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ORIGINAL ARTICLE

Burden and resistance of Gram-negative pathogens in ICU-acquired infections in Vietnam: a cross-sectional study

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ABSTRACT

Background and Objectives: This study aimed to describe the burden, pathogen distribution, antimicrobial resistance patterns, and selected clinical outcomes of intensive care unit (ICU)-acquired Gram-negative bacteria (GNB) infections in Vietnam, with exploratory comparative analyses of outcomes.

Materials and Methods: A retrospective descriptive study with comparative analyses was conducted among 102 adult patients with culture-confirmed ICU-acquired GNB infections at E Hospital, Hanoi. Demographic, clinical, microbiological, and outcome data were extracted from medical records. Antimicrobial susceptibility testing was performed according to Clinical and Laboratory Standards Institute guidelines. Comparisons between outcome groups were assessed using chi-square test, with effect sizes quantified using Cramer's V.

Results: Pneumonia was the predominant infection (70.5%), followed by urinary tract (15.2%) and bloodstream infections (10.6%). GNB accounted for 68.3% of all hospital-acquired infections (HAIs), with *Acinetobacter baumannii* (43.4%), *Pseudomonas aeruginosa* (24.8%), and *Klebsiella pneumoniae* (13.9%) being the most frequent pathogens. The predominant pathogens exhibited extensive resistance to β-lactams, cephalosporins, and carbapenems. Susceptibility was largely retained only to colistin, tigecycline, and amikacin. Mechanical ventilation was significantly associated with death or a severe clinical outcome ($p = 0.03$; Cramer's $V = 0.21$).

Conclusion: GNB dominate ICU-acquired infections in Vietnam and demonstrate alarming antimicrobial resistance, underscoring the urgent need for strengthened infection control and antimicrobial stewardship.

Keywords: Hospital-acquired infection; Gram-negative bacteria; Drug resistance; Microbial; Intensive care units; Pneumonia; Ventilator-associated; Antimicrobial stewardship

INTRODUCTION

Hospital-acquired infections (HAIs) remain a major challenge for modern healthcare systems, particularly in Intensive Care Units (ICUs), where patients are highly vulnerable because of severe illness, invasive procedures, and frequent exposure to broad-spectrum antibiotics. Gram-negative bacteria, including *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and members of the Enterobacteriaceae family, are among the most common causes of ICU-acquired infections and are increasingly asso-

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ciated with resistance to multiple classes of antimicrobial agents, including carbapenems (1, 2). These infections are linked to increased morbidity and mortality, prolonged hospital stays, and rising healthcare costs due to therapeutic failure and complications (2, 3).

Antimicrobial resistance (AMR) among Gram-negative bacteria is driven by several well-established phenotypic mechanisms, most notably the production of β-lactamases, including extended-spectrum β-lactamases and carbapenemases, which reduce or abolish the activity of β-lactam antibiotics (4). In addition, the widespread empirical use of broad-spectrum antimicrobials in critically ill patients, often initiated before definitive microbiological results are available, creates strong selective pressure that promotes the emergence and persistence of multidrug-resistant organisms (5). Together, these factors contribute to the growing difficulty of managing ICU-acquired infections using standard antimicrobial regimens.

In Vietnam, the AMR burden in ICUs reflects this global trend and poses a substantial public health concern. Previous studies have reported high rates of colonization and infection with antimicrobial-resistant organisms among ICU patients, with nosocomial transmission playing an important role in sustaining endemic resistance (6). Commonly identified pathogens include extended-spectrum β-lactamase–producing *Escherichia coli* and *Klebsiella pneumoniae*, as well as carbapenem-resistant *Acinetobacter baumannii* (6, 7). The increasing prevalence of multidrug-resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) Gram-negative bacteria underscores the need for strengthened infection prevention strategies and antimicrobial stewardship programs aimed at optimizing antibiotic use and limiting cross-transmission in critical-care settings (1, 8).

Despite growing awareness of this problem, data describing the distribution of Gram-negative pathogens and their antimicrobial resistance patterns in Vietnamese ICUs remain limited and are often derived from single-center experiences. Within this context, the present study aims to provide updated, hospital-based data on ICU-acquired Gram-negative bacterial infections in Vietnam, focusing on pathogen distribution, phenotypic antimicrobial susceptibility patterns, and selected clinical outcomes. By characterizing these features within a clearly defined analytical scope, the study seeks to contribute practical evidence to support local infection control measures and antimicrobial stewardship efforts.

