Original article

The Situation of Antibiotic Resistance in Patients with Antibiogram in Intensive Care Units

La situación de la resistencia antibiótica en pacientes con antibiograma en unidades de cuidados intensivos

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ABSTRACT

Introduction: Antibiotic resistance is one of the most emerging global health problems

today, and is particularly acute in hospital intensive care units in low- and middle-income countries.

Aim: To determine the antibiotic resistance rates of common bacteria in intensive care units of two hospitals in Vietnam.

Methods: A retrospective cross-sectional study was conducted. Data were extracted from electronic medical records of patients 18 years of age or older who had positive bacterial cultures from January 2020 to June 2022. Demographic information, medical history, and antibiotic susceptibility test results were collected from patients at two hospitals. Data were analyzed using Python 3.8.

Results: Acinetobacter spp. was most prevalent in Phu Tho hospital (27.5 %), while Klebsiella spp. was dominant in 175 Military hospital (28.0 %). Acinetobacter spp, Klebsiella spp. and Pseudomonas aeruginosa showed high levels of drug resistance to all antibiotic families, particularly to cephalosporins, carbapenems and fluoroquinolones (75 % to 100 %), their multiresistencia rates ranged from 83.8 % to 95.8 %. Conclusions: The prevalence of antimicrobial resistance among intensive care unit patients in two Vietnamese hospitals was exceptionally high, with alarming multidrug resistance rates of Acinetobacter, Klebsiella, and Pseudomonas aeruginosa.

Keywords: antibiotic resistance; intensive care units; multidrug resistance

RESUMEN

Introducción: La resistencia a los antibióticos es uno de los problemas de salud global más emergentes en la actualidad, y es particularmente grave en las unidades de cuidados intensivos de los hospitales en los países de ingresos bajos y medianos.

Objetivo: Determinar las tasas de resistencia a los antibióticos de bacterias

comunes en las unidades de cuidados intensivos de dos hospitales de Vietnam.

Métodos: Se realizó un estudio transversal retrospectivo. Se extrajeron datos de historias clínicas electrónicas de pacientes de 18 años de edad o más que tuvieron cultivos bacterianos positivos desde enero de 2020 hasta junio de 2022. Se recopiló información demográfica, historia clínica y resultados de pruebas de susceptibilidad a los antibióticos de los pacientes en dos hospitales. Los datos se analizaron utilizando Python 3.8.

Resultados: *Acinetobacter* spp. fue la más prevalente en el hospital Phu Tho (27,5 %), mientras que *Klebsiella* spp. fue la dominante en el hospital Militar 175 (28,0 %). *Acinetobacter spp, Klebsiella* spp. y *Pseudomonas aeruginosa* mostraron altos niveles de farmacorresistencia a todas las familias de antibióticos, en particular a las cefalosporinas, carbapenem y fluoroquinolonas (del 75 % al 100 %), sus tasas de multiresistencia oscilaron entre el 83,8 % y el 95,8 %.

Conclusiones: La prevalencia de resistencia antimicrobiana entre los pacientes de las unidades de cuidados intensivos en dos hospitales vietnamitas fue excepcionalmente alta, con alarmantes tasas de resistencia a múltiples fármacos de *Acinetobacter, Klebsiella* y *Pseudomonas aeruginosa*.

Palabras clave: resistencia antibiótica; unidades de cuidados intensivos; multidrogorresistencia.

