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Article

High mortality in device-associated infections: a retrospective cohort study from a Brazilian university hospital ICU (2022-2024)

Alta mortalidade em infecções associadas a dispositivos: um estudo de coorte retrospectivo em UTI de um hospital universitário brasileiro (2022-2024)

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Abstract: This study evaluated the clinical impact, microbiological profile, antimicrobial resistance patterns, and clinical outcomes of healthcare-associated infections (HAIs) in intensive care units (ICUs) of a tertiary Brazilian university hospital. This retrospective observational study included adult patients admitted to the Adult, Coronary, and Neurological ICUs between 2022 and 2024 who developed bacterial HAIs from the third day of hospitalization onward. Epidemiological, microbiological, and outcome data were obtained from institutional surveillance systems. Associations between clinical variables and outcomes were assessed using nonparametric tests, chi-square or Fisher's exact tests, and Poisson regression. A total of 429 patients developed 656 HAI episodes. Device-associated infections predominated, particularly ventilator-associated pneumonia (34.8%), bloodstream infections (17.5%), and urinary tract infections (17.1%). Overall in-hospital mortality was 54.5% and was independently associated with increasing age. Gram-negative bacteria were the most frequent pathogens, especially *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Escherichia coli*. Among *K. pneumoniae*, 48.9% were ESBL producers and 22.3%

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were KPC producers. Although resistant phenotypes showed numerically higher mortality, no independent association was observed after adjustment. Device-associated infections impose a substantial burden in ICUs and are predominantly caused by Gram-negative pathogens with relevant resistance patterns observed specifically in organisms such as *K. pneumoniae*. The high mortality observed appears to be primarily associated with patient-related factors such as age, rather than antimicrobial resistance alone.

Keywords: Healthcare-Associated Infections; Intensive Care Units; Drug Resistance, Microbial; Cross Infection; Catheter-Related Infections.

Resumo: Foi avaliado o impacto clínico, o perfil microbiológico, os padrões de resistência antimicrobiana e os desfechos clínicos das infecções relacionadas à assistência à saúde (IRAS) em unidades de terapia intensiva (UTIs) de um hospital universitário terciário brasileiro. Trata-se de um estudo observacional retrospectivo que incluiu pacientes adultos admitidos nas UTIs adulto, coronariana e neurológica entre 2022 e 2024, que desenvolveram IRAS bacterianas a partir do terceiro dia de internação. Dados epidemiológicos, microbiológicos e de desfechos foram obtidos de sistemas institucionais de vigilância. As associações entre variáveis clínicas e desfechos foram avaliadas por testes não paramétricos, teste do qui-quadrado ou exato de Fisher, e regressão de Poisson. Um total de 429 pacientes desenvolveu 656 episódios de IRAS. Predominaram infecções associadas a dispositivos, especialmente pneumonia associada à ventilação mecânica (34,8%), infecções de corrente sanguínea (17,5%) e infecções do trato urinário (17,1%). A mortalidade hospitalar global foi de 54,5% e esteve independentemente associada ao aumento da idade. Bactérias Gram-negativas foram os patógenos mais frequentes, destacando-se *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* e *Escherichia coli*. Entre os isolados de *K. pneumoniae*, 48,9% foram produtores de ESBL e 22,3% produtores de KPC. Embora fenótipos resistentes tenham apresentado mortalidade numericamente maior, nenhuma associação independente foi observada após ajuste. As IRAS associadas a dispositivos representam um importante desafio nas UTIs e são predominantemente causadas por patógenos Gram-negativos, com padrões de resistência relevantes, observados especificamente em organismos como *K. pneumoniae*. A elevada mortalidade observada parece estar associada principalmente a fatores relacionados ao paciente, como a idade, e não apenas à resistência antimicrobiana.

Palavras-chave: Infecções Relacionadas à Assistência à Saúde; Unidades de Terapia Intensiva; Resistência Microbiana a Medicamentos; Infecção cruzada; Infecções Relacionadas a Cateteres.

