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## Influenza Resurgence after Relaxation of Public Health and Social Measures, Hong Kong, 2023

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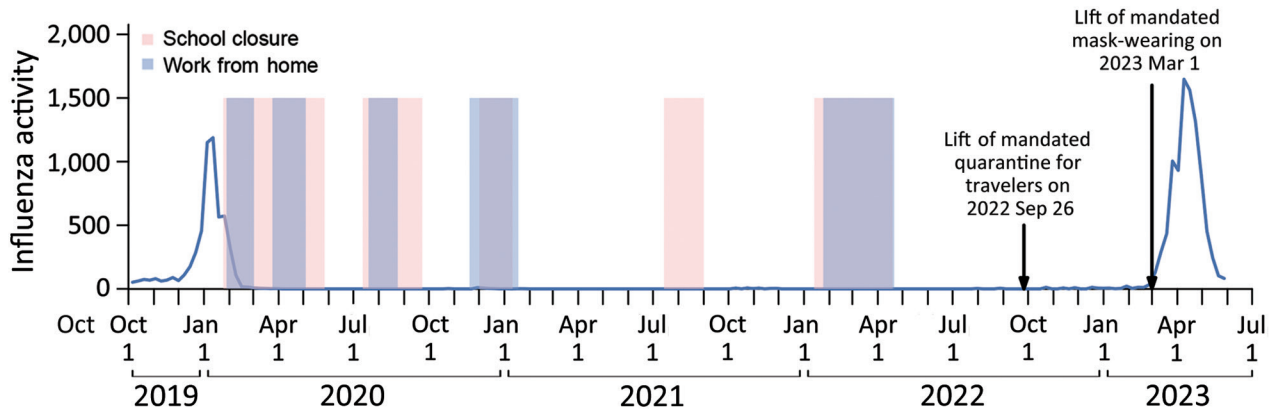
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Soon after a mask mandate was relaxed (March 1, 2023), the first post-COVID-19 influenza season in Hong Kong lasted 12 weeks. After other preventive measures were accounted for, mask wearing was associated with an estimated 25% reduction in influenza transmission. Influenza resurgence probably resulted from relaxation of mask mandates and other measures.

To control COVID-19, Hong Kong, China, put in place several public health and social measures (PHSMs), including mandatory mask wearing, school closures, hand hygiene, and avoidance of gatherings. In early 2020, those measures also reduced influenza transmission (1), and according to laboratory surveillance records, influenza virus did not circulate in the community for 3 years (2). From mid-2022 through 2023, PHSMs were progressively relaxed, and on March 1, 2023, the local mask mandate was lifted. We investigated the effects of PHSMs on influenza transmission in Hong Kong.

We collected weekly influenza-like illness consultation rates reported by private general practitioners and the weekly proportion of sentinel respiratory specimens that tested positive for influenza virus in Hong Kong during October 2010–May 2023. We established a proxy for influenza virus activity by multiplying rates of influenza-like illness by the proportion of influenza-positive samples following previous studies (3,4) (Appendix, <https://wwwnc.cdc.gov/EID/article/29/12/23-0937-App1.pdf>). We found that weekly influenza activity had decreased to almost zero since March 2020, when PHSMs against COVID-19 began (Figure). Before mandatory on-arrival quarantine of travelers started on September 26, 2022, only sporadic influenza-positive samples were detected by surveillance, all from travelers or children who had recently received live-attenuated influenza vaccine (5). After travel restrictions were removed, sporadic influenza detections increased, but overall



**Figure.** Weekly influenza activity and several preventive measures against COVID-19 in Hong Kong during 2020–2023. The blue line represents the weekly influenza activity, measured by the product of influenza-like illness rates and laboratory detections of influenza.

activity remained low. After mandatory indoor and outdoor mask wearing restrictions were lifted on March 1, 2023, influenza transmission increased substantially; the first influenza season after COVID-19 in Hong Kong started and peaked on April 9, ended on May 25, and lasted for 12 weeks (6).

