

Antibiotic Resistance Patterns and Prevalence of Common Bacterial Pathogens in Clinical Samples: A 2020-2024 Study at Hai Phong International Hospital

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ABSTRACT

This study analyzed the results of microbiological tests conducted on a total of 9,133 clinical samples collected between 2020 and 2024 at Hai Phong International General Hospital. The aim is to evaluate antibiotic resistance patterns among common bacterial pathogens and their clinical implications. The data shows a significant prevalence of multidrug-resistant strains, particularly in *Escherichia coli*, which emerged as the most frequently isolated pathogen in both urinary infections and bloodstream infections, accounting for 69.44% and 48.12% of isolates, respectively. The study also finds *Klebsiella pneumoniae*, *Staphylococcus aureus*, and *Vibrio parahaemolyticus* as notable pathogens contributing to various infections. Antibiotic sensitivity testing revealed that carbapenems such as ertapenem (94.50%), imipenem (91.40%), and meropenem (91.00%) demonstrated high efficacy against resistant strains. Ceftriaxone (92.60%) and linezolid (98.10%) also showed strong activity against susceptible strains. Among fluoroquinolones, moxifloxacin (91.10%) was the most effective, while ciprofloxacin (48.60%) and levofloxacin (62.20%) showed moderate effectiveness. Furthermore, the distribution of antibiotic resistance mechanisms was examined, revealing 709 cases of Extended Spectrum Beta-Lactamase (ESBL) production in *E. coli*, highlighting the pressing issue of multidrug resistance. *Staphylococcus aureus* isolates totaled 1,307, with 325 classified as Methicillin-Resistant *Staphylococcus aureus* (MRSA), underlining the dual threat posed by resistant strains. Overall, the findings underscore the predominance of *E. coli* in clinical infections, alongside significant resistance patterns among common pathogens. The results advocate for vigilant antibiotic stewardship, emphasizing the need for regular monitoring of resistance trends to inform treatment strategies and enhance patient outcomes in the healthcare setting.

Keywords: antibiotic resistance, *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, multidrug resistance, antimicrobial susceptibility, extended-spectrum beta-lactamase (ESBL).

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INTRODUCTION

Antibiotic resistance is a pressing global health crisis that threatens the efficacy of existing antimicrobial treatments. The World Health Organization (WHO) has

highlighted that antibiotic resistance is responsible for an estimated 700,000 deaths annually worldwide, a figure projected to rise significantly if no effective interventions are implemented [1]. The emergence of

multidrug-resistant organisms (MDROs) poses significant challenges in managing common infections, complicating treatment options and increasing morbidity and mortality rates.

In recent years, the prevalence of antibiotic-resistant bacteria has escalated, particularly in hospital settings. According to a report by the Centers for Disease Control and Prevention (CDC), at least 2.8 million antibiotic-resistant infections occur in the United States each year, leading to more than 35,000 deaths [2]. Data from the European Centre for Disease Prevention and Control (ECDC) further indicate that antibiotic resistance is a major cause of treatment failures, resulting in extended hospital stays and higher healthcare costs [3].

In Vietnam, the situation is similarly alarming. A national survey conducted in 2020 revealed that resistance rates among common pathogens such as *Escherichia coli* and *Klebsiella pneumoniae* have reached 51.9% and 50.2% for third-generation cephalosporins, respectively [4]. A study in 2019 showed that more than 60% of *E. coli* isolates from patients with urinary tract infections (UTIs) were resistant to ampicillin, and nearly 50% showed resistance to fluoroquinolones [5]. The escalating rates of antibiotic resistance in Vietnam necessitate continuous monitoring and a thorough understanding of the current resistance patterns to inform clinical practices and public health policies.

This study aims to evaluate the prevalence of bacterial species isolated from clinical samples at Hai Phong International Hospital between 2020 and 2024 and to analyze their sensitivity to commonly used antibiotics. By providing updated insights into the antibiotic resistance landscape, the

findings of this study will contribute to improved antibiotic stewardship and enhanced patient care.

METHOD

Study Design

This study is a retrospective analysis conducted at Hai Phong International Hospital, focusing on microbiological test results obtained from clinical samples collected between 2020 and 2024. The research aims to evaluate the prevalence of various bacterial species isolated from these samples and their sensitivity to different antibiotics.

Study Population

The research focuses on the results of microbiological tests, specifically identifying and analyzing the bacterial isolates from a total of 9,133 microbiological test results.

Inclusion Criteria

Microbiological test results that report on bacterial isolates from clinical samples, including urine, blood, stool, and bronchial secretions.