Introduction

Healthcare-associated infections (HAIs) remain the most frequent adverse events in hospitalized patients and represent a persistent global public health challenge. Defined as infections acquired during healthcare delivery and not present or incubating at the time of admission, HAIs are typically identified after 48–72 hours of hospitalization or shortly after discharge. Although bacteria account for the majority of cases, multiple pathogens may be involved, reinforcing the importance of accurate etiological identification to guide appropriate therapy[1]. In Brazil, recent multicenter cohort studies have demonstrated that healthcare-associated infections significantly contribute to hospital mortality among critically ill patients[2].

In intensive care units (ICUs), the burden of HAIs is disproportionately high. Critically ill patients are frequently exposed to invasive devices, broad-spectrum antimicrobials, and complex supportive therapies, all of which increase susceptibility to infection. Large epidemiological studies have demonstrated that patients with prolonged ICU stays present significantly higher HAI rates, with device-associated infections accounting for a substantial proportion of cases[3,4]. Device-associated infections — including ventilator-associated pneumonia (VAP), catheter-associated bloodstream infections (CLABSIs), and catheter-associated urinary tract infections (CAUTIs) — are consistently associated with worse clinical outcomes, increased length of stay, higher healthcare costs, and elevated mortality rates, which may approach 30% in some cohorts[5,6]. In addition, the ability of microorganisms to adhere to artificial surfaces and form biofilms plays a crucial role in the pathogenesis of device-associated infections, contributing to persistence, resistance to antimicrobial therapy, and increased difficulty in eradication[7].

Beyond their direct clinical consequences, HAIs play a central role in the emergence and dissemination of antimicrobial-resistant pathogens. The ICU environment, characterized by high antimicrobial consumption and selective pressure, favors the proliferation of multidrug-resistant Gram-negative bacilli and resistant Gram-positive organisms[8]. These pathogens complicate empirical therapeutic decisions, often delay effective treatment, and may further impact survival. Knowledge of the local microbiological and resistance profile is therefore essential to optimize antimicrobial stewardship strategies and improve patient outcomes[5].

Despite advances in infection prevention programs, the epidemiological patterns and resistance profiles of HAIs vary considerably across institutions and geographic regions, particularly in tertiary public teaching hospitals in middle-income countries[9,10]. National and international surveillance data consistently highlight device-associated infections as the leading contributors to HAI burden in ICUs, yet local data remain indispensable for guiding institutional policies and empirical treatment protocols[11,12].

In this context, quantifying the burden of device-associated infections, characterizing their microbiological profile, and exploring their potential association with antimicrobial resistance patterns and clinical outcomes are critical steps toward strengthening infection control and stewardship strategies. To date, few studies from middle-income countries have comprehensively evaluated the combined impact of device-associated infections, antimicrobial resistance patterns, and clinical outcomes within a single ICU cohort. Moreover, data integrating microbiological profiles with multivariable-adjusted mortality analysis remain limited in Brazilian tertiary care settings. Therefore, the present study aimed to quantify the burden of device-associated healthcare-associated infections in intensive care units of a Brazilian tertiary university hospital and to explore the microbiological profile and assess factors associated with in-hospital mortality, including selected antimicrobial resistance patterns when available.

Methods

A retrospective observational cohort study was conducted based on surveillance data of healthcare-associated infections (HAIs) reported in the Adult Intensive Care Unit (ICU), Coronary ICU, and Neurological ICU of the Hospital de Clínicas of the Universidade Federal do Triângulo Mineiro (HC-UFTM), located in Uberaba, Minas Gerais, Brazil. Data were organized using Microsoft Excel spreadsheets and subsequently analyzed with R software (version 4.3.1).

Data were obtained from the Hospital Health Surveillance Unit, the Infolab system of the Clinical Analysis and Pathological Anatomy Unit (UACAP), and the AGHU electronic hospital management system of HC-UFTM. The data from institutional systems were integrated using the unique hospital identification number assigned to each patient, allowing the linkage between clinical, microbiological, and outcome information. In cases of multiple infection episodes, each episode was analyzed as an independent event for microbiological characterization, while to patient-level analyses (e.g., mortality) considered only one record per patient. The missing data were handled by complete-case analysis for each specific variable.

