# Effects of COVID-19 Infection Control Strategies on Seasonal Influenza Virus Epidemiology and Evolution

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## **Dear Editor**

During the COVID-19 outbreak, non-pharmaceutical interventions (NPI) such as mask-wearing, hand rubs, quarantine on arrival, school and workplace closures and societal behavior modifications were made. Public health efforts and travel restrictions have significantly reduced global influenza circulation. Seasonal influenza epidemics occur every year and result in hundreds of fatalities and high rates of morbidity.<sup>1,2</sup> The COVID-19 pandemic has disrupted these patterns, and in many areas, the regular circulation of these viruses has been absent for more than two years. During the early phases of the pandemic, routine influenza testing was halted due to the increased demand for SARS-CoV-2 testing.<sup>3</sup>

However, by mid-2020, many nations had started or continued their influenza testing and reporting; therefore, the sharp fall in influenza virus identification cannot be attributed to this momentary interruption in laboratory testing. By reducing opportunities for reactivation and local spreading, NPIs have similarly affected the circulation of other public respiratory infections as a respiratory syncytial virus (RSV) and human metapneumovirus.<sup>4</sup> Although NPIs reduced the number of infections and the associated morbidity and death, they also generated an immunity gap— a group of vulnerable people who escaped infection but lacked particular pathogen protection to stop recurring infections. This immunity gap for diseases preventable by vaccines, including polio, influenza, and measles, results from declining childhood immunization rates and delays to healthcare delivery brought on by pandemics.<sup>5, 6</sup> Immunity modifications may also affect how some viruses evolve. For instance, vaccinations and earlier illnesses help people establish population-level immunity to influenza viruses. To select the proper strain for the influenza vaccine, it is essential to assess humoral immunity, particularly antibodies that inhibit haemagglutinin antibody levels against the different circulating strains of viruses from influenza sentinel investigation sites in both Hemispheres (Northern and the Southern).7 Due to the smaller number of characterized viruses discovered through surveillance, predicting the dominant influenza virus strains for the upcoming season is more difficult.

The potential for future endemic viral outbreaks is increased by the impact of recently born vulnerable babies, diminishing immunity with less exposure to common endemic viruses over time, and trailing vaccination proportions in some contexts. Long-term suppression of seasonal influenza virus circulation will lower population immunity and make future influenza epidemics more severe.<sup>8</sup> Regional disparities in vaccine dispensation and supply chain interruption will exacerbate this effect. Evidence shows that immunity to influenza infection, whether contracted from infection or vaccination, declines over a single season. Also, circulating antibodies diminish over six months at the individual level. Young infants may also be more susceptible to viral infections due to decreased maternal exposure and immunity to common endemic viruses, resulting in a lack of transmitted transplacental antibodies. Recent research has revealed similar circulation patterns

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Amir Emami, PhD; Department of Microbiology, Burn and Wound Healing Research Center, Shiraz University of Medical Sciences, Shiraz, Iran Tel: +98 71 36223418 Email: emami.microbia@gmail.com Received: 04 April 2023 Revised: 25 May 2023 Accepted: 17 June 2023 before and within the COVID-19 pandemic. Nonenveloped viruses, particularly rhinovirus, displayed extraordinary endurance during NPIs compared to numerous enveloped viruses.<sup>9</sup> Non-enveloped viruses may persist despite the deployment of NPI partly due to extended shedding, increased variety, and persistence on environmental surfaces.

Additionally, co-infections could become more common, especially when SARS-CoV-2 becomes firmly entrenched in the human population. Co-infections would be crucial to the development of the disease in patients and the spread of SARS-CoV-2<sup>3</sup>. Understanding how SARS-CoV-2 interacts with other respiratory viruses (i.e., all the lineages of influenza and respiratory syncytial virus) and finding the effects of this interaction is urgently needed since it would create a mixture of infections and unpredicted disease peaks. So it is crucial to be ready for additional unpredictability in future endemic virus circulation, especially among children, considering past and current pandemic disruptions.

The aggregate findings of this inquiry suggest the plausibility that the relaxation of NPI implementation may result in rapid and persistent escalation of infections in relation to the fundamental characteristics of respiratory infections, such as those caused by enteroviruses and rhinoviruses. These characteristics include the absence of a viral envelope, the genomic diversity of mentioned viruses, their tenacity on surfaces, as well as the multitude of species that co-circulate. This issue is true even while the remaining NPIs continue to suppress other respiratory viruses. Compared to other respiratory viruses, a higher percentage of rhinovirus viruses are minimally asymptomatic or symptomatic, which may result in continuous transmission in contexts where symptom screening was utilized as a part of the criterion for attendance at school or work.10 Like seasonal influenza and parainfluenza viruses, RSV, common coronaviruses, and human metapneumovirus outbreak are not far from expected. All of the mentioned viruses share similar clinical signs and modes of transmission. Our knowledge of respiratory virus evolution has been improved by the extensive use of genome sequencing to research SARS-CoV-2 molecular epidemiology.11 The development of viral medications such as vaccines and monoclonal antibodies for protection and management, as well as the tracking of changes in viral variety and mutation within and behind the COVID-19 outbreaks, will all benefit from extended sequencing of non-SARS-CoV-2 viruses. Genomic analyses may bring important insight and public health attention for the future outbreak and/or pandemic. It is suggested to pay more attention to sequencing, which would assist researchers in tracking the transmission of a virus, its evolution, and potential impacts on public

health. In addition to the COVID-19 pandemic, it is essential to consider underlying conditions and disease. Undoubtedly, the global COVID-19 pandemic required close public attention due to its impact on health issues.

Nonetheless, other surveillance system implications on the problem of disease control and health promotions should not be ignoredsince pandemic of another disease, especially a viral respiratory outbreak might happen soon. Although most processes are preventive for breaking the transmission chain during the COVID-19 crisis, it is recommended that sanitization behavior should become non-obsessive. Moreover, it is necessary to consider national immunization programs as the top priority to maintain the previous attempt about substantial gains from childhood immunization. Altogether, it is suggested to diagnose an index for identifying co-infections. Vaccination against influenza should be considered similar to prepandemic times. Rapid diagnosis and evaluation of patients with respiratory symptoms who refer emergency are critical for COVID-19 and influenza. Moreover, treating should be based on antiviral agents. Healthcare policymakers should focus on studies and multicenter clinical trials since it would be helpful in the patients' clinical management.

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