isolates, 27.0%) and Enterococcus faecalis (36 isolates, 18.0%) were the second and third most common organisms identified. Coagulase-negative Staphylococcus spp. accounted for 18 cases (9.0%), while Streptococcus spp. accounted for only 7 cases (3.5%). Three isolates (1.5%) were identified as other Gram-positive organisms (Fig. 2).

Staphylococcal and enterococcal species together made up the majority of Gram-positive isolates recovered (86.0%). The findings highlight the role of opportunistic Gram-positive pathogens, particularly resistant staphylococci and enterococci, in driving the bacterial burden associated with the ICU.

3.5 Specimen-Wise Distribution of Bacterial Pathogens

Specimen-wise distribution analysis showed significant inter-associations between clinical specimens, adult patients presenting in the ICU, and bacterial pathogens. The most commonly isolated pathogen from respiratory specimens was Acinetobacter baumannii, followed by Pseudomonas aeruginosa and Klebsiella pneumoniae (Fig. 3). Urinary specimens were predominantly cultured for Escherichia coli (E. coli); in contrast, Klebsiella pneumoniae (K. pn.) was significantly more common in bloodstream infection specimens.

Staphylococcus aureus was more prevalent in wound and pus samples, while Enterococcus spp. was more prevalent in catheter-associated infections. The overall distribution indicates pathogen-specific preferences (i.e., multidrug-resistant Gram-negative organisms predominate in respiratory infections, while Enterobacterales also play a major role in bloodstream and urinary infections). These results highlight the need for specimen-based surveillance to inform downstream decisions on empirical antimicrobial therapy and to study pathogen ecology within ICUs.

3.6 Antimicrobial Susceptibility and Resistance Patterns

Antimicrobial susceptibility testing showed high resistance among the main bacterial pathogens associated with the ICU, particularly among Gram-negative bacteria (Table 3). The most resistant isolate was Acinetobacter baumannii, with high resistance rates (88.6% and 86.4% for meropenem and imipenem, respectively) and low resistance to colistin (4.5%). Klebsiella pneumoniae was highly resistant to the third- and fourth-generation cephalosporins, ceftriaxone (75.9%) and cefepime (69.0%), and had a high rate of carbapenem resistance to meropenem (44.8%). Similarly, Pseudomonas aeruginosa was multidrug-resistant (MDR), with resistance rates of > 50% for meropenem (51.0%), imipenem (53.1%), and ciprofloxacin (61.2%) among key antipseudomonal agents.

The major Gram-negative pathogen was Escherichia coli, with high resistance to ceftriaxone (61.1%) and Ciprofloxacin (58.3%) and relatively lower sensitivity to carbapenems and Amikacin. In addition, Gram-positive pathogens were clinically significant, with 57.3% of S. aureus isolates being methicillin-resistant (MRSA) based on cefoxitin resistance. Vancomycin and linezolid, however, were completely effective against S. aureus and Enterococcus spp. Overall, these results show high levels of MDR pathogens in the ICU, including carbapenem-resistant A. baumannii and resistant E. coli, and emphasize the importance of proactive antimicrobial surveillance and targeted stewardship initiatives in critical care areas.

Table 3
Antimicrobial Susceptibility Profiles of Major Bacterial Pathogens Isolated from Adult ICU Patients

Bacterial pathogen	Antimicrobial agent	Susceptible n (%)	Resistant n (%)
Acinetobacter baumannii (n = 220)	Meropenem	25 (11.4)	195 (88.6)
	Imipenem	30 (13.6)	190 (86.4)
	Cefepime	22 (10.0)	198 (90.0)
	Piperacillin–tazobactam	18 (8.2)	202 (91.8)
	Ciprofloxacin	20 (9.1)	200 (90.9)
	Amikacin	72 (32.7)	148 (67.3)
	Colistin	210 (95.5)	10 (4.5)
Klebsiella pneumoniae (n = 145)	Ceftriaxone	35 (24.1)	110 (75.9)
	Cefepime	45 (31.0)	100 (69.0)
	Piperacillin–tazobactam	55 (37.9)	90 (62.1)
	Meropenem	80 (55.2)	65 (44.8)
	Imipenem	85 (58.6)	60 (41.4)
	Ciprofloxacin	42 (29.0)	103 (71.0)
	Amikacin	95 (65.5)	50 (34.5)
Pseudomonas aeruginosa (n = 98)	Piperacillin–tazobactam	45 (45.9)	53 (54.1)
	Ceftazidime	40 (40.8)	58 (59.2)
	Cefepime	42 (42.9)	56 (57.1)
	Meropenem	48 (49.0)	50 (51.0)
	Imipenem	46 (46.9)	52 (53.1)
	Ciprofloxacin	38 (38.8)	60 (61.2)
	Amikacin	70 (71.4)	28 (28.6)
Escherichia coli (n = 72)	Ceftriaxone	28 (38.9)	44 (61.1)
	Cefepime	35 (48.6)	37 (51.4)
	Piperacillin–tazobactam	40 (55.6)	32 (44.4)
	Meropenem	65 (90.3)	7 (9.7)
	Ciprofloxacin	30 (41.7)	42 (58.3)

Bacterial pathogen	Antimicrobial agent	Susceptible n (%)	Resistant n (%)
	Amikacin	60 (83.3)	12 (16.7)
Staphylococcus aureus (n = 82)	Cefoxitin (MRSA screening)	35 (42.7)	47 (57.3)
	Clindamycin	48 (58.5)	34 (41.5)
	Erythromycin	40 (48.8)	42 (51.2)
	Vancomycin	82 (100)	0 (0.0)
	Linezolid	82 (100)	0 (0.0)
Enterococcus spp. (n = 74)	Ampicillin	25 (33.8)	49 (66.2)
	Vancomycin	65 (87.8)	9 (12.2)
	Teicoplanin	68 (91.9)	6 (8.1)
	Linezolid	74 (100)	0 (0.0)

3.7 Resistance Patterns of Gram-Negative Bacteria

A high burden of antimicrobial resistance was observed among key ICU pathogens. Acinetobacter baumannii had the broadest spectrum of resistance, with extensive resistance to the carbapenems meropenem and imipenem, as well as other widely used antimicrobial agents. However, the activity of colistin against A. baumannii was considerably greater, and there was a comparatively low level of resistance to colistin. Multidrug resistance was also high in Klebsiella pneumoniae for third-generation cephalosporins, cefepime, and fluoroquinolones, highlighting the high burden of MDR EEA in the ICU setting (Fig. 4).