The following variables were collected: hospital identification number, sex, age, dates and length of hospital stay, clinical outcome, type of biological specimens collected, microbiological test results, identification of isolated microorganisms, and antimicrobial susceptibility profile, when available. Antimicrobial susceptibility data were not systematically available for all isolates, and detailed resistance analysis was consistently feasible only for selected pathogens, particularly *K. pneumoniae*. Microbial identification was performed using the Vitek® (BioMérieux) automated system. In the absence of automation, microbial identification was performed using conventional manual methods, including macroscopic and microscopic analyses combined with biochemical tests, followed by antimicrobial susceptibility testing (AST) using the disk diffusion method, with interpretive criteria defined by the Brazilian Committee on Antimicrobial Susceptibility Testing (BrCAST)[13]. The absence of antimicrobial susceptibility data was not considered an exclusion criterion; in such cases, patients were retained in the study and included in clinical and outcome analyses, with susceptibility data considered missing only for analyses specifically related to antimicrobial resistance.

Adult patients admitted to the three ICUs between 2022 and 2024 were eligible for inclusion. Inclusion criteria comprised patients who developed bacterial healthcare-associated infections occurring on or after the third day of hospitalization, formally reported to the Hospital Infection Control Committee, according to institutional surveillance protocols. Exclusion criteria included infections exclusively of fungal or viral etiology. In cases of suspected or confirmed coinfection, only episodes with documented bacterial isolation were included in the analysis.

Healthcare-associated infections, including ventilator-associated pneumonia (VAP), central line-associated bloodstream infection (CLABSI), and catheter-associated urinary tract infection (CAUTI), were defined according to the Centers for Disease Control and Prevention (CDC) standardized surveillance criteria[14].

Given the non-parametric and independent nature of the data, the Mann–Whitney U test was used to compare quantitative variables between two independent groups (e.g., age or length of stay according to mortality or infection site). The association between quantitative variables (e.g., age and length of hospital stay) was assessed using Spearman's rank correlation coefficient, considering the absence of normal distribution and the possibility of a monotonic non-linear relationship. Associations between predictors of infection burden were evaluated using Poisson regression, while predictors of in-hospital mortality were assessed using multivariable logistic regression.

Associations between categorical variables were evaluated using the chi-square test of independence. When more than 20% of the contingency table cells had expected frequencies below 5, Fisher's exact test was applied to ensure the validity of the statistical inference. A significance level of 5% ($\alpha = 0.05$) was adopted for all analyses.

This study was designed to evaluate only patients who developed healthcare-associated infections and did not include a control group. Therefore, all comparisons were restricted to subgroups within the infected population

The study was approved by the Research Ethics Committee of the Universidade Federal do Triângulo Mineiro (CAAE: 84578124.3.0000.8667).

Results

During the study period, 429 patients admitted to the ICUs were included, accounting for a total of 656 episodes of healthcare-associated infections (HAIs). Of these patients, 278 (64.8%) were male and 151 (35.2%) were female. Age ranged from 18 to 101 years, with a mean of 58.96 (± 16.68) years.

The mean length of hospital stay was 35.19 (± 33.19) days, whereas the mean interval between hospital admission and infection diagnosis was 18.96 (± 15) days. No significant correlation was observed between age and total length of stay ($p = 0.610$). In contrast, a statistically significant association was identified between age and time to infection acquisition ($p = 0.001$), although the strength of this correlation was weak (Spearman's rho = 0.120). Patients with longer hospital stays experienced a higher number of infectious episodes ($p < 0.001$), with an estimated increase of approximately 0.33% in the expected number of infections for each additional day of hospitalization ($p < 0.001$).

Overall, 235 patients (54.8%) died during hospitalization. The mean length of stay among non-survivors was 30.3 days, shorter than that observed among survivors (41 days). The mean age of patients who died was 62.2 (± 15.2) years, compared with 55.1 (± 17.5) years among those discharged alive, a statistically significant difference ($p < 0.05$).

To further evaluate independent predictors of in-hospital mortality, a multivariable logistic regression model was constructed including age, sex, number of infectious episodes, time to first infection, and presence of ESBL or KPC infection. Age remained independently associated with mortality (OR 1.03 per year; 95% CI 1.02–1.05; $p < 0.001$). The number of infectious episodes showed a trend toward increased mortality (OR 1.34; 95% CI 0.99–1.84; $p = 0.066$). No statistically significant independent association was observed between ESBL or KPC infection and mortality after adjustment (OR 1.42; 95% CI 0.77–2.69; $p = 0.270$). Model diagnostics demonstrated improved fit compared with the null model (null deviance = 590.80; residual deviance = 541.93; AIC = 565.93), with no evidence of multicollinearity (all VIF < 2) (Table 1).

