Proceedings of the 6th International Conference on Biological Engineering and Medical Science
DOI: 10.54254/2753-8818/2026.36887

Epidemic Evolution and Research Progress of Pathogenic Viruses Causing Respiratory Tract Infections After 2020

Jiahui Qin

School of Food Science and Engineering, Wuhan Polytechnic University, Wuhan, China
15090850759@163.com

Abstract. Respiratory tract infections are among the most common infectious diseases worldwide. Since 2020, the epidemiological characteristics of respiratory infections have changed significantly under the influence of various factors, posing persistent challenges to global public health and human health. This study reviews changes in the epidemiological characteristics of major respiratory pathogenic viruses since 2020 and related research advances using literature analysis and comparative analysis. The findings indicate that the overall positive detection rates of respiratory syncytial virus, rhinovirus, and influenza virus have declined to some extent, but these viruses remain major pathogens of respiratory infections. Children and older adults are the primary susceptible populations, with different viruses exhibiting distinct age distributions and seasonal patterns. Multiple factors have contributed to changes in the epidemiology of respiratory viruses, and mixed infections involving multiple pathogens have become an important contributor to disease complexity. In recent years, advances in viral detection and surveillance technologies have provided support for accurate diagnosis and disease prevention and control.

Keywords: Respiratory tract infections, Respiratory viruses, Viral detection, Prevention, control and surveillance

1. Introduction

From 2020 to 2022, strict containment measures, mask-wearing, environmental disinfection, and other prevention and control strategies were widely implemented worldwide, greatly disrupting the transmission of various respiratory viruses. However, in recent years, respiratory viruses have exhibited new epidemiological characteristics, including resurgent outbreaks and increased prevalence of co-infections, which pose significant threats to human health and global public health. Consequently, research on respiratory infectious diseases faces substantial challenges.

This study aims to address four key questions: (1) What changes have occurred in the nucleic acid detection positivity rates, seasonal patterns, and infected populations of the major respiratory pathogens in China (respiratory syncytial virus, rhinovirus, and influenza virus) before and after 2020? (2) What are the factors contributing to changes in respiratory pathogenic viruses in recent years? (3) What advances have been made in viral detection technologies and prevention and control strategies for respiratory viruses? (4) What are the current limitations and unresolved challenges in respiratory virus prevention and control?

© 2026 The Authors. This is an open access article distributed under the terms of the Creative Commons Attribution License 4.0 (https://creativecommons.org/licenses/by/4.0/).

DOI: 10.54254/2753-8818/2026.36887

To address these questions, this study employs literature analysis and comparative analysis methods to systematically summarize the epidemiological changes of respiratory pathogenic viruses before and after 2020. It aims to characterize the evolutionary and epidemiological patterns of different viruses, identify the major factors influencing viral changes, and elucidate the characteristics and mechanisms of multi-pathogen infections in recent years. The findings provide theoretical support for future viral origin tracing and epidemic prediction. Furthermore, this study reviews recent advances in rapid detection technologies and prevention and control measures, which may assist healthcare institutions in optimizing respiratory disease management strategies and enable public health authorities to implement more precise prevention and control measures.

2. Changes in the epidemic characteristics of main pathogenic viruses causing respiratory tract infections in China around 2020

To provide a systematic comparison of the epidemiological dynamics of major respiratory viruses before and after 2020, this section analyzes RSV, RV, and IFV across three standardized dimensions: (1) variations in positive detection rates between the pre-pandemic and post-2020 periods; (2) changes in seasonal transmission patterns; and (3) shifts in the age distribution of susceptible populations.