MATERIALS AND METHODS

Study design and patients. A retrospective single-center descriptive study was conducted in the intensive care unit (ICU) of E Hospital, Hanoi, Vietnam, from January to December 2024. The study included all adult patients (≥18 years) diagnosed with hospital-acquired infections (HAIs). HAIs were defined according to Centers for Disease Control and Prevention (CDC) criteria as infections occurring 48 hours or more after hospital admission, which were not present or incubating at admission (9). Only patients with culture-confirmed Gram-negative bacterial infections were included. A total of 102 eligible patients were analyzed. Cases lacking culture confirmation or complete medical records were excluded. The study protocol was approved by the institutional ethics committee of E Hospital. Due to the retrospective design and use of anonymized data, informed consent was waived in accordance with institutional and national regulations.

Data collection and measurements. Clinical data, laboratory results, and infection control records were reviewed using a standardized form. Microbiological cultures and antibiotic susceptibility testing were performed using the standard Kirby–Bauer disk diffusion method on Mueller–Hinton agar, with inoculum density adjusted to 0.5 McFarland turbidity and incubation at 35 ± 2°C for 16-18 hours. Inhibition zone diameters were measured in millimeters and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing (M100, 2023 edition), with quality control strains included in each run to ensure methodological validity. Disk diffusion results were classified as susceptible, intermediate, or resistant based on CLSI clinical breakpoints for Gram-negative bacteria (10). Data were securely managed using the REDCap system with coded identifiers. Variables included demographic information, comorbidities, infection type (e.g., pneumonia, bloodstream, urinary, or surgical site infection), invasive device use, laboratory findings, and treatment outcomes.

Isolates were classified as multidrug-resistant (MDR), extensively drug-resistant (XDR), or pan-drug-resistant (PDR) according to the standardized international definitions proposed by Magiorakos et al. (2012) (11). MDR was defined as non-susceptibility to at least one agent in three or more antimicrobial categories, XDR as non-susceptibility to at least one agent in all but two or fewer categories, and PDR as non-susceptibility to all agents in all antimicrobial categories (11). Non-susceptibility included resistant, intermediate, or non-susceptible results based on CLSI clinical breakpoints, and only acquired resistance was considered.

Statistical analysis and ethics. Data were analyzed using SPSS version 20.0 (IBM Corp., Armonk, NY, USA). Descriptive statistics were used to summarize demographic and clinical characteristics. Continuous variables were expressed as mean ± standard deviation or median with interquartile range, as appropriate, while categorical variables were presented as frequencies and percentages. Associations between categorical variables and clinical outcomes were assessed using the chi-square test. Effect sizes were quantified using Cramer's V to evaluate the strength of associations beyond statistical significance. Statistical significance was defined as a two-sided p-value < 0.05. Given the descriptive and single-center design, multivariate analyses were not performed.

RESULTS

This study recruited 102 ICU patients with hospital-acquired infections caused by Gram-negative bacteria. Most were aged ≥50 years (82.4%) and male (58.8%). Common comorbidities included hypertension (40.2%), diabetes (24.5%), and cardiovascular disease (22.5%). The main reasons for ICU admission were respiratory failure or pneumonia (36.3%), trauma (20.6%), and stroke (18.6%), followed by septic shock, coma, and sepsis (Table 1).

A total of 76 of 102 patients (74.5%) had an active infection at the time of ICU admission, most commonly pneumonia (62/89 infections, 69.7%), followed by urinary tract infection (12.4%) and bloodstream infection (7.9%). Among patients with infection at admission (n = 74 isolates), the most frequently identified pathogens were *Klebsiella pneumoniae* (20.3%), *Acinetobacter baumannii* (10.8%), and *Pseudomonas aeruginosa* (10.8%), followed by *Escherichia coli* (5.4%) and fungal pathogens, mainly *Candida tropicalis* (8.1%) and *Candida albicans* (5.4%) (Table 2).

A total of 189 hospital-acquired infection episodes identified during ICU hospitalization. The higher number of infections (n = 189) compared with patients (n = 102) reflects multiple infection episodes and/or polymicrobial infections occurring in individual patients during their ICU stay. Gram-negative bacteria accounted for 68.3% (129/189) of all HAIs, followed by fungi and other organisms (21.2%) and Gram-positive bacteria (10.6%) (Table 3).