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Introduction

Antibiotic resistance (AMR) is one of the most significant global health challenges facing both high-income countries (HICs) and low- and middle-income countries (LMICs).[1] Approximately 4.95 million people died from illnesses caused by

bacterial AMR in 2019, of whom 1.27 million were directly killed by AMR.[2] This number exceeds the number of deaths caused by AIDS (864000) and nearly twice the deaths caused by malaria (643000) in the same year.[3] Five of the six most deadly bacteria were

Escherichia coli, *Staphylococcus aureus, Klebsiella pneumoniae*, *Acinetobacter baumannii, and Pseudomonas aeruginosa*, which accounted for nearly three-quarters of all deaths from AMR globally.[3]

The spread of AMR leads to ineffective treatment, increased infections in communities, and the destruction of many medical achievements made in the past century. Accordingly, if AMR continues to grow without being adequately controlled, the gross domestic product (GDP) could decline by 2% to 3.5% by 2050, resulting in a loss of 100 trillion USD globally.[4] Two main factors are contributing to the development of AMR. They are the inappropriate use of antibiotics in the community and the mis prescription of broad-spectrum antibiotics.[5]

In hospitals, the greatest threat of AMR lies in intensive care units (ICUs), where the mortality rate of infections could be as high as 80%, and the overuse of antibiotics is common.[6] In a prospective study conducted in 1265 ICUs from 75 countries, hospital-acquired infections were found in nearly half of the patients admitted to these units.[7]. In Vietnam, a high incidence of nosocomial infections and AMR were found among hospitalized patients, especially in ICUs.[8] So, this study was conducted with the goal of determination of antibiotic resistance rates of some common bacteria in ICUs in two hospitals in Vietnam.

Methods

Subjects and locations

A cross-sectional study combined with retrospective was conducted from 1st January 2020 to 30th June 2022. We retrieved EMRs of patients who had positive bacterial culture results from the ICUs in Phu Tho hospital (Phu Tho province) and

175 hospital (Ho Chi Minh City) in Vietnam. All patients were 18 years of age or older on admission. The total of 3326 specimens were positive for bacteria in the two hospitals (1121 in Phu Tho hospital and 2205 in 175 hospital).

After checking for duplicates, 2432 samples, of which 856 were from Phu Tho hospital, and 1576 were from 175 hospital, were included in the final data analysis of the present study. 1625 medical records were collected, of which 643 were from Phu Tho hospital and 982 from 175 hospital. The source patients from both hospitals were 1296 people, including 600 patients in Phu Tho hospital and 696 in 175 hospital.

The demographic and clinical information (age, gender, place of residence (province and town/district), occupation, having insurance or not, diagnosis at admission by the International Code of Diseases (ICD-10), dates of admission and discharge, treatment results, and complication) were collected from the patient's medical history.

Antimicrobial resistance patterns of isolated bacteria

Different types of samples, such as, blood, cerebrospinal fluid (CSF), tracheobronchial/ bronchoalveolar fluid, urine, skin/wound/tissue specimens, catheters, pleural and peritoneal fluid, were collected and used for the Antimicrobial Susceptibility Testing (AST). The antibiotic susceptibility of isolated bacteria was detected by VITEK 2 Compact System (bioMérieux) at the Testing Center in Phu Tho hospital and BD Phoenix 100 system (Becton Dickinson, USA) at the Department of Microbiology in the 175 Hospital. All tests were standardized and performed following the criteria of the Clinical and Laboratory Standards Institute (CLSI).[9]

Data analysis

The data were cleaned and checked for missing values, then reshaped and analyzed using Python 3.8 with various packages, including Pandas, NumPy, Stats models, Matplotlib, and Seaborn. The frequency of each bacterium was expressed as a

percentage of the total samples.

Univariate analysis of variance was conducted to determine differences in mean resistance of the five bacteria in the two hospitals. A Z-test was used to compare the statistical difference in proportions between the two hospitals. Any value with $p< 0.05$ was considered to be statistically significant. Ethically, the patient's identity is kept confidential, used only for analysis as a group.

Results

Characteristics of ICU patients having positive bacterial culture results

The characteristics of the patients having positive bacterial culture were shown in Table 1. The mean (±standard deviation (SD)) age of the patients in Phu Tho hospital and 175 hospital were 60±17.6, and 59.5±15.8 years, respectively.

The proportion of the male patients was higher than that of the female group, and the rate was higher in Phu Tho hospital than in 175 hospital.

