

Preplanned Studies

Pilot Surveillance Program on Pneumonia with Public Health Risk — Shanghai Municipality, China, 2024–2025

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Summary

What is already known about this topic?

China's surveillance for pneumonia of unknown etiology, established in 2004, is vital for identifying novel pathogens early. However, limited cases have been reported, indicating potential challenges regarding sensitivity and operational efficiency.

What is added by this report?

A pilot surveillance program to detect pneumonia with public health risk was implemented in Shanghai between October 2024 and July 2025. The system was established using an optimized workflow involving refined case definitions, tiered laboratory testing network, and joint expert risk assessment process. Forty-six cases were identified in medical institutions at different levels, demonstrating the system's operational feasibility.

What are the implications for public health practice?

The pilot provides a framework for a proactive paradigm for monitoring emerging respiratory threats. Future surveillance should prioritize identifying case clusters and specific epidemiological links (e.g., suspicious animal contact and travel history). Applying advanced diagnostics, including metagenomic sequencing, and integrating multi-source data with information technology are crucial next steps for building a more responsive surveillance system.

Systematic laboratory tests, including multiplex polymerase chain reaction (PCR) and metagenomic sequencing, were conducted. Experts specializing in clinical diagnostics, laboratory tests, and epidemiology performed joint risk assessments. Surveillance data were descriptively analyzed.

Results: Forty-six risk pneumonia cases met the case definition across participating medical institutions. Reporting departments differed by hospital tier ($P < 0.001$). Median time intervals from visit to report were comparable ($H = 2.261$, $P = 0.323$). Severe or critical pneumonia constituted 93.48% of cases, and 6.52% were associated with two distinct clusters. Common indicators of severe pneumonia were shortness of breath (60.47%, 26/43) and oxygen saturation $\leq 93\%$ (58.14%, 25/43). Most patients (76.09%) were aged ≥ 60 years. Joint risk assessment showed no evidence of emerging major infectious disease among reported cases, with 33 attributed to common respiratory pathogens detected through multiplex PCR, 11 without emerging/rare pathogens being detected by metagenomic sequencing, and 2 with inadequate samples showing no evidence of major infectious disease at follow-up. The etiologic spectrum included viruses (30.43%), mixed infections (21.74%), bacteria (10.87%), and other pathogens (8.70%).

Conclusion: This pilot demonstrated the feasibility of a surveillance framework for risk pneumonia by identifying 46 cases across medical institution tiers and departments. Integrating multiplex PCR enabled rapid etiologic clarification. Tiered laboratory testing and joint risk assessment provided closed-loop management. No evidence of emerging major infectious diseases was found. Future efforts should refine case definitions to prioritize cluster detection, standardize advanced laboratory techniques, and integrate information technology to improve early warning capabilities.

The global public health landscape increasingly faces challenges from emerging and re-emerging respiratory infectious diseases, such as the 2003 severe acute

ABSTRACT

Introduction: A pilot surveillance program on pneumonia with public health risk was conducted in Shanghai to provide a practical reference for monitoring emerging respiratory infectious diseases.

Methods: A refined risk pneumonia surveillance system was implemented in 14 sentinel hospitals across nine districts between October 2024 and July 2025. Case definitions emphasized individual severity, clustering potential, and novel pathogen detection.

respiratory syndrome (SARS) outbreak and coronavirus disease 2019 (COVID-19) pandemic. These major public health incidents mainly originate from clustered severe pneumonia cases of unknown etiology (1–4). In China, a national surveillance system for such cases, based on the 2007 surveillance protocol issued by the Ministry of Health, aims to screen for potential SARS cases, human infections of avian influenza viruses, and clusters of respiratory diseases primarily presenting as pneumonia in healthcare institutions at all levels nationwide (5). This system has been crucial for detecting and reporting human avian influenza cases (6). However, challenges persist in its operation, including suboptimal sensitivity, reporting delays, and susceptibility to external non-technical factors, leading to scarce case reports (7–8). To address these limitations and shift from a reactive focus on *unknown etiology* to a more proactive, risk-based early warning approach, this study established a surveillance system for pneumonia cases with public health risk by refining case definitions and operational protocols of the current surveillance workflow. Its feasibility was evaluated through an on-site pilot in Shanghai.