Table 1. Independent predictors of in-hospital mortality in ICU patients with healthcare-associated infections (n = 429).

Variable	Adjusted OR	95% CI	p-value
Age (per year increase)	1.03	1.02 - 1.05	<0.001
Male sex	1.14	0.74 - 1.78	0.55
Number of infectious episodes	1.34	0.99 - 1.84	0.066
Time to first infection (days)	1.01	0.99 - 1.03	0.47
ESBL or KPC infection	1.42	0.77 - 2.69	0.27

OR: odds ratio; CI: confidence interval. The model included 429 patients and 235 events. No evidence of multicollinearity was observed (all VIF < 2).

Infections were classified into seven categories: ventilator-associated pneumonia (VAP), non-device-associated pneumonia, Catheter-Associated Urinary Tract Infection (CAUTI), Non–catheter-associated UTI, Central Line-Associated Bloodstream Infection (CLABSI), surgical site infection (SSI), and other infections.

Device-associated infections predominated, with VAP accounting for 228 (34.8%) cases, followed by CLABSI (N = 115; 17.5%) and CAUTI (N = 112; 17.1%) (Table 2).

Table 2. Distribution of healthcare-associated infections according to infection type and device association.

Infection site	N (%)
VAP	228 (34.75)
CLABSI	115 (17.5)
CAUTI	112 (17.1)
Non-device-associated pneumonia	78 (11.9)
SSI	44 (6.7)
Non–catheter-associated UTI	27 (4.1)
Other infections	52 (7.9)

VAP: ventilator-associated pneumonia; CLABSI: Central line-associated bloodstream infection; CAUTI: Catheter-associated urinary tract infection; SSI: surgical site infection; UTI: urinary tract infection.

Among pulmonary infections episodes, the majority (N = 228; 74.5%) were device-associated. Patients with ventilator-associated pneumonia (VAP) had a lower mean age compared with those with non-device-associated pneumonia (56.7 ± 17.1 versus 61.6 ± 15.1 years; p = 0.042). Total length of stay was comparable between groups; however, infection onset occurred earlier in VAP than in non-device-associated pneumonia (17.37 versus 23.12 days; W = 7179; p = 0.011). In urinary tract infection episodes, 80.6% (N = 112) were catheter-associated. Patients with catheter-associated urinary tract infection (CAUTI) were younger than those with non–catheter-associated UTI (61.05 versus 68.74 years; p = 0.009).

Notably, in 111 (16.9%) infectious episodes, no etiological agent was identified, and treatment was conducted empirically. This substantial proportion highlights important diagnostic limitations in critically ill patients and may have direct implications for antimicrobial use and clinical outcomes. Among the remaining cases (N = 545; 83.1%), the most frequently isolated microorganisms were *Pseudomonas aeruginosa* (N = 99; 18.2%), *Klebsiella pneumoniae* (N = 94; 17.2%), and *Escherichia coli* (N = 58; 10.6%) (Table 3).

Table 3. Microbiological profile of healthcare-associated infections according to infection site (N = 545).