2.1. Changes in the epidemiological characteristics of respiratory syncytial virus

Respiratory syncytial virus (RSV) is an important pathogen responsible for acute lower respiratory tract infections in infants and young children, and particularly causes bronchiolitis and pneumonia. According to estimates based on the original weekly surveillance reports of the *National Acute Respiratory Infectious Disease Sentinel Surveillance* released by the Chinese Center for Disease Control and Prevention, the annual average RSV positivity rate among influenza-like illness specimens collected from outpatient and emergency sentinel sites in China was approximately 4%-5% in 2025. In contrast, a report published by the Chinese Center for Disease Control and Prevention in 2021 showed that RSV accounted for 16.8% of positive cases among patients with acute respiratory infections in China from 2009 to 2019.

Using pediatric RSV infection cases from Henan Children's Hospital as an example, Wang Bohao et al. found that among children infected with RSV between 2021 and 2024, the highest positivity rate occurred in 2023 (9.09%), whereas the lowest rate was observed in 2021 (2.17%). From January 2021 to March 2023, the RSV positivity rate showed a declining trend, followed by an increase from April 2023, reaching a peak in December. From April to December 2024, the infection rate remained relatively low but increased again in December [1]. These comparisons indicate that although RSV positivity rates have fluctuated since 2021, the overall prevalence level remains lower than that observed before 2020.

Before 2020, RSV exhibited relatively stable seasonal transmission patterns, with infections typically concentrated during winter and spring and primarily affecting susceptible populations such as infants, young children, and older adults. However, among pediatric cases at Henan Children's Hospital, the highest RSV positivity rates in 2021 and 2022 were observed in the 3-6-year-old group, reaching 3.24% and 3.49%, respectively. In contrast, the highest positivity rates shifted to the 0-1-year-old group in 2023 and 2024, reaching 15.29% and 14.05%, respectively. These findings suggest that RSV infections have increasingly occurred among younger children in recent years [1].

DOI: 10.54254/2753-8818/2026.36887

2.2. Changes in the epidemiological characteristics of rhinovirus

Rhinovirus (RV) is a major pathogen responsible for the common cold and is also an important virus associated with wheezing, acute asthma exacerbations, and some lower respiratory tract infections in children. Due to the large number of rhinovirus serotypes and genotypes, RV can maintain persistent transmission within human populations over extended periods.

According to the weekly *National Acute Respiratory Infectious Disease Sentinel Surveillance* reports released by the Chinese Center for Disease Control and Prevention, the positivity rate of rhinovirus among influenza-like illness specimens collected from outpatient and emergency sentinel sites in China remained relatively low in 2025, with an estimated annual average of approximately 7%-8%. In comparison, this value reached 16.7% before 2020. Regarding seasonal patterns, rhinovirus exhibits year-round transmission, with more pronounced peaks of activity occurring in spring and autumn.

Before 2020, rhinovirus ranked second among respiratory viruses causing acute respiratory infections in children under 14 years of age. However, statistics from 2025 showed that rhinovirus ranked third among respiratory viruses detected in pediatric infection cases. Although its relative proportion has decreased, the detection positivity rate of rhinovirus infections has continued to increase.

2.3. Changes in the epidemiological characteristics of influenza virus

Influenza virus (IFV) is an important seasonal respiratory pathogen worldwide, with its transmission exhibiting distinct seasonal characteristics. In China, influenza activity generally peaks during the winter and spring seasons, although slight regional variations exist due to differences in climatic conditions and population mobility patterns. As one of the respiratory viruses with the highest positivity rates, influenza virus can infect individuals across almost all age groups at relatively high infection rates.

Using respiratory infection patients in Tongzhou District, Beijing, as an example, Gao Xiang et al. found that among specimens collected from 2018 to 2019, the positivity rates of influenza A virus (FluA) and influenza B virus (FluB) were 26.23% and 15.30%, respectively. Among specimens collected from 2020 to 2021, the positivity rate of FluB increased to 29.55%, whereas that of FluA decreased to 7.95% [2]. Furthermore, according to estimates based on the original weekly surveillance reports of the *National Acute Respiratory Infectious Disease Sentinel Surveillance* released by the Chinese Center for Disease Control and Prevention, the annual average positivity rate of influenza virus among influenza-like illness specimens collected from outpatient and emergency sentinel sites in China was approximately 12%–14% in 2025. These data indicate that the overall proportion of influenza virus infections has declined.