Results from patients of all age groups who underwent microbiological testing during the study period.

Exclusion Criteria

Incomplete laboratory records or insufficient data regarding patient demographics or clinical background.

Duplicate test results from the same patient for the same infection episode.

Data Collection

Data were collected for each type of clinical sample, documenting the quantity and percentage of the ten most common bacterial species isolated. The analysis covered bacteria from urine samples, blood samples, stool samples, and bronchial secretions.

Bacterial Culture and Antibiotic Susceptibility Testing

Clinical specimens were cultured on Blood Agar, MacConkey Agar, and Chocolate Agar and incubated at 35–37°C for 18–24 hours under proper conditions. Bacterial identification was performed using biochemical tests and an automated system (VITEK 2).

Antibiotic susceptibility testing (AST) was conducted using the Kirby-Bauer disk diffusion method on Mueller-Hinton Agar, following CLSI 2024 guidelines[6]. Minimum inhibitory concentrations (MICs) were decided using broth microdilution or

VITEK 2 where necessary. Quality control was ensured using ATCC reference strains.

Data Analysis

Quantitative data were analyzed using descriptive statistics to summarize the distribution of bacterial isolates and their antibiotic sensitivity rates. The sensitivity rates of antibiotics were compared to evaluate their effectiveness against prevalent bacterial pathogens.

Ethical Considerations

The study protocol was approved by the Ethics Committee of Hai Phong International Hospital.

RESULTS

In this study, we analyzed the results of microbiological tests from a total of 9,133 clinical samples collected between 2020 and 2024 at Hai Phong International General Hospital.

Table 1. Distribution of specimen types (n=9133)

Specimen Type	Quantity	Percentage
Urine	3168	34.69%
Pus	1940	21.24%
Genital fluid	1024	11.21%
Nasopharyngeal fluid	688	7.53%
Blood	638	6.99%
Sputum (cup)	327	3.58%
Stool	303	3.32%
Bile fluid	286	3.13%
Bronchial fluid	266	2.91%
Abdominal fluid	249	2.73%
Sputum (tube)	104	1.14%
Others	140	1.53%
Total	9.133	100%

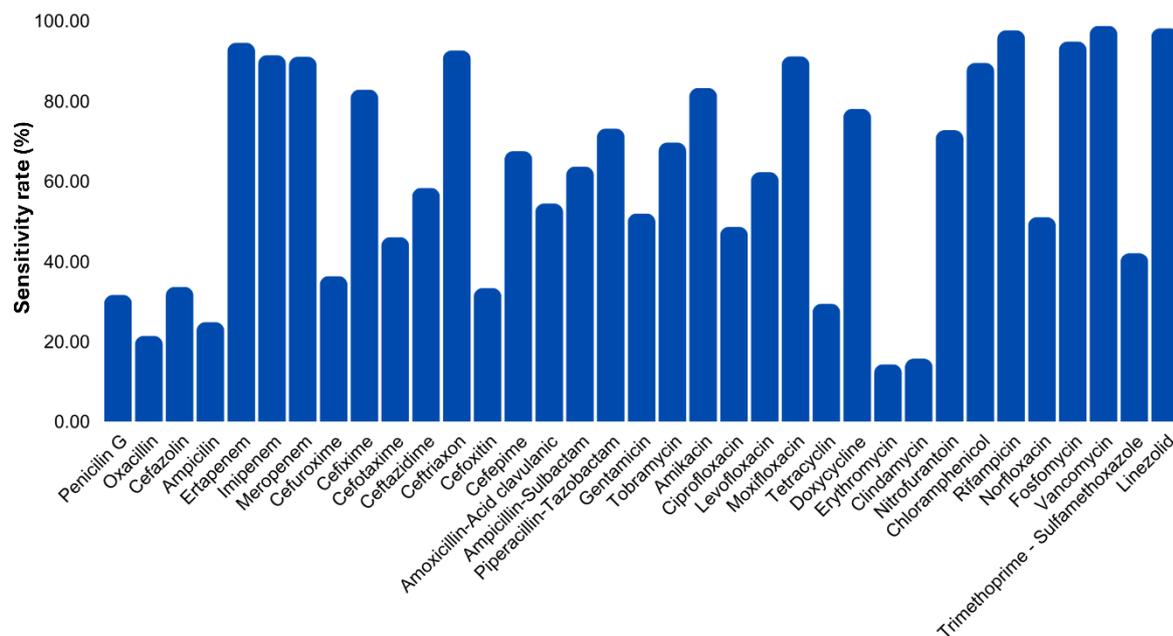


Figure 1. Antibiotic sensitivity percentages of bacterial isolates (n=9133)