All Pseudomonas aeruginosa isolates were broad-spectrum resistant to third-generation cephalosporins, fluoroquinolones, and carbapenems, consistent with an emerging multidrug-resistant phenotype. Meanwhile, Escherichia coli was more sensitive to carbapenems and showed high resistance to cephalosporins and ciprofloxacin. Overall, the heatmap underscores pathogen-specific resistance trends: carbapenems are a key resistance challenge for A. baumannii, and resistant Enterobacterales are a major challenge in ICU settings. These studies highlight the need for ongoing resistance surveillance and appropriate antimicrobial stewardship interventions in critical care settings.

3.8 Prevalence of Multidrug-Resistant Organisms

Multidrug-resistant (MDR) isolates showed a high resistance burden among bacterial isolates associated with ICUs. Acinetobacter baumannii had the highest MDR prevalence (195/220, 88.6%; 95% CI: 84.4–92.8), reflecting widespread multidrug resistance among this key ICU pathogen. Other Gram-negative organisms also showed significant MDR proportions, such as Klebsiella pneumoniae (62.1%,

95% CI: 54.2–70.0) and Pseudomonas aeruginosa (58.2%, 95% CI: 48.4–67.9). The results show a high prevalence of MDR Gram-negative bacteria, which primarily contribute to the ICU's antibiotic resistance burden (Fig. 5).

Among Gram-positive bacteria, MRSA was an important resistant phenotype in the ICU setting, comprising 57.3% (95% CI: 46.6–68.0) of all Staphylococcus aureus. E. coli had an intermediate proportion of MDR (45.8%, 95% CI: 34.3–57.3), while Enterococcus spp. had a relatively low proportion (12.2%, 95% CI: 4.7–19.6). Overall, these findings show substantial variation in MDR distribution across bacterial species, and that the most important MDR threats among isolates collected from the ICUs were A. baumannii, K. pneumoniae, and P. aeruginosa. These findings highlight the importance of pathogen-specific antimicrobial stewardship strategies and ongoing surveillance in critical care settings.

3.9 Carbapenem-Resistant Isolates

Acinetobacter baumannii isolates (192/220; 87.3%; 95% CI 82.4–91.5) showed the highest prevalence of carbapenem resistance. Significant carbapenem-negative resistance was found in P. aeruginosa (51.0%; 50/98; 95% CI: 41.3–60.6) and K. pneumoniae (42.8%; 62/145; 95% CI: 34.9–50.9), indicating a high prevalence of CGE pathogens in the ICU setting (Fig. 6).

In contrast, carbapenem resistance was relatively low in Escherichia coli (9.7%; 7/72; 95% CI: 4.1 − 18.7). In summary, the findings point to A. baumannii as the predominant carbapenem-resistant pathogen in this cohort of ICU-admitted patients, with resistant Pseudomonas and CPE as emerging pathogens to monitor and target for stewardship measures.

3.10 Risk Factors Associated with MDR Infections

Multivariable logistic regression identified several clinical factors as significant, independent predictors of MDR infections in adults in the ICU. Antibiotics used within 90 days before ICU admission were associated with the strongest presence of MDR infections (adjusted OR [aOR]: 3.18; 95% CI: 2.32–4.36; $p < 0.001$). Mechanical ventilation (aOR: 2.54; 95% CI: 1.88–3.43; $p < 0.001$) and/or a prolonged stay in the critical care unit for more than 7 days (aOR: 2.31; 95% CI: 1.72–3.11; $p < 0.001$) were further important contributors to MDR acquisition (Table 4).

Exposure to invasive devices was also associated with significantly higher rates of MDR infections with central venous catheterization (aOR: 1.74; 95% CI: 1.30–2.34, $p < 0.001$) and urinary catheterization (aOR: 1.51; 95% CI: 1.12–2.03, $p = 0.007$). Past ICU hospitalization and older age (> 65 years) were also identified as risk factors. After adjustment, the relationship of diabetes mellitus and chronic kidney disease with MDR infection was not significant, in contrast to what was seen with HIV status. However, unlike HIV status, there was no independent association of diabetes mellitus and chronic kidney disease with MDR infection after adjustment. In summary, the results indicate that health care exposure factors, such as prior antibiotic therapy, mechanical ventilation, and prolonged ICU stay, are important determinants of risk for acquiring MDR infections in critically ill individuals.

Table 4
Independent Risk Factors Associated with Multidrug-Resistant (MDR) Infections Among Adult ICU Patients.

Risk Factors	MDR Infection (n = 431) n (%)	Non-MDR Infection (n = 377) n (%)	Adjusted OR (aOR)	95% CI	p-value
Age ≥ 65 years	258 (59.9)	173 (45.9)	1.62	1.21–2.17	0.001
Male sex	276 (64.0)	224 (59.4)	1.14	0.86–1.52	0.36
ICU stay > 7 days	301 (69.8)	176 (46.7)	2.31	1.72–3.11	< 0.001
Mechanical ventilation	328 (76.1)	198 (52.5)	2.54	1.88–3.43	< 0.001
Previous antibiotic exposure within 90 days	347 (80.5)	201 (53.3)	3.18	2.32–4.36	< 0.001
Previous ICU admission	142 (32.9)	76 (20.2)	1.71	1.22–2.40	0.002
Central venous catheterization	214 (49.7)	126 (33.4)	1.74	1.30–2.34	< 0.001
Urinary catheterization	289 (67.1)	202 (53.6)	1.51	1.12–2.03	0.007
Diabetes mellitus	158 (36.7)	113 (30.0)	1.28	0.95–1.73	0.1
Chronic kidney disease	72 (16.7)	48 (12.7)	1.31	0.88–1.95	0.18

4. Discussion

This study aims to describe the bacterial epidemiology and antimicrobial resistance (AMR) patterns of pathogens in adult ICU patients, including the prevalence of multidrug-resistant (MDR) and carbapenem-resistant (CR) pathogens and associated clinical variables of MDR infections. This study shows a high prevalence of resistant bacterial pathogens in the ICU, with Gram-negative bacteria as the predominant resistant group. In particular, Acinetobacter baumannii, Klebsiella pneumoniae, and Pseudomonas aeruginosa showed significant resistive data, and prior antibiotic use, mechanical ventilation, and long stay in the intensive care unit were significantly associated with MDR infection. These findings align with global evidence that ICUs are major sites for the emergence and spread of resistant bacterial pathogens, where intensive antibiotic use and invasive procedures, coupled with prolonged patient exposure, increase the risk of antibiotic resistance [15–19].

The higher proportion of respiratory specimens in this study is likely attributable to the increased susceptibility of critically ill patients to respiratory infections, especially those who are mechanically ventilated. Invasive ventilation may disrupt normal host defense processes and predispose patients to bacterial colonization of the airway, making ventilator-associated infection (VAI) one of the most prevalent HAIs in the ICU [18, 19]. This is similar to findings from a study of bacterial isolation during hospital stay within the intensive care unit (ICU) conducted in the United States, in which respiratory samples often accounted for most of the bacterial species isolated, especially Gram-negative genera.