Regarding infected populations, children remain the primary group affected by influenza. However, cases among adolescents and adults have increased significantly in recent years. For example, among respiratory infection patients at Minhang Hospital, Fudan University, from April 2023 to July 2024, Lü, Chen, and Zhao et al. analyzed pathogen detection results from patient specimens and found that both FluA and FluB exhibited the highest positivity rates in the 7-14-year-old group (FluA: 16.5%; FluB: 10.4%). Among adults (≥15 years), the highest detection rates of FluA and FluB were observed in the 15–24-year-old group (12.5%) and the 35-44-year-old group (15.9%), respectively [3].

DOI: 10.54254/2753-8818/2026.36887

3. Major factors driving the evolution of pathogenic viruses in the respiratory tract

3.1. Mixed infection of multiple pathogens

Respiratory infections are generally not caused by a single virus but involve complex interactions among multiple viruses, bacteria, and other microorganisms. After 2020, the global epidemiological patterns of respiratory infectious diseases underwent significant changes. While various prevention and control measures reduced the transmission of SARS-CoV-2, the susceptible population increased, and the intrinsic seasonal and cyclical characteristics of pathogens contributed to the increasing occurrence of overlapping or co-circulation of multiple pathogens [4]. These changes have further complicated the diagnosis of respiratory diseases. With the development of multiplex nucleic acid detection technologies, the detected rate of respiratory multi-pathogen co-infections has gradually increased in recent years.

Respiratory co-infections mainly include three categories: virus–bacteria, virus–virus, and bacteria–bacteria co-infections. Among virus–bacteria co-detections, influenza virus and Haemophilus influenzae represent the most common combination, followed by influenza virus and Streptococcus pneumoniae. Some viral infections may disrupt the respiratory mucosal barrier and reduce local immune defense capacity, thereby increasing the risk of secondary bacterial infections. For example, influenza virus infection may increase susceptibility to bacterial infections such as S. pneumoniae. Therefore, viral infections may not only directly cause disease but also promote the infection of other pathogens by altering the host environment. Among virus–virus co-detections, the most frequently observed combination is rhinovirus and enterovirus, followed by influenza virus and rhinovirus. In bacteria–bacteria co-detections, the combination of S. pneumoniae and H. influenzae is predominant [4].

Children represent the major population affected by respiratory multi-pathogen co-infections. Wang Qing found that the overall co-infection rate among individuals of all age groups was 29.2% from October 2021 to August 2023. Children and adolescents under 18 years of age and older adults aged ≥60 years exhibited the highest positivity rates for respiratory multi-pathogen detection, while preschool children under 5 years of age showed the highest co-infection rate (42.1%) [5]. This may be attributed to the immature immune systems of younger children, which makes them more susceptible to infection by multiple pathogens.

3.2. Other factors

Changes in the epidemiological patterns of respiratory viruses are not attributable to a single factor but result from the combined effects of viral characteristics, population immunity, changes in social behavior, and interactions among pathogens. In addition to the increased complexity of respiratory virus epidemiology caused by multi-pathogen infections associated with viral variations, enhanced public health interventions, such as mask-wearing and environmental disinfection, have demonstrated significant inhibitory effects on the transmission of various respiratory viruses.

Air quality is also an important influencing factor. Increased environmental pollution exerts a moderately positive synergistic effect on the activity of certain viruses, including human coronaviruses and rhinoviruses, as well as bacteria such as Klebsiella pneumoniae. In natural environmental conditions, increased sunlight duration and precipitation have negative inhibitory effects on the activity of some viruses, whereas increased absolute humidity exhibits a positive synergistic effect on the activity of viruses and bacteria.

