Antimicrobial resistance patterns of community-acquired pneumonia pathogens: A five-year retrospective study at Hai Phong International Hospital, Vietnam (2020 – 2024)

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ABSTRACT

Background: Antimicrobial resistance (AMR) is a growing global crisis and has increasingly complicated the management of community-acquired pneumonia (CAP). In Vietnam, several studies have documented alarming resistance levels among key respiratory pathogens, but multi-year data from tertiary hospitals remain limited. ***Methods:*** We conducted a retrospective descriptive study at Hai Phong International Hospital, Vietnam, analyzing 1,418 inpatients with CAP from 2020 to 2024. Eligible patients had received at least one antibiotic, stayed ≥24 hours, and had available clinical, laboratory, and microbiology data. Data were extracted from electronic medical records and the microbiology database. Bacterial isolates were identified, and antimicrobial susceptibility was interpreted according to CLSI/EUCAST standards. Clinical outcomes were assessed based on symptom resolution, biomarker changes (WBC, CRP), and discharge status. Statistical analysis included Chi-square tests, Wilcoxon signed-rank tests, and multinomial logistic regression. ***Results:*** The cohort was predominantly elderly (≥60 years, 76.0%) and male (53.1%), with hypertension (53.3%) and diabetes (37.8%) as the most common comorbidities. Positive bacterial cultures were obtained in 22.6% of cases. Pseudomonas aeruginosa (24.9%), Acinetobacter baumannii (19.3%), and Klebsiella pneumoniae (15.3%) were the leading pathogens, while Streptococcus pneumoniae (5.0%) and Haemophilus influenzae (6.9%) were less frequent. Resistance was widespread: E. coli showed 100% resistance to ampicillin and >85% resistance to cefotaxime and ciprofloxacin; Klebsiella spp. exhibited >55% resistance to multiple agents; P. aeruginosa showed >50% resistance to fluoroquinolones and carbapenems; and A. baumannii demonstrated >85% resistance to nearly all tested drugs. Among Gram-positive isolates, S. pneumoniae displayed high resistance to erythromycin (93.3%) and clindamycin (93.8%) but preserved full susceptibility to vancomycin and linezolid. ***Conclusion:*** CAP patients at Hai Phong International Hospital demonstrated a predominance of multidrug-resistant Gram-negative pathogens and very high resistance among S. pneumoniae to macrolides. These findings highlight the urgent need for locally tailored empirical therapy, robust antimicrobial stewardship, and continuous surveillance to mitigate the growing AMR burden in Vietnam.

Keywords: community-acquired pneumonia, antimicrobial resistance, Gram-negative bacteria, Vietnam, empirical therapy

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INTRODUCTION

Antimicrobial resistance (AMR) is increasingly recognized as one of the most critical public health challenges of the 21st century. The World Health Organization (WHO) estimates that, without effective interventions, AMR could cause up to 10 million deaths annually by 2050 as common infections become more difficult to treat, complications rise, hospital stays lengthen, and healthcare costs escalate [1]. Although AMR is often associated with hospital-acquired infections, its impact on community-acquired infections, particularly community-acquired pneumonia (CAP), is also becoming severe [2]. In Vietnam, recent studies have documented alarming resistance levels among pathogens commonly associated with CAP. A cross-sectional study in Vinh Long Province (2018–2019) involving 254 CAP patients identified Streptococcus pneumoniae (12.6%), Klebsiella pneumoniae (12.2%), and Pseudomonas aeruginosa (8.3%) as the predominant pathogens, with S. pneumoniae showing resistance rates of 84.4% to erythromycin and 78.1% to tetracycline; Enterobacteriaceae isolates exhibited >30% resistance to amoxicillin/clavulanic acid [3]. Another recent study from a general hospital in Hanoi (Military Hospital 103) covering Staphylococcus aureus isolates from 2014 to 2021 reported very high resistance to macrolides (azithromycin ~82.3%, erythromycin ~82.8%) and clindamycin (~82.3%). Conversely, resistance rates to last-line agents such as vancomycin, linezolid, and teicoplanin remained very low (<3%) [4]. Regarding Pseudomonas aeruginosa, a 2019 study at Nhan Dan Gia Dinh Hospital revealed that among isolates (almost half from pneumonia in hospitalized patients), susceptibility to major antipseudomonal β-lactams (cefepime, ceftazidime, imipenem, meropenem, piperacillin-tazobactam) was modest (68%–71%), and fluoroquinolones like ciprofloxacin and levofloxacin showed susceptibility around 60-65%. However, resistance was substantial for many agents, especially where multidrug resistance (MDR) or extensively drug-resistant (XDR) phenotypes were involved [5]