This pilot surveillance program was conducted between October 2024 and July 2025. Patients were recruited from 14 sentinel hospitals (5 Level-3A, 6 Level-3B, and 3 Level-2A), which were medical institutions encompassing urban, suburban, and semi-urban areas from 9 districts in Shanghai, ensuring broad geographic representation, alongside considerations related to patient volume and clinical capacity.

Surveillance cases were patients with acute-onset pneumonia of suspected infectious origin, presenting with fever ($\geq 38^{\circ}\text{C}$) and compatible imaging or clinical diagnosis who met at least one of the following criteria:

First, individual severity. Severe (critical) pneumonia or pneumonia with a tendency toward rapidly progressing severity and was unresponsive to empirical treatment.

Second, population transmission risk. Pneumonia cases with suspicious epidemiological links were identified within two weeks.

Third, novel pathogen risk. Suspected emerging rare pathogens or novel pathogens were detected in specimens from patients.

Cases that could be explained by infection with common respiratory pathogens through routine diagnosis and management at medical institutions were excluded.

Hospital staff received standardized training on case

identification and reporting procedures under the pilot protocol [Work Plan for the Pilot Surveillance and Early-Warning Program for Pneumonia of Unknown Etiology in Shanghai; Shanghai Disease Control and Prevention Administration (2024) No.3]. Standardized checklists were used for case reporting. Attending physicians at each hospital determined which patients to enroll based on clinical judgment, mainly referencing clinical protocols. Respiratory specimens were collected if patients met the surveillance case definition. Twenty-one common respiratory pathogens (Figure 1) were tested at district CDCs within 24 hours using a commercial Multiplex Respiratory Pathogen Nucleic Acid Detection Kit [Fluorescent Polymerase Chain Reaction (PCR) Method] (Shanghai GeneDx Biotech Co., Ltd., China). When multiplex PCR results were negative, metagenomic sequencing was performed at the municipal CDC on a DNBSEQ-G99 platform (SE100) using the MGI PFI pipeline.

Epidemiological investigations were conducted for all eligible cases to collect information on demographics, clinical presentations, and epidemiological characteristics. A joint risk assessment was conducted based on laboratory tests and epidemiological investigations by experts specializing in clinical diagnostics, laboratory tests, and epidemiology (Figure 1).

All data were collected using standardized case report forms. Descriptive analyses were performed using Excel 2021 and R software (version 4.3.0, R Foundation for Statistical Computing, Vienna, Austria). Categorical comparisons were performed using chi-square or Fisher's exact tests (if expected counts were <5). Median comparisons were performed using Kruskal–Wallis tests. For key proportions, 95% Wilson confidence intervals (CIs) were calculated. Significance was defined as two-sided $P < 0.05$.

Between October 2024 and July 2025, 14 sentinel hospitals recorded 21,650,289 outpatient and emergency visits; 871,164 inpatient admissions; and 221,168 pneumonia cases, of which 46 surveillance cases met the definition. All surveillance cases were hospitalized. Most cases (76.09%, 35/46, 95% CI: 62.06%, 86.09%) were aged 60 years or older (Table 1), including 63.04% (29/46) men and 36.96% (17/46) women. Severe or critical cases constituted 93.48% (43/46, 95% CI: 82.50%, 97.76%), and 6.52% (3/46) were part of two distinct clusters. One cluster included two family members visiting the hospital. The third clustered case was identified through routine clinical investigations of an individual