A. baumannii, K. pneumoniae, and P. aeruginosa were the predominant organisms found in this cohort and agree with other studies showing these to be major pathogens of the ICU globally. These organisms are a particular threat because they can acquire resistance genes and survive in hospitals [20, 21]. However, results may vary across studies because ICUs differ in patient characteristics, antimicrobial prescribing practices, hospital infection-prevention policies, and regional epidemiology. Thus, the results may not represent the broader national or international ICU population, and further studies are needed to validate them.

The resistance levels observed in this study reflect the significant challenges posed by Gram-negative ICU pathogens. A. baumannii showed the highest resistance burden, especially to carbapenems and a wide range of commonly used antimicrobial agents. This aligns with previous reports, as carbapenem-resistant A. baumannii is a critical priority pathogen because of limited therapeutic options and its strong association with HCIs [22–25]. A. Bahmani's resistance accumulation, along with its survival under adverse environmental conditions, facilitates its persistence in intensive care environments [26, 27].

K. pneumoniae shows high resistance to cephalosporins along with other classes of antimicrobial agents. Similar patterns are frequently associated with the global dissemination of extended-spectrum β-lactamase (ESBL)-producing and carbapenem-resistant Enterobacterales (CREs), which are a concern in healthcare settings [28, 29]. Similarly, P. aeruginosa was resistant to a range of antimicrobial classes, reflecting its mutable resistance due to reduced permeability, efflux pump activity, and enzyme action. However, this study did not include molecular testing, so it did not confirm the specific resistance mechanisms.

It also highlights the continued role of resistant Gram-positive infections in ICU care; among Gram-positive organisms, MRSA-associated resistance patterns remain a focus. As seen in past studies, MRSA is a significant healthcare-associated pathogen, but rates vary widely depending on the environment's infection control practices and antimicrobial policies [30, 31]. Isolates' susceptibility to frontline agents such as vancomycin and linezolid suggests continued therapeutic effectiveness in this group. Still, ongoing monitoring of these drugs is required.

Based on the high rates of MDR strains detected in this study, bacterial isolates from the ICU present an important antimicrobial problem. The high proportion of MDR A. baumannii aligns with other ICU studies that describe this pathogen as a consistent cause of MDR infections, especially in hospitals with high

antimicrobial pressure [15, 32, 33]. Thus, fifthly, resistant K. pneumoniae, P. aeruginosa is another clinical issue because treatment options are limited.

Significant levels of carbapenem resistance were reported in A. baumannii, with noteworthy resistance in K. pneumoniae and P. aeruginosa as well. These results are similar to a large-scale surveillance of Gram-negative bacteria in Europe across multiple countries that identified carbapenem-resistant variants as the primary public health concern [34–36]. However, national or health care facility-specific carbapenem resistance rates can differ, and interpretation should account for local antibiotic use, infection-control measures, and lab methods.

The correlation between a history of antibiotic exposure and MDR infection found herein confirms that selective pressure from antimicrobial agents plays a role in the selection and survival of resistant organisms. One of the most important recognized risk factors for MDR infection is prior antibiotic use, which can change the microbial ecology and selectively favor resistant over virulent bacterial populations [27, 37, 38].

ICU stay was also associated with MDR infection, as well as mechanical ventilation. The same has been observed in Intensive Care Units, where the longer a patient is acutely exposed to the healthcare environment and has invasive devices, the greater their chance of colonization and transmission of resistant organisms [39–41]. Central venous and urinary catheterization were additional device-associated factors and underscored the need for infection prevention strategies. These findings are associations, not causation, and would require a prospective, observational study to establish causality.

The results highlight the need for ongoing AMR surveillance, infection prevention, and antimicrobial stewardship in ICUs. Local resistance data can support empirical treatment decisions and targeted interventions while minimizing unnecessary broad-spectrum antimicrobial exposure. Longitudinal monitoring, antibiotic use analysis, and resistance testing would better clarify resistance evolution and the effectiveness of interventions in future multicenter studies.

5. Conclusion

This study aimed to provide an overview of pathogens and AMR among adult ICU patients. These results show that Gram-negative organisms, specifically Acinetobacter baumannii, Klebsiella pneumoniae, and Pseudomonas aeruginosa, played a significant role in the resistance burden observed in this group. Ongoing microbiological surveillance and appropriate antimicrobial management are important, given the high levels of MDR and Carbapenem resistance among these pathogens. Previous antibiotic use, mechanical ventilation, and longer ICU stay are associated with a higher risk of MDR infection, but this may be affected by the study design. Additional multicenter and molecular studies are needed to establish resistance mechanisms and inform infection control measures.

Declarations

Ethics Approval and Consent to Participate

This study was approved by the Institutional Ethics Review Committee (Ethics Approval No.: FBS/ERC/2024/05). As a retrospective study involving the analysis of existing ICU patient records and microbiological data, informed consent was waived by the ethics committee. All patient information was anonymized, kept confidential, and used solely for research purposes in accordance with ethical guidelines.

Consent for Publication

Not applicable.

Competing Interests

The authors declare that they have no competing interests. No financial, personal, or professional relationships influenced the design, analysis, interpretation, or reporting of this study.

Authors Information

Nahid Amin[1]

E-mail: nahid2u@gmail.com

[1]Department of Public Health, Anwer Khan Modern University, Dhaka, Bangladesh.

Md Javed Alam[2]

Email: jalam866138@gmail.com

[2]Intensive Care Unit, Popular Medical College Hospital, Dhaka-1205, Bangladesh.

Dr Tufael[3]

Email: tofayelahmed083@gmail.com

[3]Department of Biochemistry, Parul University, Vadodara-391760 Gujarat, India.

Md. Abul Kashem Tang.[4]

Email: mkashemsa@gmail.com

[4]Department of Applied Nutrition and Food Technology Islamic University, Kushtia-7003, Bangladesh.

Nirmal Chandra Mahat[4]

Email: nirmal.anft.iu@gmail.com

[4]Department of Applied Nutrition and Food Technology Islamic University, Kushtia-7003, Bangladesh.

Suhel Ahmed[5]

Email: suhel.pharma@gmail.com

[5]Department of Public Health, Daffodil International University, Dhaka, Bangladesh.

Amena Khatun Manica[6]

Email: monica.95amena@gmail.com

[6]Department of Chemistry, University of New Haven, West Haven, CT, United States.

Md Abu Bakar Siddique[7]

Email: abubakars1861@gmail.com

[7]Department of Biological Sciences, St John's University, NY, USA.