Figure 1 summarizes the sensitivity percentages of various antibiotics against bacterial isolates. Notably, several carbapenems, including Ertapenem (94.50%), Imipenem (91.40%), and Meropenem (91.00%), show high efficacy, indicating their effectiveness in treating resistant infections. Ceftriaxone (92.60%) and Linezolid (98.10%) also show strong activity, suggesting they are reliable options for managing susceptible strains. Conversely, traditional antibiotics like Penicillin G (31.60%) and Erythromycin (14.30%) show low sensitivity, indicating significant resistance among the bacterial population. Among the fluoroquinolones, Ciprofloxacin (48.60%) and Levofloxacin (62.20%) reflect moderate effectiveness, while Moxifloxacin (91.10%) displays higher sensitivity.

Table 2. Top 10 Bacteria Isolated from Urine Samples (n=3168)

Bacterial Species	Quantity	Percentage
<i>Escherichia coli</i>	2200	69.44%
<i>Klebsiella pneumoniae</i>	166	5.24%
<i>Streptococcus</i> group B	152	4.80%
<i>Staphylococcus saprophyticus</i>	135	4.26%
<i>Proteus mirabilis</i>	86	2.71%
<i>Enterococcus faecalis</i>	80	2.53%
<i>Pseudomonas aeruginosa</i>	67	2.11%
<i>Enterococcus</i> (others)	41	1.29%
<i>Pseudomonas aeruginosa</i>	38	1.20%
<i>Enterobacter cloacae</i>	25	0.79%

Table 2 presents the top 10 bacteria isolated from 3,168 urine samples, with *Escherichia coli* being the most prevalent at 69.44%. This confirms its status as the leading cause of urinary tract infections (UTIs). Other significant pathogens include *Klebsiella pneumoniae* (5.24%) and *Streptococcus* group B (4.80%), both of which contribute to UTIs, especially in specific populations. Additionally, *Staphylococcus saprophyticus* (4.26%) and *Proteus mirabilis*

(2.71%) are notable, particularly in recurrent infections. The presence of *Pseudomonas aeruginosa* and *Enterobacter cloacae* indicates potential complications with more resistant or opportunistic infections. Overall, the data underscores the predominance of *E. coli* in UTIs while highlighting the diversity of other pathogens involved.

Table 3. Top 10 most common bacteria isolated from blood samples (n=638)

Bacterial Species	Quantity	Percentage
<i>Escherichia coli</i>	307	48.12%
<i>Klebsiella pneumoniae</i>	89	13.95%
<i>Streptococcus spp.</i>	49	7.68%
<i>Staphylococcus aureus</i>	44	6.90%
<i>Staphylococcus aureus</i>	17	2.66%
<i>Proteus mirabilis</i>	12	1.88%
<i>Enterococcus faecalis</i>	12	1.88%
<i>Enterobacter cloacae</i>	9	1.41%
<i>Acinetobacter baumannii</i>	8	1.25%
<i>Salmonella spp.</i>	7	1.10%

Table 3 summarizes the top 10 bacteria isolated from blood samples (n=638), with *Escherichia coli* being the most prevalent, accounting for 48.12% of the isolates. This highlights its significant role in bloodstream infections, often originating from urinary tract infections. Following this, *Klebsiella pneumoniae* represents 13.95%, indicating its importance in severe infections, especially among patients with underlying health conditions. Other notable bacteria include *Streptococcus spp.* (7.68%) and *Staphylococcus aureus* (6.90%), both of which are critical pathogens in clinical settings. The presence of multiple isolates of *Staphylococcus aureus* may suggest strain variability or contamination. Additionally, less common isolates like *Proteus mirabilis*, *Enterococcus faecalis*, and *Acinetobacter baumannii* underscore the need for vigilant infection control measures.

