

Bacterial characteristics of pediatric respiratory tract infections in Hai Phong Children's Hospital

Pham Hong Nhung¹, Nguyen Phuong Tham¹, Nguyen Khanh Ly^{1,2}, Pham Hai Yen¹, Hoang Ngoc Anh^{1,2}, Dinh Duong Tung Anh^{1,2*}

ABSTRACT

Objectives: to evaluate the microbiological patterns and antibiotic susceptibility profiles of bacterial pathogens causing lower respiratory tract infections (LRTIs) in pediatric inpatients.

Subject and Methods: a retrospective study, utilizing convenience sampling, longitudinal data comprising 310 bacterial isolates were collected from 302 children admitted to the Respiratory Department of Haiphong Children's Hospital between April 2025 and March 2026. **Results:** The results revealed that community-acquired pathogens heavily dominated the etiological profile, with the classic "respiratory triad" accounting for 97.42% of all cases: *Haemophilus influenzae* (41.29%), *Streptococcus pneumoniae* (31.61%), and *Moraxella catarrhalis* (24.52%). Infections exhibited clear seasonal dynamics with prominent early spring and winter surges. Antimicrobial susceptibility testing demonstrated profound resistance among *H. influenzae* to ampicillin, cefuroxime, and co-trimoxazole, though advanced cephalosporins and carbapenems remained highly effective. *M. catarrhalis* isolates were largely resistant to legacy drugs but highly susceptible to amoxicillin/clavulanic acid and third-generation cephalosporins. Furthermore, *S. pneumoniae* exhibited near-total resistance to macrolides and clindamycin alongside extremely low oxacillin susceptibility, yet maintained absolute susceptibility to linezolid, vancomycin, and fluoroquinolones. **Conclusions:** in conclusion, pediatric LRTIs in this hospital setting are predominantly driven by *H. influenzae*, *S. pneumoniae*, and *M. catarrhalis*. The significant resistance observed against conventional empirical therapies, such as unpotentiated penicillins and macrolides, underscores the critical need for continuous, localized antimicrobial surveillance to guide the selection of appropriate targeted treatments, such as advanced cephalosporins or specific beta-lactam/beta-lactamase inhibitor combinations.

Keywords: lower respiratory tract infections, children, *H. influenzae*, *S. pneumoniae*, *M. catarrhalis*, antibiotic resistance.

¹ Hai Phong University of Medicine and Pharmacy, Vietnam

² Hai Phong Children's Hospital, Vietnam

* Corresponding author

Dinh Duong Tung Anh
Email: ddtanh@hpmu.edu.vn

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INTRODUCTION

Lower respiratory tract infections (LRTI) remains a leading cause of pediatric hospitalization and mortality in developing nations, including Vietnam [1]. While viral, fungal, and parasitic agents can incite LRTI, bacterial pathogens remain major

contributors to the disease burden [2]. In Vietnamese tertiary centers, polymerase chain reaction (PCR) assays are increasingly utilized for etiological diagnosis; however, they are limited to pathogen identification and cannot evaluate antibiotic resistance. Because bacterial profiles exhibit substantial geographical and temporal variation,

localized surveillance is essential [3]. The objective of this study was to evaluate the bacterial etiology and determine the *in vitro* antimicrobial resistance patterns of pathogens responsible for LRTI in pediatric patients admitted to Haiphong Children’s Hospital - a tertiary referral institution in Northern Vietnam— from 4/2025 to 3/2026.

MATERIALS AND METHODS

Subjects

This retrospective, descriptive case-series reviewed medical records of pediatric inpatients aged 2–60 months admitted to the Respiratory Department of Haiphong Children’s Hospital between April 1, 2025, and March 31, 2026.

Inclusion Criteria

Patients diagnosed with lower respiratory infections (croup, pneumonia, bronchiolitis) according to the Vietnam Ministry of Health (MOH) guidelines (2015) with a positive nasopharyngeal culture [4]. Microbiological evaluation (Gram staining, culture, AST) complied with MOH Decision No.

1539/QĐ-BYT, using updated CLSI guidelines for resistance interpretation [5].

Exclusion Criteria

Active asthma treatment, wheezing, underlying chronic conditions, immunosuppression, incomplete records, or prior hospitalization >48 hours elsewhere.

Study Design, Data Collection, and Analysis

Using convenience sampling, clinical parameters (admission date, age, isolated pathogens, and AST profiles) were extracted via a standardized form from all eligible records during the study period. Data were analyzed using SPSS 23.0 (IBM®, USA) via descriptive statistics and the χ^2 test for comparing proportions.