Papiya Sultana Sharker Sharna[8]

Email: piya4p@gmail.com

[8]Acute & Intensive Care Unit, KC Hospital & Diagnostic Centre, Dhaka, Bangladesh

Hasibul Hasan[9]

Email: hasib0642@gmail.com

[9]Clinical Nutritionist, Intensive Care Unit, Rajshahi Medical College Hospital, Rajshahi, Bangladesh.

Vijay Jagdish Upadhye[10]*

Email: vijay.upadhye35296@paruluniversity.ac.in

[10]Department of Microbiology, Parul Institute of Applied Sciences and Research and Development Cell, Parul University, Vadodara, Gujarat, 391760, India.

Funding

This study received no external funding. All research activities were supported by institutional resources and authors' contributions.

Author Contribution

NA contributed to the conceptualization, methodology, investigation, data curation, and writing of the original draft. MJA contributed to literature review, formal analysis, and manuscript revision. DT contributed to data collection, methodological support, and visualization. MAKT contributed to formal analysis, validation, and interpretation of results. NCM, SA, AKM, MABS, PSSS, and HH contributed to investigation, data analysis, literature assessment, visualization, and critical revision of the manuscript. VJU contributed to conceptualization, supervision, project administration, funding acquisition, critical revision, and final approval of the manuscript. All authors read and approved the final version of the manuscript.

Acknowledgement

Not Applicable.

Availability of Data and Materials

The datasets generated and/or analyzed during the current study are not publicly available due to patient confidentiality and ethical restrictions.

References

1. Grasselli G, Scaravilli V, Mangioni D, Scudeller L, Alagna L, Bartoletti M, et al. Hospital-Acquired Infections in Critically Ill Patients With COVID-19. Chest. 2021;160:454–65. https://doi.org/10.1016/j.chest.2021.04.002.
2. Odoom A, Donkor ES. Prevalence of Healthcare-Acquired Infections Among Adults in Intensive Care Units: A Systematic Review and Meta-Analysis. Health Sci Rep. 2025;8. https://doi.org/10.1002/hsr2.70939.
3. Tillotson GS, Zinner SH. Burden of antimicrobial resistance in an era of decreasing susceptibility. Expert Rev Anti Infect Ther. 2017;15:663–76. https://doi.org/10.1080/14787210.2017.1337508.
4. Anand G, Lahariya R, Priyadarshi K, Sarfraz A. Emerging threat of WHO priority pathogens in ICU-associated CLABSI and CAUTI: an integrated analysis of resistance patterns, epidemiological trends, and stewardship strategies. Acta Clin Belg. 2025;80:135–45. https://doi.org/10.1080/17843286.2025.2546420.
5. Anand G, Lahariya R, Priyadarshi K. The rise of WHO-priority pathogens in central line associated bloodstream infection: Challenging the AWaRe paradigm in critical care. World J Microbiol

Biotechnol. 2026;42:55. https://doi.org/10.1007/s11274-026-04797-1.

6. Bereanu AS, Vintilă BI, Oprinca-Muja L-A, Bereanu R, Codru IR, Bădilă RM, et al. Prevalence and Multidrug Resistance of WHO-Priority Bacterial Pathogens in a Romanian Intensive Care Unit. J Clin Med. 2026;15:2799. https://doi.org/10.3390/jcm15072799.
7. Vance MK, Cretella DA, Ward LM, Vijayvargiya P, Garrigos ZE, Wingler MJB. Risk Factors for Bloodstream Infections Due to ESBL-Producing Escherichia coli, Klebsiella spp., and Proteus mirabilis. Pharmacy. 2023;11:74. https://doi.org/10.3390/pharmacy11020074.
8. Jalil MB, Al Atbee MYN. The prevalence of multiple drug resistance *Escherichia coli* and *Klebsiella pneumoniae* isolated from patients with urinary tract infections. J Clin Lab Anal. 2022;36. https://doi.org/10.1002/jcla.24619.
9. Hyun M, Lee JY, Lim KR, Kim Hah. Clinical Characteristics of Uncomplicated Acute Pyelonephritis Caused by Escherichia coli and Klebsiella pneumoniae. Infect Dis Ther. 2024;13:581–95. https://doi.org/10.1007/s40121-024-00940-3.
10. Pachori P, Gothalwal R, Gandhi P. Emergence of antibiotic resistance Pseudomonas aeruginosa in intensive care unit; a critical review. Genes Dis. 2019;6:109–19. https://doi.org/10.1016/j.gendis.2019.04.001.
11. Yusuf E, Van Herendael B, Verbrugghe W, Ieven M, Goovaerts E, Bergs K, et al. Emergence of antimicrobial resistance to Pseudomonas aeruginosa in the intensive care unit: association with the duration of antibiotic exposure and mode of administration. Ann Intensive Care. 2017;7:72. https://doi.org/10.1186/s13613-017-0296-z.
12. Hammoudi Halat D, Ayoub Moubareck C. The Current Burden of Carbapenemases: Review of Significant Properties and Dissemination among Gram-Negative Bacteria. Antibiotics. 2020;9:186. https://doi.org/10.3390/antibiotics9040186.
13. Eslami M, Safaripour A, Banihashemian SZ, Nikjoo Niaragh S, Hemmati MA, Shojaeian A, et al. Innovative Antibiotic Therapies for Carbapenem-Resistant Gram-Negative Bacterial Infections: Clinical Efficacy, Safety, and Comparative Studies. Microorganisms. 2025;13:295. https://doi.org/10.3390/microorganisms13020295.
14. Kerimoglu E, Catak T, Kilinc A. Evaluation of Infections Caused by Carbapenem-Resistant Pseudomonas aeruginosa, Acinetobacter baumannii, and Klebsiella pneumoniae in an Intensive Care Unit: A Retrospective Study. Antibiotics. 2025;14:700. https://doi.org/10.3390/antibiotics14070700.
15. Fahim NAE. Prevalence and antimicrobial susceptibility profile of multidrug-resistant bacteria among intensive care units patients at Ain Shams University Hospitals in Egypt—a retrospective study. J Egypt Public Health Assoc. 2021;96:7. https://doi.org/10.1186/s42506-020-00065-8.
16. Uc-Cachón AH, Gracida-Osorno C, Luna-Chi IG, Jiménez-Guillermo JG, Molina-Salinas GM. High Prevalence of Antimicrobial Resistance Among Gram-Negative Isolated Bacilli in Intensive Care Units at a Tertiary-Care Hospital in Yucatán Mexico. Med (B Aires). 2019;55:588. https://doi.org/10.3390/medicina55090588.