These findings underscore the high prevalence of AMR among key CAP pathogens in Vietnam, with notable variability in antibiotic susceptibility across regions and facilities. Nevertheless, most existing reports are geographically limited or cover narrow time spans, and systematic multi-year data from tertiary hospitals remain scarce. A comprehensive evaluation of AMR trends and antibiotic use at Hai Phong International General Hospital from 2020 to 2024 is therefore essential to guide empirical therapy, strengthen antimicrobial stewardship, and inform local treatment guidelines.

METHODS

Study Design

This was a retrospective descriptive study conducted at Hai Phong International Hospital, Vietnam. Data were obtained from the hospital's electronic medical record (EMR) system and microbiology laboratory database for the period from January 1, 2020, to December 31, 2024.

Study Population

Eligible patients were all inpatients diagnosed with community-acquired pneumonia (CAP) based on ICD-10 codes J12–J18. Patients were included if they (1) had a hospital stay ≥24 hours, (2) received antibiotic therapy, and (3) had available

respiratory specimens (sputum, endotracheal aspirate, or bronchoalveolar lavage) sent for culture and susceptibility testing.

Exclusion criteria consisted of:

– hospital-acquired pneumonia (HAP), ventilator-associated pneumonia (VAP);

– confirmed SARS-CoV-2 pneumonia;

– other virologically confirmed viral pneumonias (e.g., influenza viruses, RSV, adenovirus, parainfluenza) when no bacterial growth was identified;

– incomplete or missing microbiology records.

Microbiological Methods

Respiratory specimens were processed at the hospital microbiology laboratory using standard culture techniques. Bacterial identification was performed by conventional biochemical methods and/or automated systems (VITEK 2). Antimicrobial susceptibility testing (AST) was carried out using the Kirby–Bauer disk diffusion method or automated systems, and results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) or European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines applicable for each year [6, 7]. MDR was defined as resistance to at least three different antimicrobial classes.

Data Collection

Extracted data included demographic characteristics (age, sex, comorbidities), type of respiratory specimen, isolated pathogens, and corresponding antimicrobial susceptibility patterns. Only the first isolate per patient per hospitalization was included to avoid duplication of results from repeated cultures.

Statistical Analysis

Descriptive statistics were used to summarize the data. Categorical variables (e.g., proportion of pathogens, resistance rates) were presented as frequencies and percentages. Analyses were descriptive in nature; inferential statistics were not applied because the primary aim was to characterize pathogen distribution and antimicrobial resistance patterns over the five-year period.

Ethical Considerations

This study was a retrospective analysis using existing medical records and microbiology data. The research protocol was reviewed and approved by the Scientific Committee of Hai Phong University of Medicine and Pharmacy.

Because all data collected retrospectively and fully anonymized prior to analysis, the requirement for informed consent was waived in accordance with institutional guidelines and national ethical regulations for retrospective studies.

RESULTS

A total of 1,418 patients with community-acquired pneumonia (CAP) were included between 2020 and 2024. The cohort was predominantly male, and the majority were older adults. Table 1 summarizes the baseline clinical, laboratory, and severity characteristics on admission. Hypertension and diabetes were the most common comorbidities. Most patients had elevated inflammatory markers, and chest X-ray showed pneumonic lesions in the majority. The median neutrophil count was 6.4 G/L, and neutrophilia was observed in 48.3% of patients.

***Table 1**. Baseline clinical and laboratory characteristics of patients with CAP on admission (n=1418)*

Variable	n (%) / Mean ± SD	Median [Range]