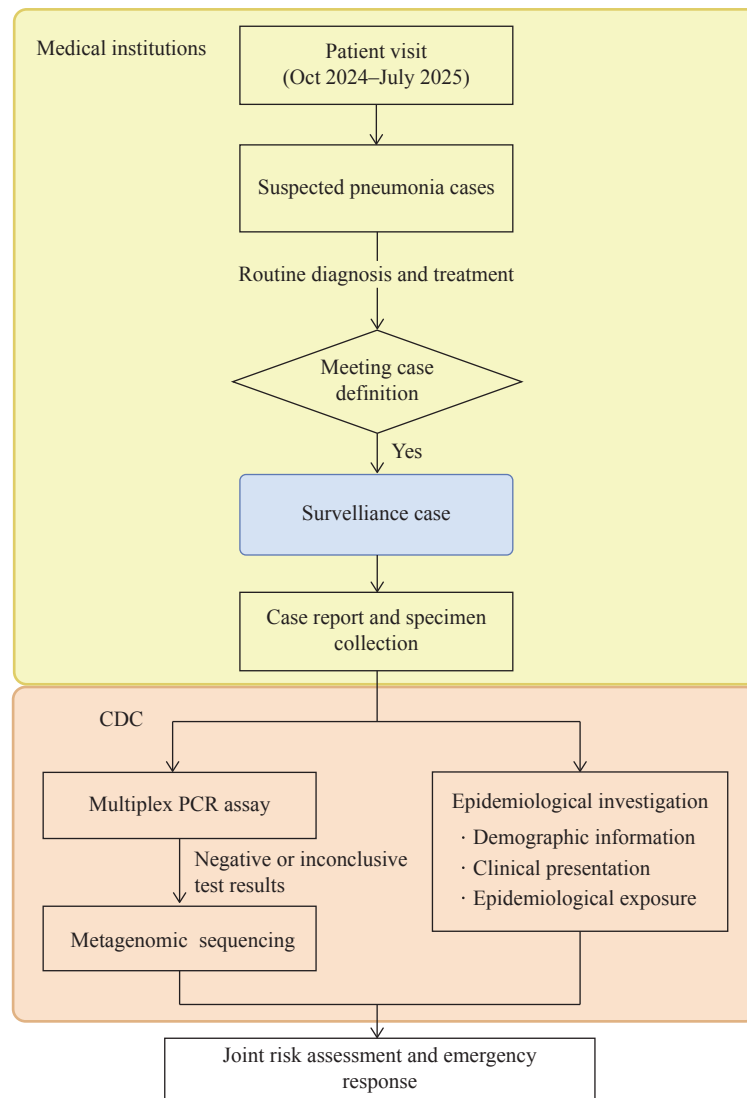


FIGURE 1. Workflow of the pilot surveillance system for pneumonia cases with public health risk.

Note: Multiplex PCR assay detected 21 common respiratory pathogens simultaneously, including SARS-CoV-2, IFV [including A(H1N1)pdm09, A(H3N2), B/Victoria, and B/Yamagata lineages], RSV (including subtypes A and B), HAdV, HMPV, HPIV (including subtypes 1–4), HCoV (including types OC43, 229E, NL63, and HKU1), HBoV, HRV, EV, *S. pyogenes* (Group A *Streptococcus*), *B. pertussis*, *S. pneumoniae*, *H. influenzae*, *L. pneumophila*, *K. pneumoniae*, *M. pneumoniae*, *C. pneumoniae*, *C. psittaci*, *Aspergillus* spp. and *Cryptococcus* spp.

Abbreviation: PCR=Polymerase Chain Reaction; CDC=Center for Disease Control and Prevention; SARS-CoV-2=severe acute respiratory syndrome coronavirus 2; IFV=influenza virus; RSV=respiratory syncytial virus; HAdV=human adenovirus; HMPV=human metapneumovirus; HPIV=human parainfluenza virus; HCoV=human coronavirus; HBoV=human bocavirus; HRV=human rhinovirus; EV=enterovirus; *S. pyogenes*=*Streptococcus pyogenes*; *B. pertussis*=*Bordetella pertussis*; *S. pneumoniae*=*Streptococcus pneumoniae*; *H. influenzae*=*Haemophilus influenzae*; *L. pneumophila*=*Legionella pneumophila*; *K. pneumoniae*=*Klebsiella pneumoniae*; *M. pneumoniae*=*Mycoplasma pneumoniae*; *C. pneumoniae*=*Chlamydia pneumoniae*; *C. psittaci*=*Chlamydia psittaci*; spp.=species.

with a family member with pneumonia without visiting the sentinel hospital. Common severity indicators for severe or critical cases included shortness of breath (60.47%, 26/43) and oxygen saturation $\leq 93\%$ (58.14%, 25/43). The most frequently reported initial symptoms were fever (71.74%, 33/46), coughing (60.87%, 28/46), and expectoration

(45.65%, 21/46). Most patients (82.61%, 38/46) were retirees. Suspicious animal contact and travel histories were reported in 13.04% (6/46) and 8.70% (4/46) of cases, respectively.