17. Gupta R, Malik A, Rizvi M, Ahmed M, Singh A. Epidemiology of multidrug-resistant Gram-negative pathogens isolated from ventilator-associated pneumonia in ICU patients. J Glob Antimicrob Resist. 2017;9:47–50. https://doi.org/10.1016/j.jgar.2016.12.016.
18. Chakraverty R, Kundu AK. Challenges Faced in Prevention and Management of Healthcare-Acquired Pneumonia (HAP) and Ventilator-Associated Pneumonia (VAP). Hospital-Acquired Infections in Intensive Care Unit and their Management. Singapore: Springer Nature Singapore; 2024. pp. 95–107. https://doi.org/10.1007/978-981-96-0018-2_9.
19. D'Souza AW, Potter RF, Wallace M, Shupe A, Patel S, Sun X, et al. Spatiotemporal dynamics of multidrug resistant bacteria on intensive care unit surfaces. Nat Commun. 2019;10:4569. https://doi.org/10.1038/s41467-019-12563-1.
20. Almouwlid A, Albenasy K, Kamel Y, Abdelmoktader A, Alaidarous M, Abdel-Hadi A. Incidence and Antibiotic Susceptibility of Gram-Negative Bacteria Associated With Chest Infections in Intensive Care Unit Patients From a Selected Hospital in the Kingdom of Saudi Arabia. Biomed Res Int. 2025;2025. https://doi.org/10.1155/bmri/5283526
21. Duhaniuc A, Sima CM, Buruiană G, Luncă C, Dorneanu OS. Antibiotic Resistance Patterns of Bacteria Involved in Colonization and/or Infection of Patients in Intensive Care Units in Northeastern Romania. Antibiotics. 2025;14:1063. https://doi.org/10.3390/antibiotics14111063.
22. Alibrahim A, Wani FA, Alruwaili OS, Altaymani S, Alharbi ZA, Alsubaiei S, et al. Prevalence and Resistance Profiles of Acinetobacter baumannii in ICU Patients in Saudi Arabia: A Systematic Review and Meta-Analysis. Antibiotics. 2025;14:1131. https://doi.org/10.3390/antibiotics14111131.
23. Hammoudi Halat D, Ayoub Moubareck C. Hospital-acquired and ventilator-associated pneumonia caused by multidrug-resistant Gram-negative pathogens: Understanding epidemiology, resistance patterns, and implications with COVID-19. F1000Res. 2024;12:92. https://doi.org/10.12688/f1000research.129080.2.
24. Phong DQ, Vinh VH, Van DH, Hieu TM, Huong TTM, Thuong LT, et al. Burden and resistance of Gram-negative pathogens in ICU-acquired infections in Vietnam: a cross-sectional study. Iran J Microbiol. 2026. https://doi.org/10.18502/ijm.v18i1.20904.
25. Chen T-A, Chuang Y-T, Lin H-Y, Chang Y-F, Hsieh Y-H, Chen C-H, et al. Serratia marcescens in Intensive Care Units: Molecular Epidemiology, Biofilm-Mediated Persistence, Antimicrobial Resistance, and Genomic Surveillance. Int J Mol Sci. 2026;27:5697. https://doi.org/10.3390/ijms27135697.
26. Darouei B, Jafari S, Rostami S, Nasri P, Mahjoobipour H, Abbasi S. Epidemiology, risk factors, and antimicrobial resistance of nosocomial infections in the intensive care unit trauma patients: A cross-sectional study. J Res Med Sci. 2025;30. https://doi.org/10.4103/jrms.jrms_469_25.
27. Da Costa P, Loureiro L, Matos A. Transfer of Multidrug-Resistant Bacteria Between Intermingled Ecological Niches: The Interface Between Humans, Animals and the Environment. Int J Environ Res Public Health. 2013;10:278–94. https://doi.org/10.3390/ijerph10010278.

28. Bahmani F, Shayanmanesh M, Safari M, Alaei A, Yasaman Pouriafar, Rasti Z, et al. Bone marrow microenvironment in myelodysplastic neoplasms: insights into pathogenesis, biomarkers, and therapeutic targets. Cancer Cell Int. 2025;25:175. https://doi.org/10.1186/s12935-025-03793-z.
29. Pérez-Nadales E, Fernández-Ruiz M, Gutiérrez-Gutiérrez B, Pascual Á, Rodríguez-Baño J, Martínez-Martínez L, et al. Extended-spectrum β-lactamase-producing and carbapenem-resistant Enterobacterales bloodstream infection after solid organ transplantation: Recent trends in epidemiology and therapeutic approaches. Transpl Infect Disease. 2022;24. https://doi.org/10.1111/tid.13881.
30. Shorr AF. Epidemiology and Economic Impact??of Meticillin-Resistant Staphylococcus aureus. PharmacoEconomics. 2007;25:751–68. https://doi.org/10.2165/00019053-200725090-00004.
31. Soe PE, Han WW, Sagili KD, Satyanarayana S, Shrestha P, Htoon TT, et al. High Prevalence of Methicillin-Resistant Staphylococcus aureus among Healthcare Facilities and Its Related Factors in Myanmar (2018–2019). Trop Med Infect Dis. 2021;6:70. https://doi.org/10.3390/tropicalmed6020070.
32. Haque S, Ahmed A, Islam N, Haque FKM. High Prevalence of Multidrug-Resistant Bacteria in the Trachea of Intensive Care Units Admitted Patients: Evidence from a Bangladeshi Hospital. Antibiotics. 2024;13:62. https://doi.org/10.3390/antibiotics13010062.
33. El mekes A, Zahlane K, Ait said L, Tadlaoui Ouafi A, Barakate M. The clinical and epidemiological risk factors of infections due to multi-drug resistant bacteria in an adult intensive care unit of University Hospital Center in Marrakesh-Morocco. J Infect Public Health. 2020;13:637–43. https://doi.org/10.1016/j.jiph.2019.08.012.
34. Dowzicky MJ, Chmelařová E. Antimicrobial susceptibility of Gram-negative and Gram-positive bacteria collected from Eastern Europe: Results from the Tigecycline Evaluation and Surveillance Trial (T.E.S.T.), 2011–2016. J Glob Antimicrob Resist. 2019;17:44–52. https://doi.org/10.1016/j.jgar.2018.11.007.
35. Piotrowski M, Alekseeva I, Arnet U, Yücel E. Insights into the Rising Threat of Carbapenem-Resistant Enterobacterales and Pseudomonas aeruginosa Epidemic Infections in Eastern Europe: A Systematic Literature Review. Antibiotics. 2024;13:978. https://doi.org/10.3390/antibiotics13100978.
36. Sakalauskienė GV, Malcienė L, Stankevičius E, Radzevičienė A. Unseen Enemy: Mechanisms of Multidrug Antimicrobial Resistance in Gram-Negative ESKAPE Pathogens. Antibiotics. 2025;14:63. https://doi.org/10.3390/antibiotics14010063.
37. Shepherd MJ, Fu T, Harrington NE, Kottara A, Cagney K, Chalmers JD, et al. Ecological and evolutionary mechanisms driving within-patient emergence of antimicrobial resistance. Nat Rev Microbiol. 2024;22:650–65. https://doi.org/10.1038/s41579-024-01041-1.
38. Fatima Z, Purkait D, Rehman S, Rai S, Hameed S. Multidrug resistance: a threat to antibiotic era. Biological and Environmental Hazards, Risks, and Disasters. Elsevier; 2023. pp. 197–220. https://doi.org/10.1016/B978-0-12-820509-9.00014-9.