Sex		
Male	753 (53.1)	
Female	665 (46.9)	
Age group		
20–59 years	336 (23.7)	
≥60 years	1,078 (76.0)	
10–19 years	4 (0.3)	
Comorbidities		
Hypertension	757 (53.3)	
Diabetes mellitus	536 (37.8)	
Heart failure	271 (19.1)	
Chronic kidney disease	240 (16.9)	
Chronic lung disease	194 (13.7)	
Dyslipidemia	170 (12.0)	
Liver disease	110 (7.8)	
CURB-65 score		
0	164 (11.6)	
1	530 (37.4)	
2	519 (36.6)	
3–5	205 (14.5)	
Laboratory findings		
WBC (G/L)	9.73 ± 4.71	8.7 [0.1–38.4]
Leukocytosis	506 (35.7)	
Leukopenia	32 (2.3)	
Neutrophils (G/L)	–	6.4 [0.3–32.1]
Neutrophilia	685 (48.3)	
CRP (mg/L)	73.9 ± 86.0	41.7 [0.2–581.8]
Elevated CRP	1,030 (72.6)	
Procalcitonin (ng/mL)*	11.9 ± 24.6	1.03 [0.04–121.5]
Elevated PCT	132/201 (65.7)	
Radiology and microbiology		
Pneumonic lesion (X-ray)	1,218 (85.8)	
Positive respiratory culture	321 (22.6)	

**Procalcitonin was measured in 201 patients.*

Among 321 positive cultures, *Pseudomonas aeruginosa* was the most frequently isolated pathogen. Table 2 presents the distribution of all identified bacteria. The previously large

"Others" group (n=31) was disaggregated into specific organisms, including *Citrobacter spp.*, *Proteus spp.*, coagulase-negative *Staphylococci*, *Corynebacterium spp.*, *Non-tuberculous Mycobacteria*, and several isolates occurring in ≤ 2 cases.

***Table 2**. Distribution of bacterial pathogens isolated from respiratory specimens (n=321)*

Pathogen	n	%
Pseudomonas aeruginosa	80	24.9
Acinetobacter baumannii	62	19.3
Klebsiella pneumoniae	49	15.3
Staphylococcus aureus	26	8.1
Haemophilus influenzae	22	6.9
Streptococcus pneumoniae	16	5
Escherichia coli	15	4.7
Enterobacter spp.	9	2.8
Stenotrophomonas maltophilia	6	1.9
Moraxella catarrhalis	5	1.6
Citrobacter spp.	4	1.2
Proteus spp.	3	0.9
Coagulase-negative *Staphylococci*	3	0.9
Corynebacterium spp.	2	0.6
Non-tuberculous Mycobacteria	2	0.6
Other organisms (≤1 case each)	17	5.3
Total	**321**	**100**

Antimicrobial resistance patterns of Gram-negative and Gram-positive isolates are shown in Tables 3 and 4. Among Gram-negative organisms, *Acinetobacter baumannii* exhibited the highest resistance rates across nearly all tested agents, while *Haemophilus influenzae* remained susceptible to several first-line therapies. Gram-positive pathogens demonstrated preserved susceptibility to vancomycin, linezolid, and rifampicin, although resistance to macrolides and clindamycin remained high.

***Table 3.** Resistance rates of Gram-negative pathogens isolated from CAP patients (n=1418)*

Pathogen (n)	AMP	AMC	CRO/CTX	CAZ	FEP	CIP	LEV	GEN	AMK	IPM	MEM	TZP	Others*
E. coli (15)	100	23.1	85.8	50	38.5	85.2	60	21.4	0	0	0	0	TMP-SMX 66.7
Klebsiella spp. (49)	83.4	45.8	57.2	47	47	55.2	45.5	38.8	20.4	40.9	42.9	52.2	TMP-SMX 59.2

P. aeruginosa (80)	–	–	–		30.4	22.8	50.7	55.7	49.2	50.8	48.8	53.9	27.8	–
A. baumannii (62)	–	–		86.6	86.7	85.5	90	88.7	85.5	82.8	85.5	85.5	69.8	–
H. influenzae (22)	95.5	31.8	–		–	–	–	18.2	–	–	–	–	–	–

Abbreviations: AMP = Ampicillin, AMC = Amoxicillin/Clavulanic acid, CRO/CTX = Ceftriaxone/Cefotaxime, CAZ = Ceftazidime, FEP = Cefepime, CIP = Ciprofloxacin, LEV = Levofloxacin, GEN = Gentamicin, AMK = Amikacin, IPM = Imipenem, MEM = Meropenem, TZP = Piperacillin–Tazobactam, TMP-SMX = Trimethoprim-Sulfamethoxazole.