Excluding 16 cases with initial medical visits at non-sentinel hospitals and thus the initial visit time for sentinel hospitals could not be accurately determined,

TABLE 1. Characteristics of surveillance cases identified through the pilot surveillance system in Shanghai.

Characteristics	All cases (N=46)	Case type	
		Severe cases (N=43)	Clustered cases (N=3)
Gender, N (%)			
Male	29 (63.04)	28 (65.12)	1 (33.33)
Female	17 (36.96)	15 (34.88)	2 (66.67)
Age group, N (%)			
Adult (18–59 years)	11 (23.91)	9 (20.93)	2 (66.67)
Older adults (≥60 years)	35 (76.09)	34 (79.07)	1 (33.33)
Medical Institution Grade, N (%)			
Level 3A	9 (19.57)	9 (20.93)	0 (0)
Level 3B	22 (47.83)	19 (44.19)	3 (100.00)
Level 2A	15 (32.61)	15 (34.88)	0 (0)
Initial symptoms, N (%)			
Fever	33 (71.74)	31 (72.09)	2 (66.67)
Coughing	28 (60.87)	27 (62.79)	1 (33.33)
Expectoration	21 (45.65)	21 (48.84)	0 (0)
Shortness of breath	9 (19.57)	9 (20.93)	0 (0)
Aching	5 (10.87)	5 (11.63)	0 (0)
Fatigue	5 (10.87)	5 (11.63)	0 (0)
Chills	4 (8.70)	4 (9.30)	0 (0)
Chest distress	3 (6.52)	3 (6.98)	0 (0)
Throat discomfort	2 (4.35)	2 (4.65)	0 (0)
Running nose	1 (2.17)	1 (2.33)	0 (0)
Sweating	1 (2.17)	1 (2.33)	0 (0)
Diarrhea	1 (2.17)	1 (2.33)	0 (0)
Indicators reflecting severity, N (%)			
Shortness of breath	27 (58.70)	26 (60.47)	1 (33.33)
Oxygen saturation ≤93%	25 (54.35)	25 (58.14)	0 (0)
Oxygenation index ≤300 mmHg	9 (19.57)	9 (20.93)	0 (0)
Rapid symptom progression	8 (17.39)	8 (18.60)	0 (0)
Respiratory failure	8 (17.39)	8 (18.60)	0 (0)
Occupation, N (%)			
Retiree	38 (82.61)	36 (83.72)	2 (66.67)
Office worker	2 (4.35)	2 (4.65)	0 (0)
Construction worker/Dust-related production line worker	2 (4.34)	1 (2.33)	1 (33.33)
Unemployed	2 (4.34)	2 (4.66)	0 (0)
Student	1 (2.17)	1 (2.33)	0 (0)
Unknown	1 (2.17)	1 (2.33)	0 (0)
Epidemiological exposure, N (%)			
None	38 (82.61)	36 (83.72)	2 (66.67)
Suspicious animal contact history	6 (13.04)	6 (13.95)	0 (0)
Travel history	4 (8.70)	4 (9.30)	0 (0)

the median time interval from symptom onset to hospital visit [interquartile range (IQR): 2–5 days] and from hospital visit to case report (IQR: 1.25–5.75 days) were 3 days. Reporting departments varied by hospital grade ($P<0.001$). Most (66.67%, 6/9) were reported by critical care medicine departments at Level 3A hospitals, whereas reporting was more balanced between infectious disease (45.45%, 10/22) and respiratory medicine (45.45%, 10/22) departments at Level 3B hospitals. Infectious disease departments were dominant, reporting 66.67% (10/15) of the cases at Level 2A hospitals.