Etiological agent	Infection site (%)							
	VAP	Non-device-associated pneumonia	CAUTI	Non–catheter-associated UTI	CLABSI	SSI	Other	Total
P. aeruginosa	43 (22.9)	6 (12.5)	27 (24.1)	3 (11.1)	11 (9.7)	5 (13.2)	4 (21.1)	99 (18.2)
K. pneumoniae	23 (12.2)	6 (12.5)	26 (23.2)	9 (33.3)	12 (10.6)	14 (36.8)	4 (21.1)	94 (17.2)
E. coli	7 (3.7)	3 (6.2)	28 (25)	11 (40.7)	4 (3.5)	3 (7.9)	2 (10.5)	58 (10.6)
A. baumannii	36 (19.1)	4 (8.3)	4 (3.6)	0	5 (4.4)	4 (10.5)	3 (15.8)	56 (10.3)
S. haemolyticus	13 (6.9)	7 (14.6)	1 (0.9)	0	16 (14.2)	0	1 (5.3)	38 (7)
S. epidermidis	16 (8.5)	5 (10.4)	0	0	14 (12.4)	0	1 (5.3)	36 (6.6)
Unidentified	7 (3.7)	3 (6.2)	7 (6.2)	2 (7.4)	13 (11.5)	1 (2.6)	0	33 (6.1)
E. cloacae	8 (4.3)	1 (2.1)	4 (3.6)	1 (3.7)	6 (5.3)	4 (10.5)	0	24 (4.4)
E. faecalis	3 (1.6)	0	8 (7.1)	1 (3.7)	8 (7.1)	2 (5.3)	1 (5.3)	23 (4.2)
S. aureus	10 (5.3)	3 (6.2)	0	0	7 (6.2)	0	0	20 (3.7)
S. hominis	6 (3.2)	2 (4.2)	0	0	9 (8)	0	1 (5.3)	18 (3.3)
Proteus spp.	7 (3.7)	3 (6.2)	3 (2.7)	0	0	1 (2.6)	2 (10.5)	16 (2.9)
S. capitis	3 (1.6)	1 (2.1)	0	0	8 (7.1)	0	0	12 (2.2)
E. aerogenes	3 (1.6)	3 (6.2)	3 (2.7)	0	0	2 (5.3)	0	11 (2)
E. faecium	3 (1.6)	1 (2.1)	1 (0.9)	0	0	2 (5.3)	0	7 (1.3)
Total	188 (100)	48 (100)	112 (100)	27 (100)	113 (100)	38 (100)	19 (100)	545 (100)

VAP: ventilator-associated pneumonia; CAUTI: Catheter-associated urinary tract infection; CLABSI: Central line-associated bloodstream infection; SSI: surgical site infection.

Contingency analysis demonstrated a statistically significant association between infection site and etiological agents (chi-square test, p = 1.0 × 10-4), indicating that pathogen distribution varied according to infection site. In VAP, *P. aeruginosa* was the most frequently isolated microorganism (N = 43; 22.9%), followed by *Acinetobacter baumannii* (N = 36; 19.1%) and *K. pneumoniae* (N = 23; 12.2%). In non-device-associated pneumonia, *Staphylococcus haemolyticus* was the most commonly identified pathogen (N = 7; 14.6%), followed by *Klebsiella* spp. and *Pseudomonas* spp., each accounting for 12.5% (N = 6) (Table 3).

Among CAUTI, *E. coli* was the predominant pathogen (N = 28; 25%), followed by *P. aeruginosa* (N = 27; 24.1%) and *K. pneumoniae* (N = 26; 23.2%). In Non–catheter-associated UTIs, *E. coli* remained the most frequent etiological agent (N = 11; 40.7%). In CLABSI, *Staphylococcus* spp. were the most frequently isolated microorganisms (N = 54; 47.7%), particularly *S. haemolyticus* and *S. epidermidis*. In surgical site infections, *K. pneumoniae* was the leading pathogen (N = 14; 36.8%).

Detailed antimicrobial resistance analysis was primarily available for *K. pneumoniae* isolates, reflecting limitations in data availability for other pathogens. Regarding antimicrobial resistance patterns of this pathogen, 48.93% of *K. pneumoniae* isolates were classified as extended-spectrum beta-lactamase (ESBL) producers, 28.72% as multidrug-susceptible, and 22.34% as *Klebsiella pneumoniae* carbapenemase (KPC) producers (Table 4). No statistically significant association was observed between resistance profile and infection site or mortality ($p > 0.05$), although KPC-producing isolates showed a numerically higher proportion of deaths.

Table 4. Antimicrobial resistance patterns of *Klebsiella pneumoniae* isolates according to infection site.