In Phu Tho hospital, the most common diagnoses at admission were respiratory diseases (37.2%) and abnormal unclassified diseases (34.7%). Meanwhile, COVID-19 and respiratory diseases accounted for the highest diagnoses in the 175 hospital (25.1% and 28.7%, respectively). 83.7% of the studied patients in Phu Tho hospital and 92.1% in 175 Hospital found at least one of five targeted bacteria. Acinetobacter spp and Klebsiella spp were the most prevalent bacterial infections identified in two hospitals.

Table 1 - Characteristics ICU patients having positive bacterial culture results in Phu Tho hospital (n = 600) and175 hospital (n = 696)

Characteristics	**Phu Tho hospital**		**175 hospitals**	
Mean [SD]	**N**	**%**	**N**	**%**
Age at admission (year)	60	[17.6]	59.5	[15.8]
Men	440	73.3	450	64.7
Having health insurance	559	93.2	561	80.6
Year of admission				
2020	254	42.3	340	48.9
2021	196	32.7	207	29.7
2022	150	25.0	149	21.4
Place of residence				
Phu Tho	566	94.3	1	0.1
Ho Chi Minh	0	0.0	497	71.4
Other provinces	34	5.7	198	28.5
Primary diagnosis at admission by ICD-10				
Respiratory (J00-J99)	223	37.2	200	28.7
COVID-19 (U07)	0	0.0	175	25.1
Abnormal and not classified (R00-R99)	208	34.7	76	10.9
Injury and poison (S00-T88)	68	11.3	39	5.6
Circulatory system (I00-I99)	50	8.3	130	18.7
Infection (A00-B99)	33	5.5	111	15.9
Digestion (K00-K95)	14	2.3	21	3.0
Genitourinary(N00-N99)	9	1.5	11	1.6
Neurology (G00-G99)	5	0.8	8	1.1
Other diseases*	15	2.7	43	6.2
Having targeted bacteria				
Klebsiella *spp.*	151	25.2	346	49.7
Pseudomonas aeruginosa	146	24.3	152	21.8
Escherichia coli	86	14.3	69	9.9
Staphylococcus aureus	30	5.0	70	10.1

Having at least one of above	502	83.7	641	92.1
Treatment result at discharge				
Recover	-	-	41	5.9
Better	-	-	213	30.6
No change	NA	NA	257	36.9
Worse	-	-	66	9.5
Dead	-	-	119	17.5
Median [IQR]				
Age at admission	61	[48-73]	61	[49-70]
Length of stay in hospital (days)	NA	NA	13	[8-22]
Length of stay in ICU (days)	NA	NA	11	[6-17]

Legend: *Other diseases included: Diseases of the musculoskeletal system, endocrine, neoplasms, skin, blood, and immune mechanism, mental disorders, and external causes of morbidity. ICU: Intensive Care Unit, COVID-19: Coronavirus disease 2019; ICD-10: International Code of Disease –10th version; IQR: Interquartile range (the difference between quartile one and quartile three); NA: Data not available.

Distribution of five targeted bacteria and antibiotic resistance rates

Table 2 showed distribution of five most prevalent bacteria isolates in two hospitals, including *Acinetobacter spp., Klebsiella spp., Pseudomonas aeruginosa, Escherichia coli,* and *Staphylococcus aureus*. In Phu Tho hospital, *Acinetobacter* species was the most prevalent identified bacteria, accounting for 27.5% of positive cases, followed by *Klebsiella species* (18.8%) and *Pseudomonas aeruginosa* (18.1%). *Escherichia coli* was present in 10.3% of isolates and *Staphylococcus aureus* in 3.6%. In 175 hospital, *Klebsiella species* were the most frequently encountered bacteria (28.0% of all positive isolates). *Klebsiella pneumoniae* was the dominant subtype of the species. *Acinetobacter species* were found in 25.4% of all isolated cases, and the most frequent subtype was *Acinetobacter baumannii*. *Pseudomonas aeruginosa* and *Escherichia coli* had a higher prevalence in Phu Tho hospital than in 175 hospital. Meanwhile, the rate of *Staphylococcus aureus* was higher in 175 hospital than in Phu Tho hospital.