Ethical Considerations

The study was approved by the Review Committee of Hai Phong University of Medicine and Pharmacy (ID: ĐTCS.Y.2025-39, Decision No. 2289/QĐ-YDHP, dated October 10, 2025) and Hai Phong Children’s Hospital. All patient data were collected anonymously and handled in strict compliance with confidentiality principles.

RESULTS

Microbiological patterns

Table 1. Baseline characteristics of the study participants (n=302).

Characteristics		n	%
Age group	2 – <12 months	108	35.76
	12 – 60 months	194	64.24
Gender	Male	184	60.93
	Female	118	39.07
Residence	Rural	169	55.96
	Urban	133	44.04
Nasopharyngeal culture results	Mono-infection	294	97.35
	Bacterial co-infection	8	2.65

Remarks: Older children (12–60 months) outnumbered infants (2–<12 months) nearly 2:1, with a male predominance (M:F: 1.56:1). Subjects were well-distributed, leaning slightly rural. Nasopharyngeal cultures predominantly yielded mono-infections.

Table 2. Distribution of bacterial strains isolated from children with LRTI.

Type	Bacterial isolates	n	%	Total	
				n	%
Gram (-)	<i>Haemophilus influenzae</i>	128	41.29	208	67.1
	<i>Moraxella catarrhalis</i>	76	24.52		
	<i>Pseudomonas aeruginosa</i>	4	1.29		
Gram (+)	<i>Streptococcus pneumoniae</i>	98	31.61	102	32.9
	<i>Staphylococcus aureus</i>	4	1.29		

Remarks: Gram-negative bacteria constituted the majority of nasopharyngeal isolates from children with LRTI. The main causative pathogens of LRTI in children in Haiphong Children's hospital were *H. influenzae*, *S. pneumoniae* and *M. catarrhalis* (Table 2).