Pathogens were detected in 71.74% of cases (33/46; 95% CI: 57.45%, 82.68%) through multiplex PCR

assay. The three most frequently identified pathogens were Influenza A(H1N1) virus (8 cases), Haemophilus influenzae (7 cases), and Human rhinovirus (5 cases). Viral infections were identified in 30.43% (14/46) of cases. Mixed infections (more than one pathogen) accounted for 21.74% (10/46). Bacterial infections were detected in 10.87% (5/46), and other pathogens (e.g., Mycoplasma and Chlamydia) in 8.70% (4/46). No pathogens were identified in 28.26% (13/46; 95% CI: 17.32%, 42.55%) of the cases after multiplex PCR and metagenomic sequencing where feasible, including two cases for which metagenomic testing could not be conducted because of unqualified sample quality (Table 2).

TABLE 2. Characteristics of surveillance cases reported by different levels of medical institutions*.

Characteristics	All cases (N=46)	Medical Institution Grade [†]			H	P
		Level 3A (N=9)	Level 3B (N=22)	Level 2A (N=15)		
Report and investigation, Median (Q1, Q3)						
Onset-to-visit interval (days) [§]	3.00 (2.00–5.00)	3.00 (3.00–3.00)	3.00 (2.00–4.50)	3.00 (1.00–5.00)	0.009	0.996
Visit-to-report interval (days) [§]	3.00 (1.25–5.75)	6.00 (6.00–6.00)	3.50 (2.00–5.25)	2.00 (1.00–4.00)	2.261	0.323
Reporting department, N (%)					–	<0.001
Infectious Disease	20 (43.48)	0 (0.00)	10 (45.45)	10 (66.67)		
Respiratory Medicine	13 (28.26)	2 (22.22)	10 (45.45)	1 (6.67)		
Critical Care Medicine	11 (23.91)	6 (66.67)	2 (9.09)	3 (20.00)		
Others	2 (4.35)	1 (11.11)	0 (0)	2 (4.35)		
Pathogen detected, N (%)					–	0.080
Virus detected	14 (30.43)	5 (55.56)	4 (18.18)	5 (33.33)		
No pathogen detected	13 (28.26)	2 (22.22)	6 (27.27)	5 (33.33)		
Mixed infection [¶]	10 (21.74)	2 (22.22)	8 (36.36)	0 (0)		
Bacteria detected	5 (10.87)	0 (0)	3 (13.64)	2 (13.33)		
Others detected**	4 (8.70)	0 (0)	1 (4.55)	3 (20.00)		
Specimen type, N (%)					–	0.212
Oropharyngeal swab	23 (50.00)	2 (22.22)	12 (54.55)	9 (60.00)		
Nasopharyngeal swab	13 (28.26)	2 (22.22)	6 (27.27)	5 (33.33)		
Sputum	6 (13.04)	3 (33.33)	2 (9.09)	1 (6.67)		
Nasal swab	3 (6.52)	1 (11.11)	2 (9.09)	0 (0)		
Bronchoalveolar lavage fluid	1 (2.17)	1 (11.11)	0 (0)	0 (0)		
Assay performed, N (%)					–	0.834
Multiplex PCR+Metagenomic sequencing	13 (28.26)	2 (22.22)	6 (27.27)	5 (33.33)		
Multiplex PCR only	33 (71.74)	7 (77.78)	16 (72.73)	10 (66.67)		

* Categorical variables are presented as N (%); Comparisons across hospital grades use Fisher's exact tests because of small expected cell counts; Median intervals are compared using the Kruskal–Wallis test. All tests are two-sided with $\alpha=0.05$.

[†] Medical institution grade is defined under the Chinese hospital grading system, Level-3 and Level-2 denote tertiary and secondary hospitals by service scope, and Grade A/B (e.g., Level-3A, Level-3B, Level-2A) denotes the accreditation ranking within each level.

[§] Sixteen patients with a history of seeking medical care at non-pilot hospitals before visiting the pilot hospital are excluded (including eight cases reported as level-3A, six as level-3B, and two as level-2A).

[¶] Mixed infection refers to the detection of more than one pathogen.