Table 2 - Distribution of targeted bacteria isolated from ICU patients in two hospitals

Bacteria isolates	**Phu Tho hospital** (n=856)		**175 hospital** (n = 1576)	
	n	**%**	**n**	**%**
*Acinetobacter species**	235	27.5	401	25.4
Acinetobacter baumannii	229	26.8	380	24.1
Acinetobacter lwoffii	3	0.4	0	0.0
Acinetobacter haemolyticus	2	0.2	1	0.1
Acinetobacter junii	1	0.1	0	0.0
Acinetobacter spp	0	0.0	20	1.3
*Klebsiella species***	162	18.8	441	28.0
Klebsiella pneumoniae	155	18.1	397	25.2
Klebsiella oxytoca	6	0.7	1	0.1
Klebsiella aerogenes	0	0.0	11	0.7
Klebsiella ozaenae	0	0.0	6	0.4
Klebsiella spp	0	0.0	25	1.6
Pseudomonas aeruginosa	155	18.1	216	13.7
Escherichia coli	88	10.3	71	4.5
Staphylococcus aureus	31	3.6	72	4.6
Other bacteria	186	21.7	375	23.8

* In this study, *Acinetobacter spp* was used for all kinds of *Acinetobacter species*
** In this study, *Klebsiella spp* was used for all kinds of *Klebsiella species*

Table 3 showed the AMR of four targeted bacteria towards 20 antibiotics most used in the AST in two hospitals. The AMR of the Gram-negative bacteria, including *Acinetobacter spp, Klebsiella spp, Pseudomonas aeruginosa*, and *Escherichia coli*, were described in Table 3. For the Gram-negative bacteria, the level of AMR in 175 hospital was higher than that in Phu Tho hospital for 80% of antibiotics used in AST, exception Doripenem, Tobramycine, Trimethoprim-sulfamethoxazole. In 175 Hospital, the rates of bacteria having Extended-spectrum beta-lactamase (ESBL) were 35.2% for *Escherichia coli* and 10.9% for *Klebsiella spp*. The proportion of carbapenemase producing bacteria was 63.6% for *Acinetobacter spp*, 63.9% for *Klebsiella spp*, 52.9% for *Pseudomonas aeruginosa*, and 16.9% for *Escherichia coli* (table 3).

Table 3 - Antibiotic resistance rate of *Acinetobacter spp, Klebsiella spp, Pseudomonas aeruginosa* and *Escherichia coli* towards 20 antibiotics most used in the Antibiotic Susceptibility Test (units: %)