DOI: 10.54254/2753-8818/2026.36887

Interactions also exist among respiratory viruses. SARS-CoV-2 and rhinovirus show the most pronounced inhibitory effects on influenza A virus activity. Interactions among respiratory bacteria are primarily characterized by bidirectional synergistic effects, while interactions between respiratory bacteria and viruses are mainly characterized by unidirectional synergistic effects [5].

4. Current research progress in respiratory tract diagnosis, treatment and prevention & control technologies

Given the substantial shifts in the epidemiological landscape of respiratory viruses described above—especially the growing incidence of multi-pathogen co-infections and the ongoing evolution of circulating pathogen profiles—conventional single-pathogen-based diagnostic approaches are increasingly inadequate for supporting precise clinical decision-making. Concurrently, the changing dynamics of viral transmission have placed additional demands on surveillance and early warning systems. Accordingly, the following section summarizes recent technological advances in pathogen detection, as well as surveillance and control strategies developed to address these emerging challenges.

4.1. Virus detection technology

Respiratory viral infections are characterized by a wide variety of pathogens and similar clinical manifestations, making it difficult to accurately distinguish different pathogens based solely on clinical symptoms. Therefore, rapid and accurate laboratory diagnostic technologies have become essential components of disease management and epidemic control.

Traditional viral detection methods mainly include virus isolation and culture, antigen detection, and serological assays. Among these methods, virus isolation and culture exhibit high accuracy and can be used for viral characterization and antiviral susceptibility analysis. However, their application in rapid clinical diagnosis is limited due to the long detection period and stringent operational requirements. Antigen detection methods offer advantages such as simple operation and rapid detection, making them useful for large-scale screening and primary healthcare settings; however, their sensitivity may be affected by factors including sample quality and viral load.

With the advancement of molecular diagnostic technologies, nucleic acid detection has become a critical approach for respiratory virus identification. Real-time fluorescence quantitative PCR (qPCR) demonstrates high sensitivity and specificity. Jia Yan et al. established a triple fluorescence quantitative PCR assay for the detection of human rhinovirus (HRV), human metapneumovirus (hMPV), and human bocavirus (BoV), and evaluated its specificity and sensitivity. The results showed that the detection limit reached 10^3 copies/mL, with a linear range of 10^3–10^9 copies/mL. Reproducibility analysis demonstrated a coefficient of variation (CV) ≤5%, and no cross-reactivity with other respiratory viruses was observed, indicating high specificity [6]. In addition, the development of multiplex PCR technology enables simultaneous identification of multiple respiratory pathogens in a single test. Gu Wuyang et al. used multiplex PCR and direct immunofluorescence assay (DFA) to detect pharyngeal swab samples from children with respiratory infections in a hospital in Xuzhou. The results showed that the number of positive cases detected by multiplex PCR was significantly higher than that detected by DFA, and the sensitivity, specificity, and accuracy of multiplex PCR for detecting RSV, ADV, FluA, FluB, HPIV1, HPIV2, and HPIV3 were superior to those of DFA [7]. Multiplex PCR technology improves the ability to identify co-infections and changes in pathogen spectra, providing important support for precision clinical diagnosis and treatment.

DOI: 10.54254/2753-8818/2026.36887

In recent years, novel detection technologies based on genomic sequencing have gradually been applied in respiratory virus research. High-throughput sequencing technology enables comprehensive analysis of viral genomes and can not only facilitate the discovery of unknown pathogens but also contribute to investigations of viral variation, transmission patterns, and evolutionary trends. Zhang Haixiang applied targeted high-throughput sequencing technology to identify pathogens causing community-acquired pneumonia in children at a hospital in Fujian. The results demonstrated that targeted high-throughput sequencing exhibited high pathogen detection rates and high sensitivity for bacteria, viruses, fungi, and Mycoplasma pneumoniae, showed a high detection rate for mixed infections, and was less affected by antibiotic exposure [8].