Table 4. Top 10 most common bacteria isolated from stool samples (n=303)

Bacterial Species	Quantity	Percentage
<i>Vibrio parahaemolyticus</i>	90	29.70%
<i>Salmonella spp.</i>	89	29.37%
<i>Aeromonas hydrophila/caviae</i>	33	10.89%
<i>Plesiomonas shigelloides</i>	24	7.92%
<i>Salmonella paratyphi B</i>	17	5.61%
<i>Aeromonas sobria</i>	14	4.62%
<i>Aeromonas spp.</i>	10	3.30%
<i>Salmonella paratyphi C</i>	6	1.98%
<i>Pseudomonas aeruginosa</i>	5	1.65%
<i>Vibrio haemolyticus</i>	3	0.99%

Table 4 presents the distribution of the top 10 bacteria isolated from stool samples, totaling 303 isolates. *Vibrio parahaemolyticus* is the most frequently isolated organism, representing 29.7%

of the total, which highlights its significance in gastrointestinal infections, particularly in coastal areas or regions with seafood consumption. Following closely, *Salmonella spp.* accounts for 29.37%, indicating its major role in foodborne illnesses.

Other notable isolates include *Aeromonas hydrophila/caviae* (10.89%) and *Plesiomonas shigelloides* (7.92%), both associated with gastroenteritis. Specific strains of *Salmonella*, such as *Salmonella paratyphi B* and *C*, are present but less common, emphasizing the diverse nature of salmonella infections.

Table 5. Top 10 most common bacteria isolated from bronchial secretions (n=266)

Bacterial Species	Quantity	Percentage
<i>Pseudomonas aeruginosa</i>	53	19.92%
<i>Acinetobacter baumannii</i>	43	16.17%
<i>Klebsiella pneumoniae</i>	39	14.66%
<i>Pseudomonas aeruginosa</i>	29	10.90%
<i>Staphylococcus aureus</i>	15	5.64%
<i>Acinetobacter baumannii</i>	12	4.51%
<i>Haemophilus influenzae</i>	12	4.51%
<i>Staphylococcus aureus</i>	8	3.01%
<i>Escherichia coli</i>	8	3.01%
<i>Pseudomonas spp.</i>	5	1.88%

Table 5 presents the top 10 bacteria isolated from bronchial secretions in a total of 266 samples. The predominant species is *Pseudomonas aeruginosa*, which comprises 19.92% of the isolates, indicating its significant role in respiratory infections, particularly among immunocompromised patients. *Acinetobacter baumannii* follows closely at 16.17%, highlighting its prevalence in healthcare-associated infections. *Klebsiella pneumoniae* accounted for 14.66%, marking it as a crucial pathogen in both community and hospital settings. The repeated entries for *Pseudomonas aeruginosa* and *Acinetobacter baumannii* may suggest strain variation or potential contamination issues.

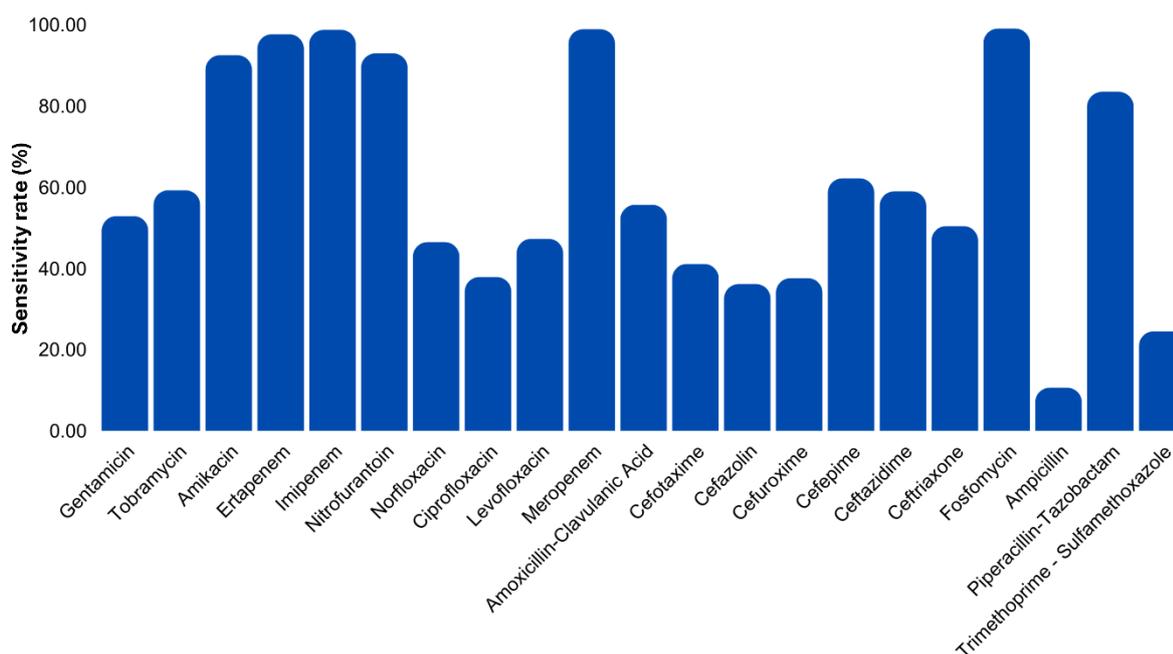


Figure 2. Sensitivity rates of antibiotics against *Escherichia coli* isolated from urine samples (n=2200)