Name of antibiotics	*Acinetobacter spp*			*Klebsiella spp*			*Pseudomonas aeruginosa*			*Escherichia coli*		
	Phu Tho	175	*p*	Phu Tho	175	*p*	Phu Tho	175	*p*	Phu Tho	175	*p*
Amikacin	71.6	87.4	***	37.9	42.9	-	79.7	51.8	***	7.1	8.5	-
Ampicillin-Sulbactam	68.7	89.2	***	79.5	89.9	**	100	100	-	53.3	52.6	-
Cefazolin	-	100	-	-	92.0	-	-	100	-	-	82.1	-
Cefepime	90.2	92.7	-	75.6	87.5	***	84.3	70.8	***	60.7	66.7	
Cefotaxime	91.9	97.1	-	80.1	72.3	**	98.7	-	-	61.1	37.5	*
Ceftazidime	88.0	96.8	***	77.6	91.3	***	62.7	66.7		60.9	82.1	**
Ceftriaxone	89.7	87.5	-	72.5	86.1	**	88.9	100	***	58.6	69.1	
Ciprofloxacin	82.5	91.5	***	75.7	87.6	**	76.4	78.3	--	64.1	77.6	***
Colistin	-	3.3	-	-	37.4	-	-	19.1	-	-	0.0	-
Doripenem	80.0	-	-	73.3	12.5	***	85.5	-	-	12.5	-	
Ertapenem	71.4	100	***	73.3	85.2	***	100	96.7	***	13.5	22.0	**
Gentamicin	73.1	93.6	***	56.4	58.2	-	81.2	63.6	***	45.2	48.3	
Imipenem	77.8	90.0	***	73.8	75.9	-	82.7	77.5	-	12.1	23.2	***
Levofloxacin	74.7	91.5	**	70.4	76.9	-	85.7	81.0	-	60.0	40.0	-
Meropenem	78.2	92.7	***	75.2	84.5	*	82.9	81.9	-	10.0	30.6	***
Minocycline	-	9.7	-	-	54.5	-	-	97.2	-	-	50.0	-
Piperacillin-Tazobactam	85.2	89.2	-	76.8	83.0	-	60.0	57.7	-	18.1	17.2	-
Tobramycine†	69.0	3.2	***	65.2	0.0	-	84.8	37.5	***	43.8	-	-
Trimethoprim-sulfamethoxazole	70.6	18.6	***	55.7	22.5	***	100	6.1		68.9	29.1	-
ESBL (+)	-	-	-	-	10.9	-	-	0.0	-	-	35.2	-
Carbapenemase (+)	-	63.6	-	-	63.9	-	-	52.9	-	-	16.9	-

Legend: ESBL: Extended – Spectrum Beta – Lactamase.Z-test is used to compare the difference in proportions between two hospitals. * p<0.05, ** p<0.01, *** p<0.001

Table 4 - demonstrates the multi-drug resistance of five targeted. Acinetobacter spp had the highest rate of multi-drug resistance (90.2% in Phu Tho and 95.8% in 175 hospital.

Table 4 - Multi-drug resistance of bacteria in two hospitals

Bacteria	Phu Tho Hospital		175 Hospital	
	n	%	n	%
Acinetobacter spp	235	90.2	401	95.8
Klebsiella spp	161	85.1	441	90.0
Pseudomonas aeruginosa	155	87.5	216	83.8
Escherichia coli	88	76.1	71	76.1
Staphylococcus aureus	31	90.3	72	51.4

Table 5 demonstrates the antibiotic resistance of four targeted bacteria to different antibiotic families. The resistance rates of *Acinetobacter spp* in 175 hospitals were higher for cephalosporins, carbapenems, beta-lactams, aminoglycosides, and fuoroquinolones than that in Phu Tho hospital.

Table 5 - Antibiotic resistance rate of *Acinetobacter spp, Klebsiella spp, Pseudomonas aeruginosa and Escherichia coli* to antibiotic families used in the antibiotic susceptibility test

Antibiotics	*Acinetobacter spp*		*Klebsiella spp*		*Pseudomonas aeruginosa*		*Escherichia coli*	
	Phu Tho hospital	175 hospital	Phu Tho hospital	175 hospital	Phu Tho hospital	175 hospital	Phu Tho hospital	175 hospital
Aminoglycosides	80.3	94.3	67.5	57.6	83.9	66.4	48.8	44.1
Beta-lactam	86.5	92.0	83.1	87.4	61.3	75.3	39.1	48.6
Carbapenems	79.2	95.7	75.5	82.9	84.3	86.8	13.8	24.3
First gen. cephalosporin	-	100	-	92.0	0.0	100	-	82.1
Second generation cephalosporin	90.0	100	88.1	84.0	100	100	72.7	38.9
Third gen. cephalosporin	90.2	95.8	78.1	88.6	89.5	79.1	63.2	71.0
Forth gen. cephalosporin	90.2	92.7	75.5	87.5	84.3	70.8	60.7	66.7
Fluoroquinolones	80.6	91.5	75.7	87.6	80.0	79.4	62.2	77.6
Glycylcyclines	-	31.0	-	9.1	-	91.8	-	1.8
Lincosamides	50.0	-	0.0	-	-	-	-	-
Macrolides	0.0	100	75.0		100	100	-	-
Monobactams	85.7	100	60.0	77.4	72.2	79.3	33.3	100
Nitrofuran	100	50.0	72.0	52.2	100	100	9.8	10.0
Oxazolidinones	100	-	-	-	100	-	-	-
Penicillins	100	98.8	99.1	99.2	100	97.2	83.3	94.6
Phosphonics	-	77.8	62.0	68.0	-	100	10.8	16.7
Polymyxins	-	3.3	-	37.4	-	19.1	-	0.0
Tetracyclines	42.6	9.7	70.8	55.6	66.7	97.2	75.0	50.0
Trimethoprim derivatives	70.6	81.4	55.4	77.5	100	93.9	68.9	70.9