Meanwhile, isothermal amplification technologies, gene chip technologies, and emerging detection methods based on nanomaterials and biosensors are continuously developing, providing new approaches for rapid, portable, and point-of-care testing in the future. Li Weigang and colleagues developed a multi-target rapid detection method for common upper respiratory tract viruses based on a digital microfluidic RT-qPCR chip. The study demonstrated that this method achieved a sensitivity of 94% and a specificity of 100%, providing a novel approach for early clinical identification of respiratory pathogens [9]. Zhang Ning further developed a digital isothermal amplification chip integrating viral nucleic acid extraction, reagent storage, digital partitioning, and amplification functions. This platform not only improves detection efficiency and reduces operational complexity but also enhances the stability, accuracy, and sensitivity of quantitative analysis [10].

4.2. Prevention, control and monitoring technology

Respiratory viruses are characterized by rapid transmission, pronounced seasonality, and a high propensity for genetic variation. Therefore, establishing a comprehensive surveillance and early warning system is essential for the timely identification of changes in epidemic patterns.

During the COVID-19 pandemic, respiratory infectious disease surveillance systems were further strengthened worldwide, encompassing case surveillance, pathogen surveillance, viral genomic surveillance, and environmental surveillance. In particular, advances in pathogen genomic surveillance have enabled continuous tracking of viral genetic variations, providing a basis for assessing viral transmission characteristics and for formulating prevention and control measures In addition, integrated surveillance of multiple pathogens has gradually become an important trend in respiratory disease prevention and control. Traditional surveillance systems typically focused on individual priority pathogens. In recent years, however, with the increasing co-circulation of multiple respiratory viruses, including influenza virus, RSV, and SARS-CoV-2, integrated surveillance systems can more comprehensively characterize changes in the respiratory infection disease spectrum, thereby supporting the allocation of medical resources and public health decision-making.

Meanwhile, digital technologies and artificial intelligence (AI) methods have been increasingly applied to respiratory disease surveillance. For example, integrating clinical case data, laboratory test results, and epidemiological information can enhance the capacity of AI to analyze epidemic trends and predict disease risks. Furthermore, the development of telemedicine platforms and digital reporting systems has facilitated the rapid collection and sharing of infectious disease information.

DOI: 10.54254/2753-8818/2026.36887

5. Problems and challenges in current research

Although significant advances have been achieved in respiratory virus research and prevention and control technologies in recent years, ongoing changes in viral epidemiological patterns continue to present numerous challenges.

First, respiratory viruses possess strong mutation capabilities and adaptability, resulting in uncertainty in disease transmission trends. Changes in viral genomes may affect transmissibility, immune evasion capacity, and the applicability of diagnostic methods. Therefore, continuous surveillance of viral mutations and timely assessment of the potential public health impacts of emerging variants remain important research priorities.

Meanwhile, the co-circulation of multiple respiratory viruses and the increasing prevalence of multi-pathogen co-infections have further complicated disease diagnosis and prevention and control. Different viral infections often exhibit similar clinical manifestations, making it difficult to accurately identify pathogens based solely on symptoms. Therefore, the development of rapid, accurate, and cost-effective multiplex pathogen detection technologies remains a key focus of future research.

In addition, some existing surveillance systems still face limitations in data integration. The transmission of respiratory viruses is influenced by multiple factors, including population mobility, seasonal variations, environmental conditions, and social behaviors. Reliance on data from a single source is insufficient to fully characterize disease transmission patterns. Therefore, strengthening data sharing among different regions and institutions and utilizing emerging technologies such as artificial intelligence to improve predictive capabilities are important challenges that need to be addressed in future public health research.

6. Conclusion

This study primarily investigated changes in the epidemiological characteristics of major respiratory pathogenic viruses after 2020 and reviewed related research advances. The findings showed that the positive detection rates of respiratory syncytial virus, rhinovirus, and influenza virus have all declined after 2020. Although temporary fluctuations occurred due to the implementation of epidemic prevention and control measures, these three viruses remain major pathogens responsible for respiratory infections. Children and older adults continue to represent the primary susceptible populations. Notably, respiratory syncytial virus infections have shown a trend toward younger age groups, while the proportion of influenza virus infections among adolescents and adults has increased. Although the peak seasons of the three viruses differ, respiratory virus activity generally remains higher during the winter and spring months.