The sensitivity rates of various antibiotics against *Escherichia coli* isolates from urine samples indicate significant variations in effectiveness. Notably, Fosfomycin (99.03%) and Imipenem (98.72%) showed the highest sensitivity, suggesting they are highly effective against this pathogen. Other antibiotics like Ertapenem (97.62%) and Meropenem (98.86%) also demonstrated strong efficacy. In contrast, Ampicillin exhibited the lowest sensitivity rate at only 10.65%, indicating a high resistance level. Amikacin (92.48%) and Nitrofurantoin (92.94%) were also effective, while Ciprofloxacin (37.87%) and Levofloxacin (47.28%) displayed lower sensitivity rates. Overall, the data highlights the importance of selecting the appropriate antibiotic for treating infections caused by *E. coli*, particularly in urinary tract infections.

Table 6. Distribution of Antibiotic Resistance Mechanisms Among Common Bacterial Species

Bacterial Species	AntiResult	Total
Citrobacter freundii	ESBL	1
Total Citrobacter freundii		1
Escherichia coli	AmpC	77
	Carbapenemase	3
	ESBL	709
Total Escherichia coli		3074
Klebsiella oxytoca	ESBL	1
Total Klebsiella oxytoca		14
Klebsiella pneumoniae	AmpC	1
	ESBL	19
Total Klebsiella pneumoniae		596
Proteus mirabilis	AmpC	1
	ESBL	21
Total Proteus mirabilis		144
Staphylococcus aureus	MRSA	325
	MSSA	982
Total Staphylococcus aureus		1307
Staphylococcus saprophyticus	MRSS	5
Total Staphylococcus saprophyticus		132

The data presented in table 6 summarizes the distribution of various antibiotic resistance mechanisms among several common bacterial species. Among the notable findings, *Escherichia coli* exhibits the highest number of resistance cases, with 709 instances of Extended Spectrum Beta-Lactamase (ESBL) production, followed by AmpC (77 cases) and carbapenemase (3 cases). This indicates a significant prevalence of multidrug resistance in this species, which is a major concern in clinical settings due to its association with severe infections. *Staphylococcus aureus* is another critical pathogen, with a total of 1307 isolates,

including 325 Methicillin-Resistant *Staphylococcus aureus* (MRSA) and 982 Methicillin-Sensitive *Staphylococcus aureus* (MSSA), highlighting the dual threat of resistance among staphylococcal infections.

DISCUSSION

This study provides valuable insights into the prevalence and antibiotic susceptibility patterns of bacterial pathogens isolated from clinical samples at Hai Phong International General Hospital between 2020 and 2024. The findings indicate a high prevalence of *Escherichia coli*, accounting for 69.44% of isolated organisms, consistent with previous studies that highlight *E. coli* as a dominant pathogen in urinary tract infections (UTIs) globally [7, 8]. The second most common pathogen identified was *Klebsiella pneumoniae* (5.24%), which aligns with reports from other regions showing its rising incidence and associated resistance challenges. Notably, our results reveal a significant level of antibiotic resistance, particularly against commonly used antibiotics like ampicillin (10.65% sensitivity) and ciprofloxacin (37.87% sensitivity). These findings mirror trends observed in various studies indicating an increase in multidrug-resistant (MDR) strains of *E. coli* and *K. pneumoniae*, raising concerns for public health and treatment efficacy [9, 10]. These results are consistent with trends noted in the Ministry of Health's annual antibiotic resistance surveillance reports, which indicate a rising prevalence of multidrug-resistant (MDR) strains in these bacterial species across Vietnam. According to the Ministry of Health (2022), the resistance rates for ampicillin and ciprofloxacin were reported at 11.5% and 38.2%, respectively, highlighting a situation similar to our findings [4]. For instance, ertapenem (97.62%) and meropenem (98.86%) exhibited high sensitivity rates, suggesting that carbapenems remain

effective against the predominant bacterial isolates. This is particularly important given the increasing resistance to beta-lactams and fluoroquinolones. Conversely, the low sensitivity rates to trimethoprim-sulfamethoxazole (24.49%) and nitrofurantoin (92.94%) warrant attention, as they indicate potential treatment limitations for common infections.