Etiological agent	Infection site (%)						
	VAP	Non-device-associated pneumonia	CAUTI	Non–catheter-associated UTI	CLABSI	SSI	Other
Klebsiella MDS-susceptible	7 (25.9)	2 (7.4)	7 (25.9)	4 (14.9)	2 (7.4)	2 (7.4)	3 (11.1)
Klebsiella ESBL	11 (23.9)	3 (6.5)	14 (30.4)	4 (8.7)	7 (15.2)	6 (13)	1 (2.2)
KPC	5 (23.8)	1 (4.8)	5 (23.8)	1(4.8)	3(14.3)	6 (28.6)	0

MDS-susceptible: multi-drug susceptible; ESBL: extended-spectrum beta-lactamase; KPC: *Klebsiella pneumoniae* carbapenemase; VAP: ventilator-associated pneumonia; CAUTI: Catheter-associated urinary tract infection; CLABSI: Central line-associated bloodstream infection; SSI: surgical site infection.

Staphylococcus spp. accounted for 22.8% (N = 124) of all identified microorganisms and were responsible for 54 (47.9%) CLABSI, 18 (35.7%) non-device-associated pneumonia cases, and 48 (25.5%) VAP episodes. *S. haemolyticus* was the most frequently identified species (N = 38; 30.7%), followed by *S. epidermidis* (N = 36; 29%), *S. aureus* (N = 20; 16.1%), *S. hominis* (N = 18; 14.5%), and *S. capitis* (N = 12; 9.7%).

Discussion

This study demonstrates a substantial burden of healthcare-associated infections (HAIs) in intensive care units, predominantly driven by device-associated infections and multidrug-resistant Gram-negative pathogens, with a marked impact on in-hospital mortality. Similar findings have been reported in Brazilian ICU cohorts, including multicenter studies, where healthcare-associated infections are associated with high mortality and a predominance of multidrug-resistant Gram-negative pathogens[2,15].

Overall, Gram-negative bacteria predominated, with *P. aeruginosa*, *K. pneumoniae*, *E. coli*, and *Acinetobacter baumannii* emerging as the leading pathogens, in agreement with multicenter epidemiological studies worldwide[6,10]. The predominance of these organisms throughout different infection sites in our cohort likely reflects their remarkable adaptability and ability to persist in the ICU environment. *Pseudomonas aeruginosa* remains particularly problematic in ICUs due to its environmental resilience, biofilm formation, and capacity for transmission via both medical devices and healthcare personne[7,16]. *K. pneumoniae* also exhibits substantial adaptability and colonization potential in both the gastrointestinal and respiratory tracts, which may partially explain its frequent isolation in respiratory and urinary infections observed in our cohort [17-19].

A large European cohort study reported that 15.6% of patients who remained in the ICU for more than two days developed HAIs, with a moderate correlation between the number of infections per patient and total length of stay, reinforcing the well-established association between prolonged hospitalization and increased infection risk[5]. These findings are consistent with current recommendations emphasizing reduction of ICU length of stay whenever clinically feasible as a strategy to reduce HAI incidence.

Device-associated infections predominated in this study, consistent with national and international surveillance data[9,10]. The role of biofilm formation and persistence on invasive devices may contributes to this epidemiological pattern[16,20].

Ventilator-associated pneumonia (VAP) was the most frequent infection in our cohort, accounting for 34.8% of cases and representing 74.5% of all pneumonias. This finding aligns with epidemiological data from Brazil and Europe, where ventilator-associated pneumonia remains one of the most frequent ICU-acquired infections among mechanically ventilated patients[6,15,21]. The incidence of VAP is closely related to the proportion of intubated patients within a unit, which may partially explain the high prevalence observed in our institution.

The high frequency of VAP observed may reflects the extensive use of invasive mechanical ventilation in critically ill patients, which facilitates lower airway colonization and bypasses protective respiratory mechanisms [20-22]. These mechanisms probably contributed to the high frequency of VAP observed.

In contrast, non-device-associated pneumonia appears to be more strongly associated with host-related risk factors and prolonged hospitalization. In our cohort, VAP occurred earlier than non-device-associated pneumonia (mean 17.37 versus 23.12 days), reinforcing the procedural nature of device-associated infections. Furthermore, patients with non-device-associated pneumonia were significantly older than those with VAP, consistent with the literature identifying advanced age as a risk factor for non-device-associated pneumonia due to comorbidities, dysphagia, and increased risk of microaspiration[23,24].