Changes in respiratory virus epidemiology are influenced by multiple factors, including social and environmental conditions, population immunity, interactions among pathogens, and multi-pathogen co-infections. In recent years, advances in detection technologies and surveillance approaches have continuously improved the sensitivity, accuracy, and cost-effectiveness of respiratory virus identification, providing important support for disease diagnosis and prevention and control. However, this study has several limitations. Epidemiological data on viral prevalence remain subject to certain limitations and uncertainties, the mechanisms underlying multi-pathogen co-infections are not yet fully understood, and the practical value of some emerging detection technologies requires further investigation.

DOI: 10.54254/2753-8818/2026.36887

References

[1] Wang, B., Wang, J., Sun, Z., Sun, G., Wang, W., Li, P., Wang, H., Huang, X., & Zhen, X. (2026). Epidemiological characteristics of respiratory syncytial virus in children during 2021-2024. *Journal of Virological Methods, 345*, 115433.

[2] Gao, X., Zou, L., Zhang, C., Gao, J., Zhou, J. L., Wang, J. G., & Zhao, H. Q. (2025). Changes in the epidemiological characteristics of respiratory viruses before and after the implementation of strict control measures for the COVID-19 pandemic in Tongzhou District, Beijing. *Chinese Journal of Viral Diseases, 15*(6), 594–598. https://doi.org/10.16505/j.2095-0136.2025.0052.

[3] Lü, P., Chen, M., & Zhao, Z. (2025). Etiological and epidemiological characteristics of respiratory infection cases in a tertiary hospital in Shanghai after the COVID-19 pandemic. *Fudan University Journal of Medical Sciences, 52*(2), 242–248.

[4] Su, R., Zheng, J., Zhao, H., et al. (2026). Epidemiological characteristics of respiratory multi-pathogen co-detection in China during the 2023–2025 surveillance years based on influenza-like illness surveillance. *Chinese Journal of Epidemiology, 47*(4), 603–611.

[5] Wang, Q. (2024). *Analysis of the epidemiological patterns of multiple respiratory pathogens and their influencing factors* (Doctoral dissertation, Peking Union Medical College). https://doi.org/10.27648/d.cnki.gzxhu.2024.000190.

[6] Jia, Y., Luo, Z., Lei, Y., Chen, J., Lu, Z., Chen, X., … Yao, J. (2026). Establishment and validation of a triplex fluorescent quantitative PCR method for the detection of human rhinovirus, human metapneumovirus, and human bocavirus. *Chinese Journal of Nosocomiology*, (19), 3074–3078.

[7] Gu, W., Fang, L., Li, Y., & Chen, Y. (2025). Application value of multiplex PCR technology in the detection of common respiratory pathogens in children. *Modern Instruments & Medical Treatment, 31*(1), 58–62.

[8] Zhang, H. (2023). *Application value of targeted high-throughput sequencing in children with community-acquired pneumonia* (Master's thesis, Fujian Medical University). https://doi.org/10.27020/d.cnki.gfjyu.2023.000762

[9] Li, W., Jiang, X., Wang, H., Wang, M., Zhou, A. B. X., Luo, D. S., … Dong, C. (2022). Establishment of a rapid multi-target detection method for susceptible upper respiratory tract viruses based on digital microfluidic technology. *Journal of Tropical Medicine, 22*(11), 1487–1492.

[10] Zhang, N. (2023). *Research on rapid quantitative detection technology for respiratory viruses based on digital isothermal amplification chips* (Doctoral dissertation, Academy of Military Sciences). https://doi.org/10.27193/d.cnki.gjsky.2023.000154