Discussion

Distribution of targeted bacteria in two hospitals

The study found differences in bacteria strain patterns between the Phu Tho hospital (in the northern region) and the 175 hospitals (in the southern region). Phu Tho hospital had similar results to the review study on ICUs in LMICs, where *Acinetobacter spp* were the most commonly isolated bacteria (24%), followed by *Pseudomonas aeruginosa* and *Klebsiella spp.* (16% and 15%).[10] Similarly, a study in a Vietnamese ICU in the southern region in 2015 found the highest proportion of *Acinetobacter species* (42.3%) over *Klebsiella species* (22.1%).[11] In the present study, the bacteria pattern at 175 hospital was inconsistent with other studies in LMICs and Asia.[12] Between 2020 and 2022, *Klebsiella spp.* accounted for the highest percentage of isolated specimens in the ICU of 175 hospital, except in 2021, when *Acinetobacter spp.* ranked first (25.4%), and *Klebsiella spp.* ranked second (28.0%).

One possible explanation for this result is the outbreak of carbapenem-resistant *Klebsiella pneumonia* in ICU patients who had low respiratory tract infections in China and Saudi Arabia.[13,14] In 175 hospital, the rate of carbapenems- resistance of *Klebsiella spp* was 82.9% compared to 75.5% in Phu Tho hospital.

Moreover, in a recent study, *Klebsiella species* were also the leading cause of ventilator-related pneumonia in ICU patients and accounted for up to 85% of nosocomial pneumonia.[15] Another explanation is the high likelihood of *Klebsiella spp* infection in the bloodstream infection.[10,16]

The impact of the COVID-19 pandemic could contribute to the highest number of *Acinetobacter spp* isolates in 175 hospitals in 2021. When the COVID-19 pandemic happened in Ho Chi Minh City from April 2020 until September 2021, 175 hospital was one of the centers for treating COVID-19 patients.[12]

The opportunistic *Acinetobacter spp.* infection might increase due to the heavy use of ventilators among ICU patients having breathing problems, especially the COVID-

19 disease. Research in LMICs also confirmed the association between the presence of *Acinetobacter spp.* with ventilator-associated pneumonia.[16]

Antibiotic resistance profiles and multi-drug levels of bacteria

In this study, *Acinetobacter spp., Klebsiella spp., and Pseudomonas aeruginosa* were predominant (from 65%-67% of total isolated samples) compared to the minor proportion (only 34%) in the national study in 2012-2013.[17]

The results also showed the widespread resistance of these bacteria to all kinds of antibiotics. Among all observed bacteria, *Acinetobacter spp.* had the highest rate of multi-drug resistance (90.2% in Phu Tho and 95.8% in hospital 175). *Acinetobacter spp* were resistant to all commonly used antibiotic families at a very high rate of resistance (>80%) in both hospitals. These rates were higher than those in the national study in Vietnam 10 years ago, when the resistance rates were from 68% to 77% in all 16 hospitals under the survey.[17] A possible cause may be the overuse of third and fourth generation cephalosporins and quinolone antibiotics in ICU patients, and another one is the abuse of antibiotics for prophylaxis. According to the Ministry of Health of Viet Nam, 74% of antibiotic treatments were incompliant with AST.[18] In a recent study in Vietnam, the healthcare-acquired infection could happen due to overcrowding of patients, healthcare workers' habit of broad-spectrum antibiotics, or incomplete sterilization of the material.[19]