39. Fodor A, Abate BA, Deák P, Fodor L, Gyenge E, Klein MG, et al. Multidrug Resistance (MDR) and Collateral Sensitivity in Bacteria, with Special Attention to Genetic and Evolutionary Aspects and to the Perspectives of Antimicrobial Peptides—A Review. Pathogens. 2020;9:522. https://doi.org/10.3390/pathogens9070522.
40. Abbas A, Barkhouse A, Hackenberger D, Wright GD. Antibiotic resistance: A key microbial survival mechanism that threatens public health. Cell Host Microbe. 2024;32:837–51. https://doi.org/10.1016/j.chom.2024.05.015.
41. Terreni M, Taccani M, Pregnolato M. New Antibiotics for Multidrug-Resistant Bacterial Strains: Latest Research Developments and Future Perspectives. Molecules. 2021;26:2671. https://doi.org/10.3390/molecules26092671.

Figures

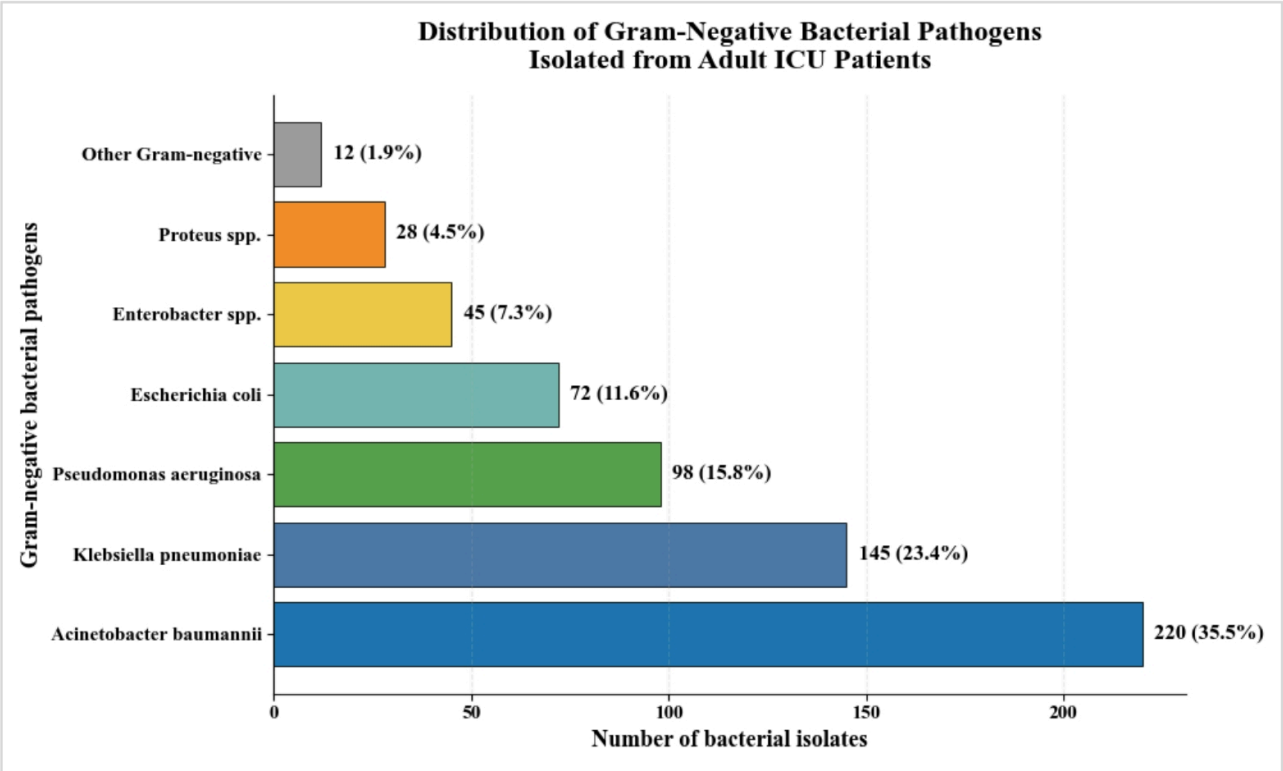


Figure 1

Distribution of Gram-negative bacterial pathogens isolated from adult ICU patients. Bars represent the number of recovered Gram-negative bacterial isolates, with percentages indicating the relative contribution of each pathogen among the total Gram-negative isolates.