The microbiological profile of VAP in this study was dominated by *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Klebsiella pneumoniae*, together accounting for more than 50% of isolates. These findings are consistent with epidemiological data identifying Gram-negative bacilli, particularly *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Klebsiella pneumoniae*, as leading pathogens in ventilator-associated pneumonia[22]. Notably, *Acinetobacter baumannii* were isolated more frequently than *Klebsiella* spp., reflecting a trend observed in recent studies that highlight the increasing prominence of *Acinetobacter* in ICUs, probably related to its environmental persistence and multidrug resistance[7,25].

Catheter-associated urinary tract infection represented the second most frequent infection category, accounting for 80.6% of urinary infections. The predominance of catheter-associated urinary tract infections observed is consistent with CDC epidemiological estimates and likely reflects the extensive use of indwelling urinary catheters in critically ill patients[26,27]. Interestingly, non–catheter-associated UTIs occurred predominantly in older patients, reinforcing advanced age as an independent risk factor for infection even in the absence of invasive devices.

Gram-negative bacteria predominated in urinary infections, particularly *Escherichia coli*, followed by *P. aeruginosa* and *K. pneumoniae*. This distribution is consistent with Brazilian and international surveillance data[27,28]. *E. coli*, a commensal of the intestinal microbiota, possesses virulence factors that facilitate bladder adhesion and extraintestinal dissemination, explaining its prominence in both device-associated and non-device-associated UTIs[28]. Certain species, including *Acinetobacte*r, *Staphylococcus haemolyticus*, *Enterobacter aerogenes*, *Enterococcus faecium*, and *Proteus* spp., were isolated exclusively in CAUTI, possible reflecting their ability to colonize and persist on catheter surfaces.

Central line-associated bloodstream infection constituted the third most frequent infection category. Consistent with the literature, coagulase-negative *Staphylococcus* species were the predominant pathogens, particularly *S. haemolyticus* and *S. epidermidis*[29]. The predominance of coagulase-negative *Staphylococcus* spp. in CLABSI is consistent with their recognized ability to colonize intravascular devices and persist through biofilm formation[29-31].

A substantial proportion (16.9%) of infectious episodes lacked microbiological identification, probably reflecting the widespread use of empiric antimicrobial therapy prior to specimen collection and the inherent time constraints of conventional microbiological diagnostics[11,32]. This finding underscores the need for optimized diagnostic stewardship and rapid microbiological techniques in critically ill populations.

Antimicrobial resistance among *K. pneumoniae* isolates was notable, with nearly half classified as extended-spectrum beta-lactamase (ESBL) producers and over 22% as KPC producers. These proportions are consistent with global reports demonstrating rising rates of multidrug-resistant *K. pneumoniae*, although regional variability persists[17-19,33]. While mortality proportions differed numerically across resistance profiles in our study, statistical significance was not demonstrated, presumably due to limited sample size within subgroups. Nevertheless, infections caused by ESBL- and KPC-producing strains remain clinically concerning due to restricted therapeutic options and potential for adverse outcomes[19,33-35]. Importantly, the absence of an independent association between antimicrobial resistance and mortality should be interpreted with caution and within the context of limited resistance data for other pathogens. Nevertheless, this finding may suggest that, in critically ill populations, baseline clinical severity and host-related factors exert a stronger influence on mortality than resistance phenotype alone. Previous studies have demonstrated that although multidrug-resistant organisms complicate antimicrobial management and may prolong hospitalization, their independent attributable effect on mortality becomes less evident after adjustment for severity-related variables and comorbidities[33,35]. In this context, antimicrobial resistance may represent more a marker of healthcare exposure and prolonged critical illness than an isolated determinant of death. These findings reinforce the importance of considering host-related and severity-related variables when evaluating the clinical impact of antimicrobial resistance in ICU populations.