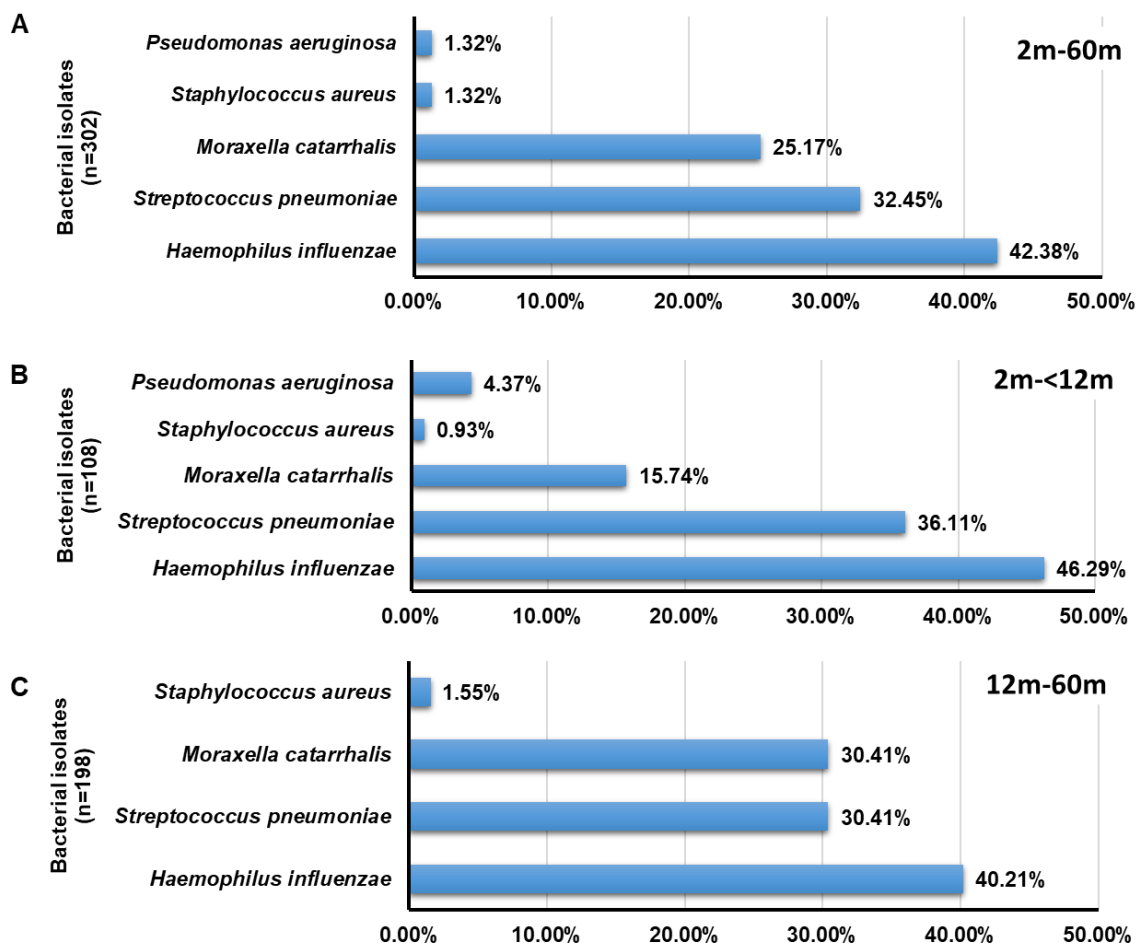


Figure 1. Distribution of bacterial isolates following age groups of children with LRTI.

Remarks: There were clear differences in the ratio of main bacterial pathogens responsible for LRTI among the age groups of patients (Fig. 1B and 1C).

Table 3. Age-specific distribution of common bacterial pathogens in children with LRTI.

Age Bacteria	2m - <12m (n=108) n (%)	12m – 60m (n=194) n (%)	p (*)
<i>Haemophilus influenzae</i>	50 (46.29)	78 (40.21)	0.3047
<i>Streptococcus pneumoniae</i>	39 (36.11)	59 (30.41)	0.3107
<i>Moraxella catarrhalis</i>	17 (15.74)	59 (30.41)	0.0049
<i>Staphylococcus aureus</i>	1 (0.93)	3 (1.55)	N/A
<i>Pseudomonas aeruginosa</i>	4 (3.70)	0 (0.00)	N/A

(*): Chi-square test; N/A: not applicable; m: month.

Remarks: *H. influenzae* and *S. pneumoniae* were most prevalent overall, peaking in infants (2m–<12m) without statistical significance ($p > 0.05$). Conversely, *M. catarrhalis* rates significantly doubled from 15.74% in infants to 30.41% in older children (12m–60m) ($p = 0.0049$). *S. aureus* and *P. aeruginosa* were rare; *P. aeruginosa* was exclusively isolated in infants (3.70%) (Table 3).

Analysis of patient distribution by month of admission revealed two distinct peaks in the prevalence of the most common pathogens based on the time of hospital admission (Figure 2): from March to April and from November to December. A highly similar seasonal pattern was observed among the three most prevalent bacterial species in this study (*H. influenzae*, *S. pneumoniae* and *M. catarrhalis*).