Among Gram-negative HAIs (n = 132 infection episodes), pneumonia was the predominant infection type (93/132, 70.5%), followed by urinary tract infection (15.2%) and bloodstream infection (10.6%). In contrast to infections present at admission (Table 2), ICU-acquired Gram-negative infections were dominated by *Acinetobacter baumannii*, which accounted for 43.4% (56/129) of isolates, followed by *Pseudomonas aeruginosa* (24.8%) and *Klebsiella pneumoniae* (13.9%). This shift in pathogen distribution highlights the increased contribution of non-fermenting Gram-negative bacilli to ICU-acquired infections. The apparent differences in frequencies of *Klebsiella pneumoniae* and *Acinetobacter baumannii* between Tables 2 and 3 reflect distinct clinical contexts (infection at admission versus hospital-acquired infection) rather than data inconsistency.

Acinetobacter baumannii (n = 46) showed high levels of resistance to most tested β-lactams and fluoroquinolones, including piperacillin/tazobactam, ceftazidime, cefepime, meropenem, and ciprofloxacin, while lower resistance was observed to amikacin and colistin. *Pseudomonas aeruginosa* (n = 27) demonstrated substantial resistance to ceftazidime, cefepime, meropenem, and ciprofloxacin, with comparatively lower resistance rates to amikacin and colistin. *Klebsiella pneumoniae* (n = 19) exhibited high resistance to β-lactams and fluoroquinolones, whereas resistance to amikacin, colistin, and tigecycline was less frequent. *Escherichia coli* (n = 7) showed marked resistance to cephalosporins and fluoroquinolones, with lower resistance rates to carbapenems and aminoglycosides, and retained susceptibility to colistin and tigecycline (Table 4).

Table 1. General characteristics and admission causes of patients with hospital-acquired infections caused by Gram-negative bacteria (n = 102)

Characteristics	Category	Frequency (n)	Percent (%)
Age group	< 50 years	18	17.6
	≥ 50 years	84	82.4
Gender	Male	60	58.8
	Female	42	41.2
Comorbidities / Medical history	Diabetes mellitus	25	24.5
	Hypertension	41	40.2
	Cardiovascular disease	23	22.5
	Cance	9	8.8
	Stroke	14	13.7
	Chronic kidney disease	11	10.8
	Chronic obstructive pulmonary disease	5	4.9
	Autoimmune disease	18	17.6
	Alcohol abuse	4	3.9
	Polytrauma with prior surgery	6	5.9
Reason for ICU admission	Respiratory failure – pneumonia – OPA	37	36.3
	Coma	8	7.8
	Septic shock – multiple organ failure	14	13.7
	Intracerebral / ischemic stroke	19	18.6
	Polytrauma	21	20.6
	Sepsis	8	7.8
	Peritonitis – necrotizing infection	3	2.9
	Poisoning	1	1.0

Abbreviations: OPA, Opportunistic pulmonary abscess; ICU, Intensive Care Unit.

Table 2. Types and causative agents of infections at admission among patients with hospital-acquired infections caused by Gram-negative bacteria (n = 102)

Category	Type / Pathogen	Frequency (n)	Percent (%)
Infection status at admission	With infection at admission	76	74.5
	- Pneumonia	62	69.7
	- Urinary tract infection	11	12.4
	- Bloodstream infection	7	7.9
	- Intra-abdominal infection	3	3.4
	- Surgical site infection	2	2.2
	- Skin and soft tissue infection	4	4.5
	Without infection at admission	26	25.5
Causative agents among patients with infection at admission (n = 74)	*Klebsiella pneumoniae*	15	20.3
	Escherichia coli	4	5.4
	Acinetobacter baumannii	8	10.8
	Staphylococcus aureus	1	1.4
	Pseudomonas aeruginosa	8	10.8
	Candida tropicalis	6	8.1
	Candida albicans	4	5.4
	Klebsiella aerogenes	4	5.4

Table 2. Continuing...