Additionally, our study emphasizes the need for continuous surveillance of antibiotic resistance patterns in clinical settings. Previous studies have reported similar resistance profiles, underscoring the global nature of this public health issue [7, 8]. Therefore, implementing antibiotic stewardship programs and promoting rational antibiotic use in both hospital and outpatient settings is critical to mitigating the emergence of resistant strains. The data presented in this study highlights trends in antibiotic resistance mechanisms among several common bacterial species, particularly focusing on *Escherichia coli* and *Staphylococcus aureus*. The findings indicate that *E. coli* exhibits the highest number of resistance cases, with 709 instances of Extended Spectrum Beta-Lactamase (ESBL) production, 77 cases of AmpC, and 3 cases of carbapenemase. The significant prevalence of ESBL-producing *E. coli* is alarming, as these enzymes confer resistance to a broad range of beta-lactam antibiotics, which are commonly used to treat serious infections. This high incidence of multidrug resistance in *E. coli* underscores a critical public health concern, as these resistant strains are associated with increased morbidity and mortality in clinical settings [9].

In addition, the presence of 325 Methicillin-Resistant *Staphylococcus aureus* (MRSA) isolates among a total of 1307 *Staphylococcus aureus* cases. This further exemplifies the dual threat posed by this pathogen. MRSA infections are particularly difficult to treat due to their resistance to methicillin and other beta-lactam antibiotics. The high prevalence of both MRSA and Methicillin-Sensitive *Staphylococcus aureus* (MSSA) strains emphasizes the need for vigilant infection control measures and the development of effective antimicrobial stewardship programs. The coexistence of MRSA and MSSA within the same patient populations complicates treatment strategies and necessitates a nuanced approach to antibiotic prescribing [11].

CONCLUSIONS

This study emphasizes the significant prevalence of antibiotic resistance among common bacterial pathogens. Notably, *Escherichia coli* was the most frequently isolated organism, accounting for 69.44% of urinary tract infections (UTIs) and 48.12% of bloodstream infections. Additionally, it exhibited 709 instances of Extended Spectrum Beta-Lactamase (ESBL) production, indicating a high level of multidrug resistance. *Staphylococcus aureus* also poses a considerable threat, with 1,307 isolates, including 325 MRSA cases, underscoring the challenges in managing staphylococcal infections. These findings highlight the urgent need for effective antibiotic stewardship and targeted infection control measures to combat rising resistance levels in clinical settings.

REFERENCES

1. World Health Organization. Global antimicrobial resistance and use surveillance system. 2022.

2. Centers for Disease Control and Prevention (U.S.). Antibiotic resistance threats in the United States. . 2019.
3. (ECDC). ECfDPaC. Antimicrobial Resistance in the EU/EEA. 2020.
4. Bộ Y tế Việt Nam. Báo cáo giám sát kháng kháng sinh tại Việt Nam 2020. 2023.
5. Hưng TTM. Thực trạng kháng kháng sinh của vi khuẩn ở cộng đồng và các yếu tố liên quan ở Việt Nam, năm 2018-2019: Viện vệ sinh dịch tễ trung ương 2022.
6. CLSI. Performance Standards for Antimicrobial Susceptibility Testing.14th ed. CLSI supplement M02. Clinical and Laboratory Standards Institute; 2024.
7. Kahlmeter G. An international survey of the antimicrobial susceptibility of pathogens from uncomplicated urinary tract infections: the ECO.SENS Project. *The Journal of antimicrobial chemotherapy*. 2003;51(1):69-76.
8. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clinical microbiology and infection : the official publication of the European Society of Clinical Microbiology and Infectious Diseases*. 2012;18(3):268-81.
9. Liu C, Sun S, Sun Y, Li X, Gu W, Luo Y, et al. Antibiotic resistance of *Escherichia coli* isolated from food and clinical environment in China from 2001 to 2020. *Science of The Total Environment*. 2024;939:173498.
10. Paul M, Carrara E, Retamar P, Tängdén T, Bitterman R, Bonomo RA, et al. European Society of Clinical Microbiology and Infectious Diseases (ESCMID) guidelines for the treatment of infections caused by multidrug-resistant Gram-negative bacilli (endorsed by European society of intensive care medicine). *Clinical Microbiology and Infection*. 2022;28(4):521-47.

11. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet* (London, England). 2022;399(10325):629-55.