According to the results in two hospitals, there were very few effective antibiotics for *Acinetobacter* infections, which is alarming. *Acinetobacter* infection is primarily associated with nosocomial infections rather than community-acquired infections.[20] Therefore, empiric antibiotic treatment therapies must be carefully considered before being prescribed in the ICU and other departments.

Klebsiella spp. represented a higher level of carbapenem resistance than other countries in South East Asia.[21] Approximately 75.5% of the *Klebsiella spp.* in Phu Tho hospital and 82.9% in 175 hospital were resistant to carbapenem, while the rate in Southeast Asia was 0- 8%.

The resistance of *Klebsiella spp.* to third-generation cephalosporin in this study was also at the top ranking in Southeast Asia. In this region, 34-81% of *Klebsiella spp.* isolates resisted third-generation cephalosporin,[21] while 78.1% and 88.6% of these bacteria in Phu Tho hospital and 175 hospital resisted this antibiotic family, respectively. In the United States and European, the prevalence of *Klebsiella spp.* is falling sharply, and the proportion of *Klebsiella spp.* in LMICs, such as China, India, Pakistan, Egypt, and Vietnam, is increasing.[10,22] Despite the low mortality rate due to Klebsiella spp. (2.8% in this study), similar outbreaks of *Klebsiella* pneumonia could occur as they did in Ho Chi Minh City in 2019.[23] *Klebsiella spp.* were increasingly resistant to all antibiotics, even with strong antibiotics like colistin (37.4%). In the 2012-2013 study, the resistance rate of *Klebsiella spp.* was only 17% for imipenem and 66% for third-generation cephalosporins.[17] This trend in Vietnam has not yet been fully explained, but in some studies in China, carbapenemase production was the primary cause of *Klebsiella* pneumonia's resistance to carbapenem.

The overuse of antibiotics also contributed to the spread of carbapenem-resistant *Klebsiella* pneumonia.[24] The prevalence of *Klebsiella spp.* containing carbapenemase in 175 hospital was 63.9%, which may explain why this organism was becoming more prevalent. In one study in southern Vietnam in 2016, moderate to heavy drinking of alcohol weekly, being old, smoking, and living in rural areas were associated with a high risk of *Klebsiella* pneumonia carriage in communities.[25]

Pseudomonas aeruginosa was the second-highest infection among patients with respiratory and circulatory diseases (only after *Acinetobacter spp.*) in Phu Tho hospital. These results were similar to the study in Southeast Asia, where these bacteria were the second highest contributor to nosocomial infections after *Acinetobacter baumannii*.[16] The prevalence of carbapenem resistance of *Pseudomonas aeruginosa* in South East Asian countries was 31.1% in the Philippines, 23.3% in Singapore, 28.7% in Thailand, and 46.7% in Vietnam.[26] While in this study, the carbapenem-resistant rate in Phu Tho hospital was 75.5%, and in 175 hospital was 82.9%.

Besides, the ciprofloxacin-resistant rate was also high (76.4% in Phu Tho hospital and 78.3% in 175 hospital). Ten years ago, Vietnam only had about 55.7% of these bacteria resistant to carbapenem in the ICU and less than 40% in other departments; now, the resistance rate has reached 75-80%.[17]

In conclusion, the prevalence of AMR among ICU patients in two Vietnamese hospitals was exceptionally high, with alarming multidrug resistance rates of *Acinetobacter, Klebsiella,* and *Pseudomonas aeruginosa*.

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