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# Epidemiological characteristics of respiratory

## Abstract

**Objective** It is now understood that the COVID-19 pandemic and its associated containment measures have affected the epidemiology of other respiratory viruses. This study aimed to investigate respiratory pathogen infections in Shenzhen during and after the COVID-19 pandemic.

**Methods** A retrospective analysis was conducted on test data from 24,814 patients at Shenzhen Third People's Hospital between January 2021 and December 2023. The analysis focused on changes in detection rates, epidemiological characteristics, and clinical features of respiratory pathogens, including three viruses and eight bacteria.

**Results** The overall positivity rate for respiratory viruses increased after the COVID-19 epidemic ( $P < 0.05$ ), whereas no significant difference was detected in the overall positivity rate of most respiratory bacteria. Notably, the detection rates of influenza A and B increased after the COVID-19 epidemic, with influenza A showing the most significant increase from 4.5 to 10.8% ( $P < 0.05$ ). Conversely, the detection rates of PAE and MRSA decreased significantly ( $P < 0.05$ ), whereas those of H1N1 and SMA increased significantly ( $P < 0.05$ ). The seasonal patterns of influenza A changed markedly, with a shift in peak occurrence and extended periods of high positivity. The age distribution of infections also shifted, with adults showing higher detection rates after the pandemic than school-aged children and elderly individuals did.

**Conclusion** The removal of non-pharmaceutical interventions following the COVID-19 pandemic has significantly affected the epidemiological and seasonal patterns of certain respiratory pathogens in Shenzhen. These findings highlight the need for continuous surveillance of multiple respiratory pathogens and adaptive public health strategies in the post-pandemic era.

**Keywords** Respiratory infections, COVID-19 pandemic, Epidemiology, Non-pharmaceutical interventions, Seasonal patterns

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## Background

Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has spread rapidly around the world since December 2019, leading to a public health emergency declared by the World Health Organization (WHO) [1, 2]. In response to the ongoing COVID-19 pandemic, many countries have implemented a wide range of measures known as non-pharmaceutical interventions (NPIs). China is one of the countries that implemented more stringent measures, particularly during the first year of the pandemic. These measures included immediate detection and full inclusion of suspected cases through multiple rounds of mass screening tests for entire cities; upgrading of viral testing capacity for rapid diagnosis; establishment and construction of temporary hospitals to isolate cases; and strict tracking and quarantine of close contacts via global positioning system (GPS) technology and electronic health cards [

## Results

respectively ( $P < 0.05$ ). After the COVID-19 pandemic, the proportion of males among positive samples was also greater than that among females (viruses for 55.2% vs. 44.8%,  $P < 0.05$ ; bacteria for 63.8% and 36.2%,  $P < 0.05$ ) (Table S1). During the COVID-19 pandemic (Fig. S1A), MRSA, HIN, KP, IVA and RSV were the main pathogens in males, whereas HIN, RSV, IVA and PAE were the main

occurred in April, followed by September. Correlation analysis revealed changes in the relationship patterns among the three viruses during and after the epidemic (Figure S3). The correlation between IVA and IVB shifted from negative to positive ( $\rho=-0.23$  vs.  $\rho=0.29$ ), while the positive correlation between IVA and RSV became stronger ( $\rho=0.30$  vs.  $\rho=0.41$ ). The negative correlation between IVB and RSV also intensified ( $\rho=-0.27$  vs.  $\rho=-0.44$ ). However, none of these changes reached statistical significance (all  $p>0.05$ ).

### Discussion

SARS-CoV-2 is a highly contagious respiratory virus that

positivity rates during and after the pandemic, contrasting with viral pathogens. is lack of dramatic change might be explained by the commensal nature of many bacterial pathogens [26]. Unlike respiratory viruses,

many bacterial pathogens are part of the normal human microbiota [27

measures [29]. However, we did observe changes in specific bacteria. The decrease in PAE and MRSA after the pandemic could be attributed to improved hygiene measures and reduced hospital admissions [30]. The increase in HIN and SMA might reflect shifts in the respiratory tract microbiome, possibly due to viral-bacterial interactions [31]. Studies have shown that COVID-19 vaccination can influence respiratory microbiome composition [32, 33], potentially contributing to the observed changes in bacterial detection rates.

Regarding age distribution, while the overall positive rate peaked in the 0–5 year age group both during and after the pandemic, we observed higher detection rates in adults compared to school-aged and elderly people post-pandemic. Adults may have resumed social activities more quickly, increasing their exposure risk, and different age groups may have varied in their adherence to NPIs. Notably, some studies reported age distribution trends that revealed that school-aged people [34] or elderly people [25] were at high risk for respiratory infection in their populations after the pandemic, which dif-

## Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12889-025-22884-0>.

Supplementary Material 1

### Author contributions

J.Q. conceived the original idea; Q.J. and S.Y. collected the data and performed statistical analysis; Q.J. organized the data and wrote the manuscript.

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### Data availability

No datasets were generated or analysed during the current study.

### Declarations

#### Ethical approval

This retrospective study was approved by the Ethics Committee of Shenzhen Third People's Hospital and was conducted in accordance with the 1964 Helsinki Declaration and its later amendments or comparable



31. Edouard S, Million M, Bachar D, et al. The nasopharyngeal microbiota in patients with viral respiratory tract infections is enriched in bacterial pathogens. *Eur J Clin Microbiol Infect Dis*. 2018;37(9):1725–33.
32. De Maio F, Posteraro B, Ponziani FR, et al. Nasopharyngeal microbiota profile of SARS-CoV-2 infected patients. *Biol Proced Online*. 2020;22:18.
33. Lee KH, Gordon A, Foxman B. The role of respiratory viruses in the etiology of bacterial pneumonia: an ecological perspective. *Evol Med Public Health*. 2016;2016(1):95–109.
34. Zheng PP, Zhao YN, Wang ZK, et al. Prevalence of respiratory pathogens among hospitalised patients with acute respiratory infection during and after