** "Others" refers to infections caused by pathogens other than viruses or bacteria (e.g., mycoplasma, chlamydia).

Abbreviation: PCR=polymerase chain reaction.

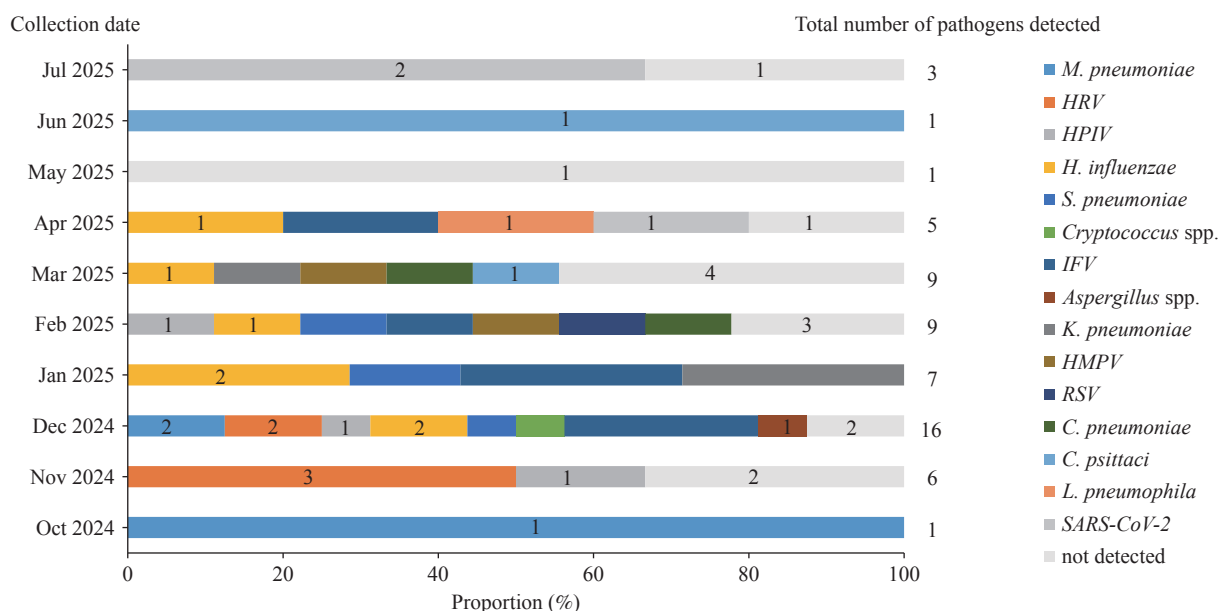


FIGURE 2. Proportion of different pathogens detected from October 2024 to July 2025.

Note: The proportion of each pathogen was calculated as the number of specific pathogen detections divided by the total number of pathogens detected by month. Absolute counts of each detected pathogen are shown in the bar. The undetected category represents cases in which no pathogen was identified by multiplex PCR or subsequent metagenomic sequencing.

Abbreviation: *M. pneumoniae*=*Mycoplasma pneumoniae*; *HRV*=human rhinovirus; *HPIV*=human parainfluenza virus; *H. influenzae*=*Haemophilus influenzae*; *S. pneumoniae*=*Streptococcus pneumoniae*; *IFV*=influenza virus; *K. pneumoniae*=*Klebsiella pneumoniae*; *HMPV*=human metapneumovirus; *RSV*=respiratory syncytial virus; *C. pneumoniae*=*Chlamydia pneumoniae*; *C. psittaci*=*Chlamydia psittaci*; *L. pneumophila*=*Legionella pneumophila*; *SARS-CoV-2*=severe acute respiratory syndrome coronavirus 2; spp.=species; PCR=polymerase chain reaction.

Based on the monthly proportion of pathogens detected from pilot surveillance (Figure 2), the most frequently detected Influenza A(H1N1) virus was identified in eight cases over four months (December 2024, January 2025, February 2025, and April 2025). Other common respiratory viruses, such as Human rhinovirus (5 cases) and Human metapneumovirus (3 cases), were also primarily detected in winter (November 2024 to February 2025). *Haemophilus influenzae* (7 cases) and *Streptococcus pneumoniae* (3 cases) were the most common bacterial pathogens. Both cases detected with *Chlamydia psittaci* had a history of suspicious bird contact. *Aspergillus* spp., *Cryptococcus* spp., and *L. pneumophila* were detected in cases of mixed infections.