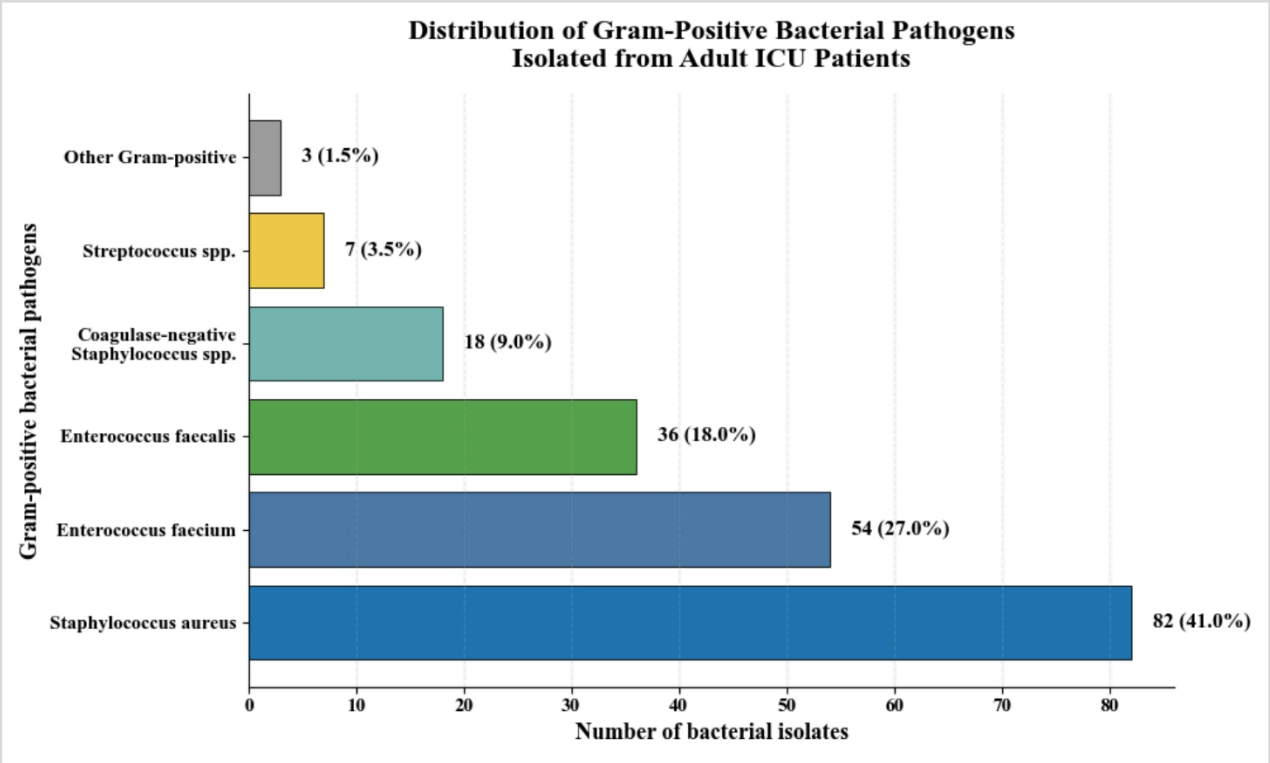


Figure 2

Distribution of Gram-positive bacterial pathogens isolated from adult ICU patients. Bars represent the number of recovered Gram-positive bacterial isolates, with percentages indicating the relative contribution of each pathogen among total Gram-positive isolates.

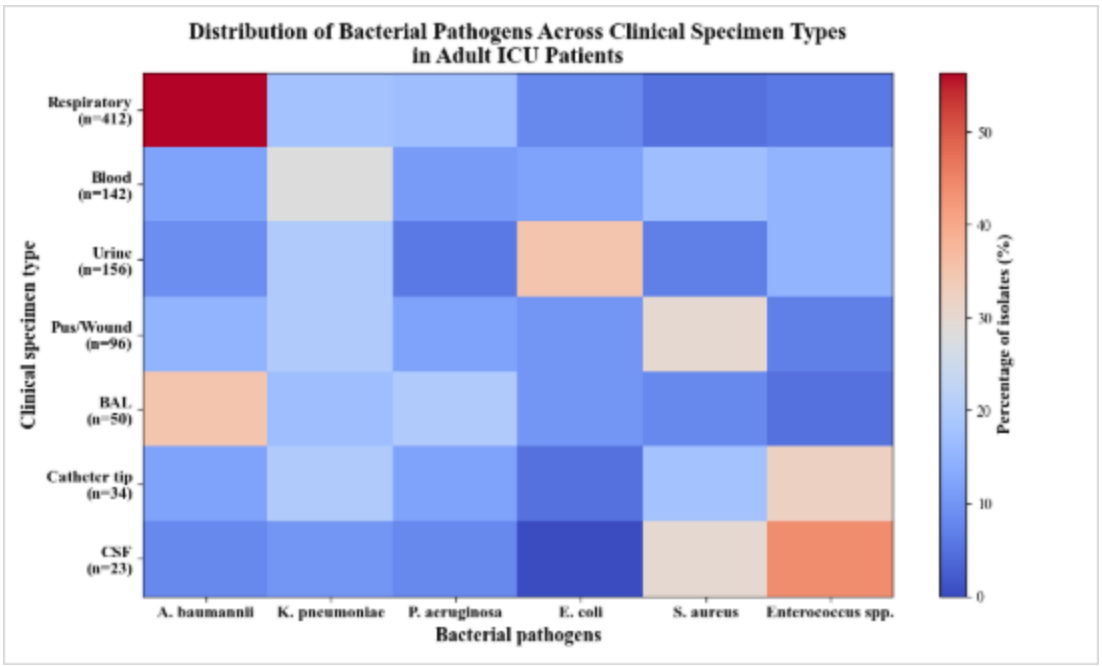


Figure 3

Specimen-wise distribution of bacterial pathogens isolated from adult ICU patients. The heatmap represents the relative contribution of individual bacterial pathogens within each clinical specimen category. Color intensity indicates the percentage distribution of isolates recovered from each specimen type, with higher intensity representing greater pathogen predominance.

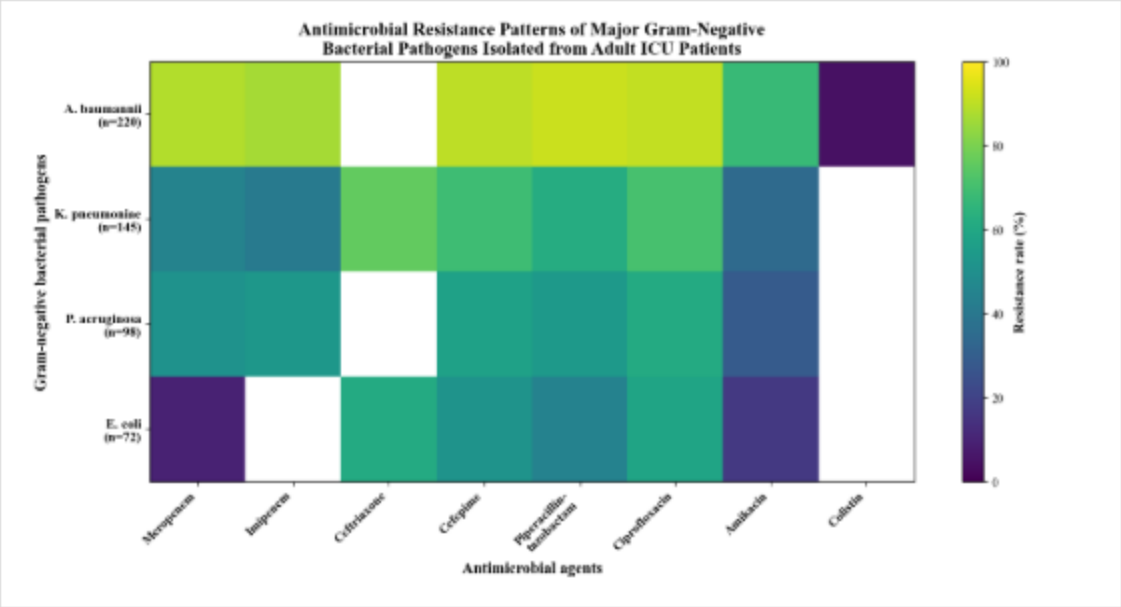


Figure 4

Antimicrobial resistance patterns of major Gram-negative bacterial pathogens isolated from adult ICU patients. The heatmap shows resistance rates (%) for each pathogen–antimicrobial combination; higher color intensity indicates greater resistance. NA indicates not tested or not applicable.