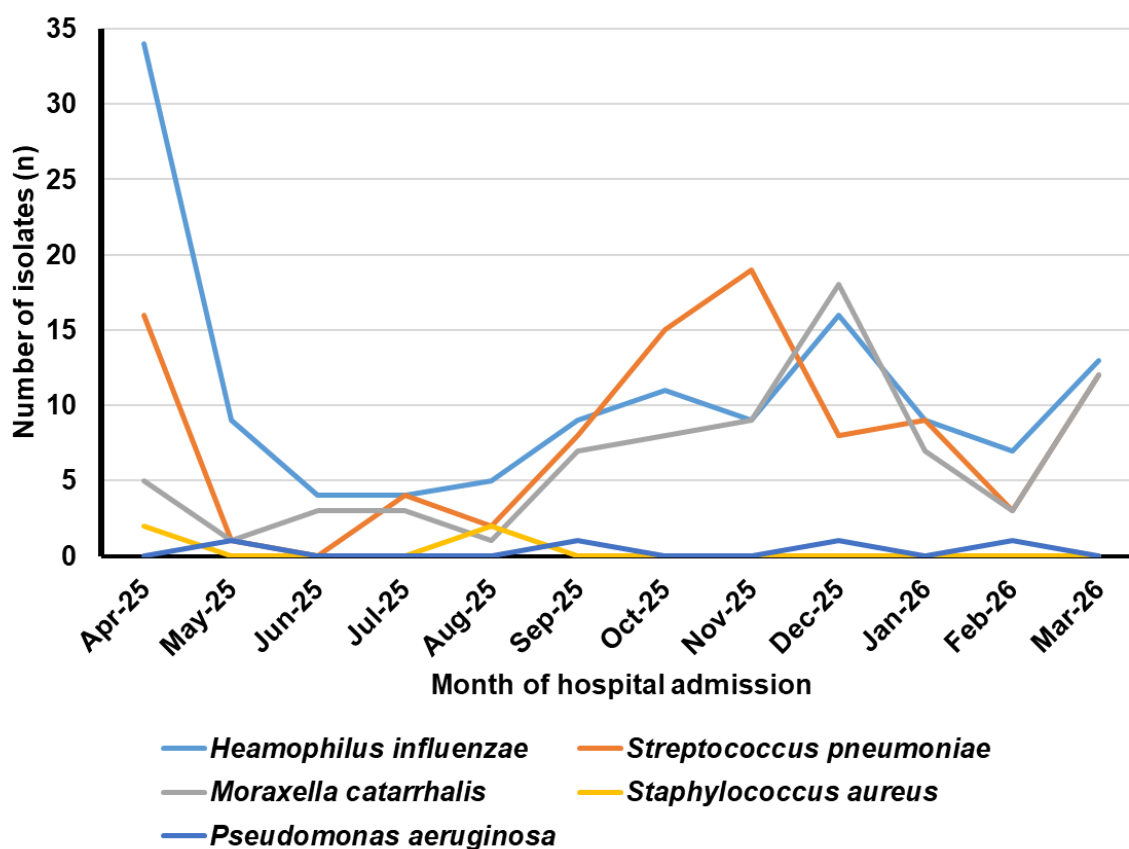


Figure 2. The distribution of the pathogens according to the time of diagnosis.

Remarks: Analysis of patient distribution by month of admission revealed two distinct peaks in the prevalence of the most common pathogens based on the time of hospital admission (Figure 2): from March to April and from November to December. A highly similar seasonal pattern was observed among the three most prevalent bacterial species in this study (*H. influenzae*, *S. pneumoniae* and *M. catarrhalis*).

***In vitro* antibiotic susceptibility of bacteria causing LRTI in children**

Here, we assessed the *in vitro* antibiotic susceptibility of the main causative bacteria found in children with LRTI using antibiogram of nasopharyngeal swab samples.

Table 4. Antibiotic susceptibility of the most common Gram (-) bacteria isolated from inpatients with LRTI.

Group	Bacteria	Antibiotics	<i>H. influenzae</i>	<i>M. catarrhalis</i>
Penicillins		Ampicillin	1.6	N/A
Cephems		Ceftriaxone	99.21	58.33
		Cefotaxime	99.18	100.00
		Cefuroxime	5.56	34.67
		Ceftazidime	100.00	100.00
		Cefepime	98.35	78.26
Fluoroquinolones		Ciprofloxacin	90.48	72.86
		Levofloxacin	89.76	75.00
Folate Inhibitors		Trimethoprim/ Sulfamethoxazole	17.74	35.14
Beta-lactam/beta-lactamase Inhibitors		Amoxicillin/Clavulanic acid	63.78	100.00
		Ampicillin/Sulbactam	24.41	N/A
		Piperacillin/Tazobactam	98.38	N/A
Carbapenems		Imipenem	96.50	98.11
		Meropenem	100.00	95.77

N/A: not applicable

Remarks: *H. influenzae* isolates resisted ampicillin, cefuroxime, and co-trimoxazole, but maintained near-absolute susceptibility to carbapenems, fluoroquinolones, and advanced cephalosporins (ceftazidime 100%, ceftriaxone 99.21%, cefotaxime 99.18%). *M. catarrhalis* also resisted cefuroxime and co-trimoxazole, but responded optimally to amoxicillin/clavulanic acid, 3rd-generation cephalosporins, carbapenems, and secondary fluoroquinolones.

Table 5. Antibiotic susceptibility of *S. pneumoniae* isolated from inpatients with LRTI.

Group	Bacteria	Antibiotics	Number of test	% Susceptible
Penicillins		Oxacillin	57	1.75
		Ampicillin	2	50.00
Macrolides		Erythromycin	95	1.05
		Azithromycin	92	2.17
Lincosamides		Clindamycin	95	4.21

Glycopeptides	Vancomycin	94	97.88
Oxazolidinones	Linezolid	98	100.00
Fluoroquinolones	Levofloxacin	98	100.00
	Ciprofloxacin	1	100.00
Folate Inhibitors	Trimethoprim/ Sulfamethoxazole	96	29.17
Cephems	Ceftriaxone	3	100.00
	Cefotaxime	3	66.67
	Cefepime	1	0
	Cefuroxime	1	100.00
Beta-lactam/beta-lactamase Inhibitors	Amoxicillin/ Clavulanic acid	1	100.00
	Ampicillin/Sulbactam	2	50.00
Carbapenems	Imipenem	57	1.75
	Meropenem	2	50.00

Remarks: *S. pneumoniae* exhibited near-total resistance to macrolides and clindamycin. The extremely low oxacillin susceptibility (1.75%) served as a strong surrogate marker for Penicillin-Resistant *Streptococcus pneumoniae* (PRSP). Linezolid, vancomycin and fluoroquinolones demonstrated absolute or near-absolute efficacy. Inconsistent beta-lactam and carbapenem efficacy indicated atypical cross-resistance patterns among the beta-lactams.