Enterococcus faecium	4	5.4
Enterococcus faecalis	1	1.4
Enterobacter cloacae	2	2.7
Burkholderia cepacia	1	1.4
Streptococcus pyogenes	1	1.4
Proteus mirabilis	1	1.4
Chryseobacterium indologenes	1	1.4
Klebsiella oxytoca	1	1.4

Table 3. Distribution of hospital-acquired infections by microbial group, type, and Gram-negative pathogens (n = 189)

Category	Type / Pathogen	Frequency (n)	Percent (%)
Microbial group distribution in hospital-acquired infections	Gram-negative bacteria	129	68.3
	Gram-positive bacteria	20	10.6
	Fungi and others	40	21.2
Types of hospital-acquired infections caused by Gram-negative bacteria (n = 132)	Pneumonia	93	70.5
	Urinary tract infection	20	15.2
	Bloodstream infection	14	10.6
	Surgical site infection	5	3.8
Distribution of Gram-negative bacterial species in hospital-acquired infections (n = 129)	*Acinetobacter baumannii*	56	43.4
	Pseudomonas aeruginosa	32	24.8
	Klebsiella pneumoniae	18	13.9
	Klebsiella aerogenes	12	9.3
	Escherichia coli	8	6.2
	Enterobacter cloacae	1	0.8
	Proteus mirabilis	1	0.8
	Elizabethkingia meningoseptica	1	0.8

Among the evaluated characteristics, mechanical ventilation was the only variable that differed significantly between outcome groups, with all survived/discharged patients requiring mechanical ventilation (100.0%) compared with 91.5% in the death/severe outcome group ($p = 0.03$; Cramer's $V = 0.21$). No statistically significant differences were observed between the two outcome groups for bloodstream infection, hospital-acquired pneumonia, urinary tract infection, or surgical site infection (all $p > 0.05$). Overall, hospital-acquired pneumonia was the most common infection in the study population (91.2%), and the death/severe outcome rate was 46.1% (47/102) (Table 5).

DISCUSSION

HAIs in ICUs remain a critical global concern, especially those caused by Gram-negative bacteria (GN), due to their high morbidity, mortality, and economic impact. In the present study, Gram-negative bacteria accounted for 68.3% of all hospital-acquired infections, underscoring their predominance in the ICU setting. This finding directly addresses the primary study objective of describing the burden of GNB-associated HAIs in a Vietnamese ICU and confirms their dominant role in severe nosocomial infections. This result is consistent with international data showing that GNB are responsible for the majority of ICU-associated infections. The EUROBACT-2 study reported that 59% of hospital-acquired bloodstream infections in ICUs were due to GNB, with *Klebsiella* spp., *Acinetobacter* spp., and *Escherichia coli* being the leading pathogens (12). Similarly, a multicenter study in Italy found that carbapenem-resistant *Enterobacterales* (CRE) and *Pseudomonas aeruginosa* occurred at rates of 3.57 and 1.74 per 1,000 patient-days, respectively, accounting for

19.2% and 26.8% of all infections caused by these organisms (13).

Comparable patterns have been reported from Vietnam and other low- and middle-income countries, where ICU settings are characterized by high antimicrobial pressure and limited infection-control resources. Large-scale Vietnamese studies consistently demonstrate a predominance of Gram-negative bacteria in ICU-acquired infections, with a national survey of adult ICUs reporting that Gram-negative organisms accounted for 84.2% of all hospital-acquired infection isolates, most commonly *Acinetobacter baumannii* (24.4), *Pseudomonas aeruginosa* (13.8%), *Klebsiella pneumoniae* (11.6%), and *Escherichia coli* (5.4%) (14). These national data closely align with the present study, in which pneumonia accounted for 70.5% of Gram-negative HAIs and *A. baumannii*, *P. aeruginosa*, and *K. pneumoniae* were the leading pathogens. Resistance patterns reported in Vietnam further underscore the clinical impact of these infections, with carbapenem resistance rates reaching 89.2% for *A. baumannii*, 55.7% for *P. aeruginosa*, and 14.9% for *K. pneumoniae* (14), alongside a high prevalence of extended-spectrum β-lactamase–producing *E. coli* and *Klebsiella* spp. (7, 15). Together, these findings reflect a persistent and severe burden of multidrug-resistant Gram-negative pathogens in Vietnamese ICUs, consistent with both regional and global trends in critically ill, mechanically ventilated populations.