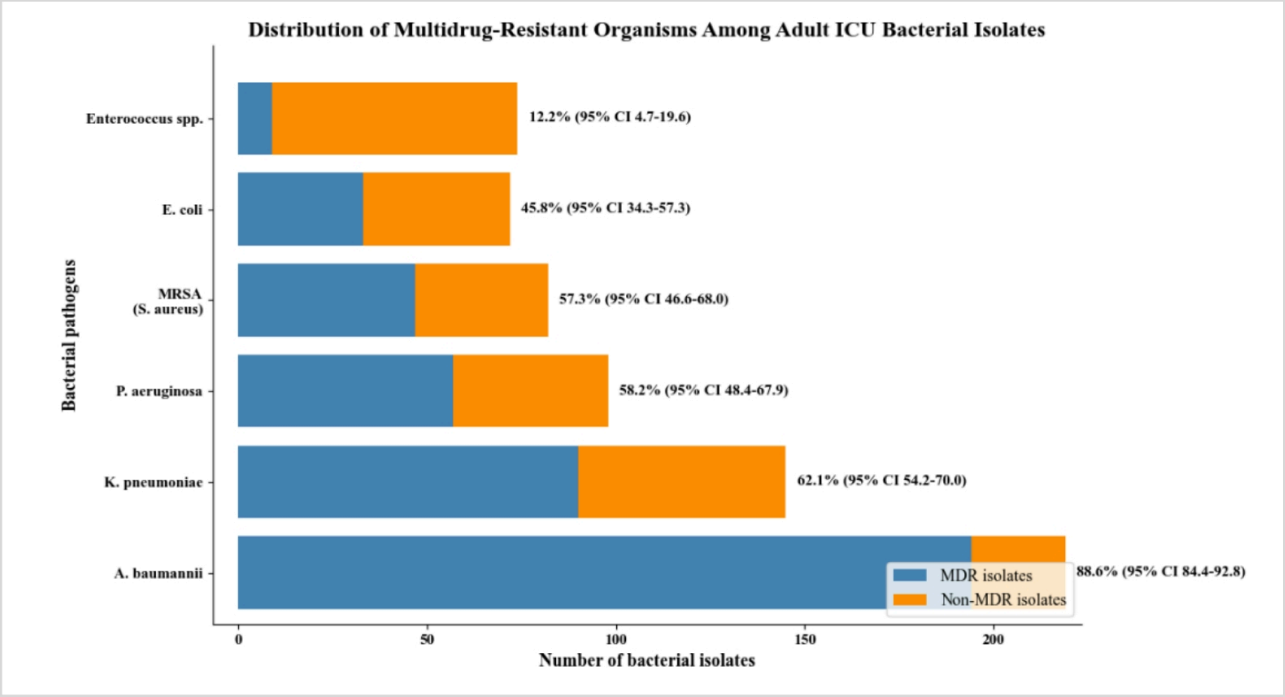


Figure 5

Distribution and prevalence of multidrug-resistant organisms among bacterial isolates recovered from adult ICU patients. Stacked bars represent MDR and non-MDR isolates for each bacterial pathogen, with MDR prevalence estimates calculated among total isolates.

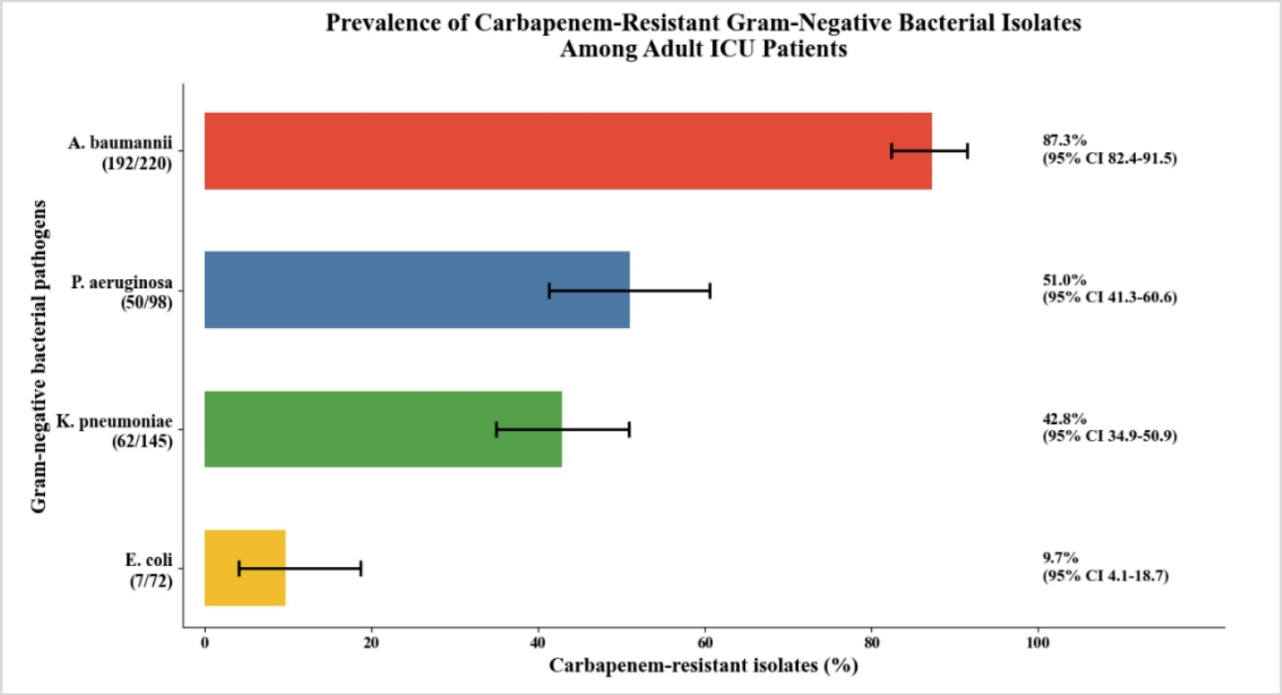


Figure 6

Prevalence of carbapenem-resistant Gram-negative bacterial isolates among adult ICU patients. Bars represent the proportion of carbapenem-resistant isolates among tested bacterial species, with error bars indicating 95% confidence intervals.