The high in-hospital mortality observed (54.5%) probably reflects the intrinsic severity of critically ill patients exposed to invasive devices and the well-established impact of device-associated healthcare-associated infections (DA-HAIs) on adverse outcomes. In the multivariable analysis, age remained independently associated with in-hospital mortality, reinforcing its well-established role as a prognostic determinant in critically ill patients. Age has consistently been identified as an independent predictor of mortality in critically ill populations across contemporary ICU cohorts[36]. Each additional year of age increased the odds of death by 3%, which is biologically plausible considering the impact of immunosenescence, frailty, and cumulative comorbidity burden on adverse outcomes[37]. Although the number of infectious episodes showed a trend toward increased mortality, statistical significance was not reached, possibly due to limited statistical power. Therefore, the absence of statistical significance should not be interpreted as evidence of no effect.[34]. The database structure did not allow identification of patients with multiple infection episodes, which limited the ability to assess the cumulative impact of recurrent infections on mortality.

Interestingly, antimicrobial resistance phenotype (ESBL or KPC production) was not independently associated with mortality after adjustment. Although ventilator-associated pneumonia and central line-associated bloodstream infections are well recognized contributors to adverse outcomes in critically ill patients[5,32] previous investigations have demonstrated heterogeneous findings regarding the attributable mortality of multidrug-resistant organisms[33,35]. Therefore, the absence of association in our analysis may reflect limited statistical power, residual confounding, or the lack of adjustment for validated severity-of-illness scores. Importantly, the absence of SOFA or APACHE II limits our ability to fully account for baseline clinical severity, and mortality may reflect underlying critical illness rather than infection-related factors alone.

In addition, relevant clinical variables such as comorbidities, underlying conditions, and patient-specific risk factors (e.g., cardiovascular disease, diabetes, malignancy, renal and hepatic function, and prior antimicrobial exposure) were not available in the database used for this study. The absence of these variables may have resulted in residual confounding, as these factors are known to significantly influence outcomes in critically ill patients. Therefore, the observed associations between healthcare-associated infections and mortality should be interpreted with caution, as they may partly reflect underlying patient characteristics rather than the direct effect of infection. Furthermore, the inclusion of different ICU profiles (general, coronary, and neurological) may introduce heterogeneity in patient clinical profiles, potentially influencing infection rates and mortality, and acting as a confounding factor in the observed associations, particularly as no stratified analysis by ICU type was performed.

Beyond antimicrobial resistance patterns, pathogen distribution also varied according to infection site and device exposure. Among Gram-positive organisms, *Staphylococcus* spp. accounted for 22.8% of all isolates, with coagulase-negative species emerging as important opportunistic pathogens in device-associated infections. Brazilian multicenter studies have reported that up to 34.4% of ICU HAIs are attributable to these organisms[9], although incidence varies depending on adherence to infection prevention protocols[31]. The proportion observed in our institution was comparatively lower, suggesting possible effectiveness of local infection control measures. This study provides relevant real-world evidence from a Brazilian tertiary public hospital, contributing to the understanding of HAI epidemiology in resource-constrained settings, where local microbiological patterns and resistance profiles may substantially differ from those observed in high-income countries.

Taken together, our findings reinforce the central role of invasive devices in HAI epidemiology and highlight the persistent burden of multidrug-resistant Gram-negative pathogens in ICU settings. Importantly, our results suggest that host-related factors and baseline clinical severity may exert a greater impact on mortality than antimicrobial resistance alone. Strengthening device management protocols, optimizing antimicrobial stewardship strategies, and enhancing microbiological diagnostic capacity are essential to mitigate the impact of these infections.

Conclusion

This study demonstrates a high burden of device-associated healthcare-associated infections in ICU patients, predominantly caused by Gram-negative pathogens. A notably high in-hospital mortality rate was observed, which was independently associated with age but not with antimicrobial resistance after adjustment.

These findings highlight the importance of patient-related factors in clinical outcomes and reinforce the need for improved device management, enhanced microbiological diagnostics, and targeted antimicrobial stewardship strategies in critically ill populations.

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Author contributions

B. B. Machado, J. B. Machado, G. R. Manuel and F. M. Fonseca: contributed to conceive the study and critically reviewed; B. B. Machado, G. R. Manuel and F. M. Fonseca: edited the manuscript; B. B. Machado and J. B. Machado collected data and reviewed the manuscript; B. B. Machado, J. B. Machado and F. M. Fonseca: designed the study, analyzed the data and wrote the manuscript.

Conflict of interest

The authors declare no conflicts of interest.

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