The antimicrobial resistance (AMR) profiles observed in this study highlight the second core objective, namely characterization of resistance patterns among ICU-acquired GNB. *A. baumannii*, *P. aeruginosa*, and *K. pneumoniae* demonstrated very high resistance rates to β-lactams, carbapenems, and fluoroquinolones, confirming their role as major ESKAPE pathogens. In this cohort, *A. baumannii* exhibited 100% resistance to ceftazidime, cefepime, meropenem, and piperacillin/tazobactam, while *P. aeruginosa* showed resistance rates of approximately 70-80% to the same antibiotic classes. *K. pneumoniae* also displayed widespread resistance to carbapenems (89.5%) and cephalosporins (100%), whereas *E. coli* retained comparatively lower resistance to carbapenems and tigecycline.

Globally, *A. baumannii* remains among the most resistant Gram-negative species, with 91.1% of isolates in Brazil classified as multidrug-resistant (MDR)

Table 4. Comparative antibiotic susceptibility results of major Gram-negative bacteria isolated from hospital-acquired infections

Antibiotic	*A. baumannii* (n = 46)			*P. aeruginosa* (n = 27)			*K. pneumoniae* (n = 19)			*E. coli* (n = 7)		
	I n (%)	R n (%)	S n (%)	I n (%)	R n (%)	S n (%)	I n (%)	R n (%)	S n (%)	I n (%)	R n (%)	S n (%)
Ticarcillin	–	9 (19.6)	–	–	4 (14.8)	–	–	–	–	–	–	–
Piperacillin	–	9 (19.6)	–	–	4 (14.8)	–	–	–	–	–	–	–
Piperacillin/tazobactam	–	46 (100.0)	–	–	17 (63.0)	3 (11.1)	–	18 (94.7)	1 (5.3)	–	4 (57.1)	3 (42.9)
Ceftazidime	–	46 (100.0)	–	–	19 (70.4)	8 (29.6)	1 (5.3)	17 (89.5)	1 (5.3)	1 (14.3)	6 (85.7)	–
Ceftazidime/Avibactam	–	–	–	–	14 (51.9)	9 (33.3)	–	11 (57.9)	8 (42.1)	–	3 (42.9)	4 (57.1)
Ceftolozane/Tazobactam	–	–	–	–	10 (37.0)	7 (25.9)	–	17 (89.5)	2 (10.5)	–	4 (57.1)	3 (42.9)
Cefepime	–	46 (100.0)	–	–	19 (70.4)	8 (29.6)	–	19 (100.0)	–	–	6 (85.7)	1 (14.3)
Imipenem	–	9 (19.6)	–	–	3 (11.1)	1 (3.7)	–	–	–	–	–	–
Meropenem	–	46 (100.0)	–	–	20 (74.1)	7 (25.9)	–	17 (89.5)	2 (10.5)	–	3 (42.9)	4 (57.1)
Gentamicin	–	44 (95.7)	2 (4.3)	–	16 (59.3)	7 (25.9)	–	15 (78.9)	4 (21.1)	–	6 (85.7)	1 (14.3)
Amikacin	6 (13.0)	24 (52.2)	3 (6.5)	–	5 (18.5)	11 (40.7)	–	2 (10.5)	5 (26.3)	–	1 (14.3)	2 (28.6)
Ciprofloxacin	–	46 (100.0)	–	–	22 (81.5)	4 (14.8)	–	19 (100.0)	–	–	7 (100.0)	–
Colistin	27 (58.7)	8 (17.4)	–	2 (7.4)	2 (7.4)	–	14 (73.7)	3 (15.8)	–	–	–	6 (85.7)
Tigecycline	–	–	–	–	–	–	2 (10.5)	14 (73.7)	3 (15.8)	–	–	7 (100.0)

Abbreviations: I – Intermediate; R – Resistant; S – Susceptible

Table 5. Comparison of hospital-acquired infections between outcome groups (n = 102)

Characteristic	All patients (n = 102)	Survived / Discharged (n = 55)	Death / Severe outcome (n = 47)	p-value	Cramer's V
	n (%)	n (%)	n (%)		
Bloodstream infection	14 (13.7)	6 (10.9)	8 (17.0)		
Hospital-acquired pneumonia	93 (91.2)	48 (87.3)	45 (95.7)	0.37	0.09
Urinary tract infection	20 (19.6)	12 (21.8)	8 (17.0)	0.13	0.14
Surgical site infection	5 (4.9)	2 (3.6)	3 (6.4)	0.54	0.06
Mechanical ventilation	98 (96.1)	55 (100.0)	43 (91.5)	0.52	0.07
Total	102 (100.0)	55 (53.9)	47 (46.1)	0.03	0.21

(16) and 41.9% of isolates in Thailand reported as extensively drug-resistant (XDR) (17). Although molecular testing was not performed in the present study, these resistance patterns are consistent with global reports dominated by carbapenemase-producing strains, supporting the external validity of the findings. Despite this, colistin and tigecycline continue to demonstrate partial activity against *A. baumannii*, with susceptibility rates of up to 96% reported in Taiwan (18). In the present study, 58.7% of *A. baumannii* isolates remained intermediate to colistin, confirming its continued, albeit limited, therapeutic relevance.