Risk assessments by epidemiological, laboratory testing, and clinical experts were conducted for all 46 reported cases. Combined with laboratory tests and epidemiological investigation results, 33 were considered to be caused by common respiratory tract pathogens, and 11 were excluded from emerging or rare pathogen infection through metagenomic sequencing. Metagenomic sequencing could not be performed in 2 cases because of poor sample quality. As for the 2 cases, given the following three findings-

no suspicious sequences were detected, no secondary transmission was observed among close contacts at follow-up, the clinical course and response to standard care were consistent overall, no evidence of a major infectious disease was identified during the pilot period.

DISCUSSION

This pilot risk pneumonia surveillance system demonstrated operational feasibility by examining a structured framework for early identification of severe and clustered pneumonia cases with potential public health risk. The system's integration of multifaceted case definitions, systematic laboratory testing, and joint risk assessment effectively captured cases that met severity or clustering criteria, establishing a closed-loop monitoring and management process.

Although the pilot program significantly improved surveillance sensitivity, the demographic profiles revealed that most (76.09%) reported cases were aged 60 years or older. This likely reflects the higher background incidence of severe pneumonia in the older adult population owing to comorbidities and age-related immune decline. Although severe disease

monitoring in vulnerable groups is clinically important, from a public health perspective focused on detecting emerging major respiratory infectious diseases, an over-representation of sporadic cases among older adults may dilute the signal for real threats. This concern is particularly notable considering that historical pandemics (e.g., SARS and COVID-19) have often manifested significantly in younger populations at an early stage (2,9). Future iterations of surveillance system should strategically enhance the focus on cases with greater epidemic potential, including those involving clusters (e.g., in familial settings, workplaces, schools, or healthcare facilities) or unusual epidemiological links, such as suspicious animal contact or travel history. Recalibrating resources and alert thresholds to prioritize investigating such target populations could improve the system's efficiency in detecting genuine public health emergencies. The cross-tier differences in reporting departments found in this study can inform where surveillance capacity and targeted training should be prioritized in resource-constrained settings.

The high proportion (71.74%) of cases infected with common respiratory pathogens underscores the importance of implementing multiplex molecular diagnostics within the surveillance system. This enables timely differentiation between known pathogens and truly unexplained cases, enabling more efficient distribution of public health resources. Influenza A(H1N1) virus was the most frequently detected pathogen, aligning with seasonal influenza activity. Detection of *Chlamydia psittaci* in cases with a history of bird contact illustrates the system's sensitivity to zoonotic links. However, the persistent fraction of cases (28.26%) with no identified pathogens, even after metagenomic sequencing, highlights ongoing diagnostic challenges and the importance of joint risk assessment by experts from related disciplines. This undetected fraction may be related to factors such as specimen type and quality, suboptimal sampling timing relative to illness onset, prior antimicrobial use, and limitations of reference databases, warranting closer attention.

Interpreting metagenomic sequencing results requires considerable clinical and microbiological expertise to distinguish true infection from colonization or environmental contamination, and epidemiological exposure should be considered (10). Operationally, a tiered approach rather than sequencing every PCR-negative specimen is recommended, given the high cost of metagenomic

sequencing. The following factors could be assessed: 1) case-level public health risk (preferring cases with strong epidemiological links to clusters or outbreaks and severe clinical manifestations); 2) specimen quality and type (preferring lower respiratory tract specimens); 3) prior antimicrobial use (potentially reducing bacterial detection), and 4) collection timing relative to symptom onset.