Table 4. *Resistance rates of Gram-positive pathogens isolated from CAP patients*

Pathogen (n)	**PEN**	**CRO/CTX**	**ERY**	**CLI**	**TET**	**DOX**	**LEV**	**VAN**	**LZD**	**RIF**	**CHL**	**TMP-SMX**
S. pneumoniae (16)	30.8	28.6–30.8	93.3	93.8	84.6	50	0	0	0	0	0	64.3
S. aureus (26)	–	–	–	–	–	–	62.5	–	–	–	–	16

Abbreviations: PEN = Penicillin G, CRO/CTX = Ceftriaxone/Cefotaxime, ERY = Erythromycin, CLI = Clindamycin, TET = Tetracycline, DOX = Doxycycline, LEV = Levofloxacin, VAN = Vancomycin, LZD = Linezolid, RIF = Rifampicin, CHL = Chloramphenicol, TMP-SMX = Trimethoprim-Sulfamethoxazole.

DISCUSSION

This study provides novel multi-year data on pathogen distribution and antimicrobial resistance (AMR) among *community-acquired pneumonia* (CAP) cases in northern Vietnam, specifically at Hai Phong International Hospital from 2020-2024. Several key findings emerge, with important clinical and public health implications.

First, the predominance of Gram-negative bacilli isolated (with *Pseudomonas aeruginosa* ~24.9%, *Acinetobacter baumannii* ~19.3%, *Klebsiella pneumoniae* ~15.3%) in our culture-positive CAP cases is concerning. While *Streptococcus pneumoniae* and *Haemophilus influenzae* are classically reported as leading CAP pathogens globally, recent Vietnamese studies also show shifts toward Gram-

negative dominance in many settings. For example, Nguyen Quoc Phuong et al. (2025) described that among pneumonia patients in intensive care units in northern Vietnam, *A. baumannii* (32.8%), *P. aeruginosa* (23.6%), and *K. pneumoniae* (20.4%) were major pathogens, and that sensitivity in CAP was higher than in hospital-acquired pneumonia (HAP) [8].

Second, the resistance patterns observed in our study echo national trends, but in some aspects are more severe. In particular, high resistance of *E. coli* to ampicillin, cephalosporins, and fluoroquinolones (as >80% in many cases) leaves few oral options. A cross-sectional study of ESBL-producing Enterobacteriaceae in An Giang (2020-2021) reported that *E. coli* had ~96.5% resistance to ampicillin and high resistance to other common agents[9]. Therefore, our findings are consistent with these and further underscore the shrinking efficacy of first-line antimicrobials in CAP settings.

Third, for *P. aeruginosa*, our observations of high resistance to fluoroquinolones and carbapenems are similar to those reported by a study at Nhan Dan Gia Dinh Hospital, where antipseudomonal β-lactams had susceptibilities in the range 68-71%, and fluoroquinolones ~60-65% among pneumonia isolates[5]. However, our data suggest that in Hai Phong, resistance may be even higher for many of these agents, which may reflect local antibiotic usage patterns or delayed initiation of appropriate therapy.

Fourth, while Gram-positive organisms were fewer, the pattern of resistance was still alarming in some respects. For *S. pneumoniae*, we observed very high resistance to macrolides and tetracyclines, consistent with other Vietnamese CAP studies. For example, the Vinh Long CAP study (2018-2019) found *S. pneumoniae* resistance to erythromycin ~84.4%, and tetracycline ~78.1%. This persistence of resistance among Gram-positives reinforces the need to avoid empirical reliance on macrolide therapy without susceptibility data. Overall, our data reveal that empirical therapy for CAP in this region must be reconsidered. Antibiotics that were formerly reliable may no longer be suitable as first-line agents for many patients, especially those likely to harbor multidrug-resistant Gram-negative pathogens. The findings support strengthened antimicrobial stewardship, local susceptibility surveillance, and tailored empirical guidelines.

This study has several limitations. First, being a single-center retrospective study, findings may not be generalizable across Vietnam. Second, only culture-based diagnostics were included; atypical bacteria and viruses were not systematically investigated, so some pathogens may have been under-detected. Third, resistance testing methods and interpretative standards (CLSI/EUCAST) may have changed over the study period, potentially affecting comparability.

CONCLUSION

The bacteriological landscape of CAP at Hai Phong International Hospital is characterized by a predominance of Gram-negative organisms and high levels of resistance to many commonly used antibiotics. Empirical treatment protocols should be updated to reflect local AMR patterns; stewardship and continuous surveillance are essential to preserve treatment efficacy and reduce the public health burden of CAP.

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