DISCUSSION

Microbiological patterns of LRTI in children

Among 310 bacterial isolates, Gram-negative pathogens predominated (67.1%), driven by *H. influenzae* (41.29%) and *M. catarrhalis* (24.52%). Gram-positive bacteria accounted for 32.37%, mainly *S. pneumoniae* (31.36%). This "respiratory triad" caused 97.42% of community-acquired infections. Compared to a 2019 study (638 isolates) at the same site, a sharp shift occurred: *S. aureus* declined drastically from 28.06% to 1.28% in 2025 [3]. The high prevalence of *H. influenzae* and *M. catarrhalis* necessitates using beta-lactam/beta-lactamase inhibitors or advanced cephalosporins per CLSI guidelines [5], as widespread beta-lactamase production and BLNAR strains render un-potentiated ampicillin ineffective [6, 7]. For *S. pneumoniae*, the primary Gram-positive pathogen, MIC monitoring remains vital to mitigate invasive disease [8]. Conversely, the

minimal presence (1.29% each) of *S. aureus* and *P. aeruginosa* indicates that nosocomial or healthcare-associated complications were rare in this community population [9].

The 12-month longitudinal data (April 2025 – March 2026) revealed distinct temporal fluctuations: an anomalous spring spike in April 2025 driven by *H. influenzae* due to climate-driven mucosal alterations [10], and a classic winter surge peaking in December. In winter, *S. pneumoniae* peaked in November and *M. catarrhalis* in December, a wave facilitated by indoor crowding and viral-induced epithelial damage [11], consistent with 2019 dynamics [3]. Regionally, a Hai Phong study [12] corroborated the dominance of this bacterial triad, whereas a Colombian cohort [13] reported *M. pneumoniae* and *S. pneumoniae* as primary pathogens, highlighting that pediatric respiratory etiology varies substantially across geographic and temporal boundaries.

Antibiotic susceptibility of bacteria inducing LRTI in children

Regarding antibiotic susceptibility, *H. influenzae* showed profound resistance to ampicillin, cefuroxime, co-trimoxazole, and ampicillin/sulbactam, but remained highly sensitive to advanced cephalosporins, carbapenems, piperacillin/tazobactam, and fluoroquinolones. Conversely, *M. catarrhalis* exhibited significant resistance to cefuroxime and co-trimoxazole, but absolute susceptibility to amoxicillin/clavulanic acid, cefotaxime, and ceftazidime. These profiles align with a pediatric CAP study where both leading pathogens demonstrated widespread legacy drug and macrolide resistance, yet remained highly susceptible to newer-generation cephalosporins, carbapenems, and select targeted agents [14]. A recent Chinese pediatric LRTI study reported 92.0% beta-lactamase positivity and ampicillin resistance in *H. influenzae*. While susceptibility to amoxicillin/clavulanate was moderate (70.2%), efficacy remained high (>90.0%) for cefotaxime, ofloxacin, tetracycline, chloramphenicol, and rifampicin [15].

Regarding antibiotic susceptibility, *S. pneumoniae* demonstrated profound resistance to macrolides, clindamycin, oxacillin, cefepime, and imipenem, while linezolid, vancomycin, fluoroquinolones, and select beta-lactams maintained high efficacy. This pattern exhibits regional variations: a Hai Phong study [16] found high susceptibility to imipenem and cephalosporins but severe ciprofloxacin resistance. Conversely, a Quang Nam-Da Nang study aligned with the current findings regarding near-total macrolide resistance and absolute linezolid, vancomycin, and levofloxacin efficacy, while reporting low beta-lactam resistance and an 83.9% multidrug-resistance (MDR) rate [17].

CONCLUSION

The most common pathogens inducing LRTI in children at Haiphong Children's hospital in 2025 were *S. pneumoniae*, *H. influenzae* and *M. catarrhalis*. Our study has also recorded a dramatic reduction in the prevalence of isolated *S. aureus* while provided valuable data on the antibiotic sensitivity and raised alarm over presence of antibiotic-resistant bacteria inducing LRTI in children. The above findings underscore the necessity of ongoing monitoring regarding both the changing bacterial patterns causing community-acquired LRTI in children and their evolving antibiotic resistance profiles over time at the same study site.

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