This study was subject to at least two limitations. First, surveillance was limited to 14 sentinel hospitals, which may not have captured the complete spectrum of pneumonia cases with public health risk. Without data on the catchment population and estimated coverage, selection bias related to hospital participation and demographic profiles cannot be excluded. Therefore, this pilot supports conclusions regarding operational feasibility rather than citywide representativeness. Variations in reporting patterns across hospital tiers suggest potential differences in clinical pathways and diagnostic practices that warrant further standardization. Second, surveillance currently relies heavily on manual case identification and reporting by clinicians. For example, physician-based judgments used to apply the severity-tendency and common-pathogen exclusion criteria may vary across clinicians and hospitals and could introduce selection bias in case ascertainment. Despite facilitating an established initial workflow, this manual approach requires a shift toward more automated and active surveillance.

Future efforts should 1) refine case definitions emphasizing cluster detection to enhance sensitivity for novel outbreaks that could lead to significant public health hazards; 2) standardize the application of advanced laboratory technologies, such as metagenomic sequencing, in the surveillance of major emerging infectious diseases; 3) strengthen integration of multi-source data and application of information technologies, such as artificial intelligence, to improve the surveillance system's sensitivity; and 4) develop region-specific early warning thresholds based on different districts' epidemiological characteristics and capacities.

This pilot demonstrated the operational feasibility and value of a proactive multidimensional risk framework for pneumonia surveillance. By integrating syndromic screening, tiered laboratory testing, and joint risk assessment, it provides a feasible model for enhancing the sensitivity and timeliness of early warning systems for emerging respiratory infections. Refining this model will be crucial for building a more

resilient, intelligent, and precise national surveillance system capable of meeting the evolving challenges of infectious disease prevention and control.

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Conflicts of interest: No conflicts of interest.

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REFERENCES

1. Qi BE, Wang Q, Wang J, Li TT, Cao YL, Shen R, et al. Surveillance for pneumonia of unknown etiology: current status, challenges, and implementation ways. *Chin J Epidemiol* 2025;46(5):914 – 20. <https://doi.org/10.3760/cma.j.cn112338-20241022-00648>.
2. Cao WC, De Vlas SJ, Richardus JH. The severe acute respiratory syndrome epidemic in mainland China dissected. *Infect Dis Rep* 2011;3(1):e2. <https://doi.org/10.4081/idr.2011.1794>.
3. Berry M, Gamielien J, Fielding BC. Identification of new respiratory viruses in the new millennium. *Viruses* 2015;7(3):996 – 1019. <https://doi.org/10.3390/v7030996>.
4. Gao RB, Cao B, Hu YW, Feng ZJ, Wang DY, Hu WF, et al. Human infection with a novel avian-origin influenza A (H7N9) virus. *N Engl J Med* 2013;368(20):1888 – 97. <https://doi.org/10.1056/NEJMoa1304459>.
5. Ministry of Health of the People's Republic of China. National protocol for surveillance, identification and management of pneumonia of unknown etiology. 2007. <https://www.nhc.gov.cn/bgt/pw10708/200708/638e481ad2814ecd9a2598411908bc49.shtml>. [2007-08-06]. (In Chinese).
6. Wang JQ, Wang HW, Yang JJ. Analysis of the surveillance of pneumonia of unknown etiology in Fuzhou City from 2013 to 2015. *J Appl Prev Med* 2016;22(5):453-5. <http://dx.doi.org/10.3969/j.issn.1673-758X.2016.05.025>.
7. Wang Y. Evaluation of the surveillance system for Pneumonia of Unknown Etiology.
8. Zhang JM, Chai ZK, Zuo SJ, Zhang XH. Discussion on the surveillance of pneumonia of unknown etiology. *Chin J PHM* 2013;29(3):366 – 7. <https://doi.org/10.19568/j.cnki.23-1318.2013.03.036>.
9. Chen NS, Zhou M, Dong X, Qu JM, Gong FY, Han Y, et al. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. *Lancet* 2020;395(10223):507 – 13. [https://doi.org/10.1016/S0140-6736\(20\)30211-7](https://doi.org/10.1016/S0140-6736(20)30211-7).
10. Chen Y, Fan LC, Chai YH, Xu JF. Advantages and challenges of metagenomic sequencing for the diagnosis of pulmonary infectious diseases. *Clin Respir J* 2022;16(10):646–656. <https://doi.org/10.1111/crj.13538>.