P. aeruginosa also exhibited substantial multidrug resistance, particularly to carbapenems and cephalosporins. Similar trends have been reported internationally; for example, in burn ICUs, 41.4% of *P. aeruginosa* isolates were MDR (19). Although newer β-lactam/β-lactamase inhibitor combinations have demonstrated promising activity, their availability remains limited in many Vietnamese hospitals. The partial preservation of amikacin susceptibility (40.7%) observed in this study therefore has direct clinical relevance in resource-constrained settings, where treatment options are restricted.

K. pneumoniae poses a particularly serious threat due to the global dissemination of carbapenem-resistant strains. In Thailand, 17.2% of isolates were carbapenem-resistant, driven largely by the bla_NDM and bla_OXA-48-like genes (17). Similarly, in Spain, 16.4% of isolates were MDR, with the bla_CTX-M and aac(6')-Ib genes being dominant (20). The high resistance rates observed in the present study mirror these global findings, with only 15.8–26.3% of isolates remaining susceptible to tigecycline and amikacin, underscoring the limited therapeutic arsenal available for ICU-acquired *K. pneumoniae* infections.

Regarding clinical outcomes, the study demonstrated a high proportion of death or severe outcomes (46.1%), reflecting the severity of Gram-negative HAIs in ICU patients. Pneumonia was the predominant infection in both outcome groups and was particularly frequent in the death/severe outcome group (95.7%). To improve interpretability beyond p-values, effect size measures (Cramer's V) were incorporated, allowing assessment of the strength of associations despite the modest sample size. Mechanical ventilation showed a statistically significant association with death/severe outcome ($p = 0.03$) and a moderate effect size (Cramer's $V = 0.21$), supporting its clinical relevance as a marker of disease severity rather than an isolated risk factor. No other infection types demonstrated meaningful effect sizes, suggesting limited discriminatory power in this cohort. The use of effect size measures strengthens the clinical interpretation of findings by distinguishing statistically significant but weak associations from those with potential practical importance, particularly in ICU populations where exposure prevalence is high and sample sizes are limited. This approach aligns with current recommendations for observational clinical research and enhances the robustness of the study conclusions.

Several Vietnam-specific factors may contribute to the high burden of AMR observed, including widespread empirical use of broad-spectrum antibiotics, delayed microbiological diagnostics, high device utilization, and variable adherence to infection-control bundles. Limitations in antimicrobial stewardship programs, particularly in resource-limited ICUs, further exacerbate selective pressure and facilitate the persistence of MDR organisms (21-23).

Limitations. Several limitations warrant careful consideration. First, the retrospective, single-center design limits generalizability to other ICUs in Vietnam. Second, the modest sample size reduces statistical power, particularly for subgroup analyses and rare pathogens. Third, the absence of molecular testing precluded identification of specific resistance genes (e.g., bla_NDM, bla_OXA-48-like) and assessment of clonal transmission, largely due to resource constraints. Fourth, potential selection bias cannot be excluded, as only culture-confirmed cases with complete records were included. Despite these limitations, the study provides valuable, context-specific evidence on the burden, resistance patterns, and clinical impact of Gram-negative HAIs in a major Vietnamese ICU, with important implications for infection control and antimicrobial stewardship.

CONCLUSION

Hospital-acquired infections caused by Gram-negative bacteria remain a critical issue in ICU settings, driven by high rates of multidrug resistance and limited therapeutic options. *A. baumannii*, *P. aeruginosa*, and *K. pneumoniae* were the predominant pathogens, showing extensive resistance to commonly used antibiotics. Strengthening infection prevention, antimicrobial stewardship, and continuous surveillance is essential to control resistance dissemination and improve clinical outcomes among critically ill patients.

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