Because various other PHSMs were implemented concurrently with the mask mandate, resurgence of influenza activity could not be attributed to relaxation of the mask mandate alone. Therefore, we used a previous approach that estimated the time-varying effective reproductive number ( $R_t$ ) (7) and a multivariable log-linear regression model on  $R_t$  that could allow for adjustment of other factors affecting influenza transmission, including depletion of susceptible persons, seasonal differences, and meteorologic predictors and preventive measures (Appendix). Because the

predominating influenza strain in 2023 was influenza A(H1N1)pdm09, we identified previous influenza A(H1N1)pdm09 epidemics that had occurred during 2010–2020. To construct a preventive score, we used data from cross-sectional telephone surveys among the general adult population in Hong Kong from 2020 to 2023 as a proxy for the intensity of preventive measures, other than mask wearing, against COVID-19 (1). The preventive score included the average proportion of persons who avoided visiting crowded places, avoided going to healthcare facilities, avoided touching public objects, or used protective measures when touching public objects, and washed hands immediately after going out. Before 2020, the proportion of those preventive measures was established as baseline. When constructing a preventive score, we compared the Akaike information criterion of 4

**Table.** Effects of public health and social measures to protect against COVID-19 on  $R_t$  for influenza, Hong Kong, 2010–2023\*

Model†	PHSM description	% Change in $R_t$ (95% CI)	$\Delta$ AIC‡
Model 1			3.62
Mask		-25 (-43 to -1)	
Preventive score 1	Avoid social gatherings. Wash hands after being outside. Avoid touching or use protective measures with shared objects.	-82 (-91 to -63)	
Model 2			9.55
Mask		-26 (-44 to -2)	
Preventive score 2	Avoid going out as much as possible. Wash hands after being outside. Avoid touching or use protective measures with shared objects.	-80 (-91 to -55)	
Model 3 (main model)			0
Mask		-25 (-43 to -1)	
Preventive score 3	Avoid going to crowded places. Avoid going to healthcare facilities. Avoid touching or use protective measures with shared objects.	-77 (-88 to -60)	
Model 4			2.79
Mask		-24 (-43 to 0)	
Preventive score 4	Avoid going to crowded places. Avoid going to healthcare facilities. Avoid touching or use protective measures with shared objects. Wash hands after being outside.	-81 (-90 to -62)	

\*AIC, Akaike information criterion;  $R_t$ , time-varying effective reproductive number.

†Models were adjusted for depletion of susceptible persons, between-season effects, and absolute humidity.

‡ $\Delta$ AIC<sub>model*i*</sub> = AIC<sub>model*i*</sub> - AIC<sub>min</sub>, AIC<sub>min</sub> = min(AIC<sub>model*i*</sub>),  $i = 1, \dots, 4$ .

combinations of those protective measures. Meteorologic variables provided by the Hong Kong Observatory (<http://hko.gov.hk>) were temperature, wind speed, and relative and absolute humidity. To quantify the effects of meteorologic variables, we fitted the models to data before the COVID-19 pandemic.

Among the 9 epidemics of 2010–2023, the estimated  $R_t$  varied from 0.62 to 1.38 (median 1.02) (Appendix Figure 1). The estimated  $R_t$  showed a decreasing pattern in each season, ranging from  $\approx 1.2$  at the beginning of an epidemic period to 0.8 at the end of an epidemic period. After model selection (Appendix), we found that a model of absolute humidity, mask wearing, and preventive score 3 (Table) explained 92% of the observed variance in estimated  $R_t$  (Appendix Table 1). Changes in absolute humidity (Appendix Figure 2, panel A), the proportion of mask wearing, and preventive score 3 (Appendix Figure 2, panel B) strongly correlated with changes in  $R_t$ . After adjusting for other factors, such as depletion of susceptible persons, between-season effects, and absolute humidity, we found that mask wearing was associated with a 25% (range 1%–43%) reduction in  $R_t$  and that other preventive measures (combined) were associated with a 77% (range 60%–88%) reduction (Table).

We found that that influenza increased after PHSMs were relaxed and influenza transmission increased shortly after the mask mandate was relaxed. Our results are consistent with those of several studies that found that PHSMs against COVID-19 may reduce influenza transmission (8) and that mask wearing may have a low to moderate protective effect against influenza virus transmission in the community (9,10).

A limitation of our analysis was that we used results of survey reports to generate a proxy of intensity of implemented PHSMs over time, which may not be accurate. Also, we used a proxy measure of influenza activity based on surveillance data, and the reliability of our analysis depended on the accuracy of this proxy. In addition, influenza vaccination coverage (Appendix Figure 5) was not included in the model because our model included the effect of vaccination via season-specific intercept. Nevertheless, our study results suggest that the resurgence of influenza after relaxation of PHSMs was most likely affected by the lifting of mask mandate and other PHSMs.

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## SARS-CoV-2 Variants BQ.1 and XBB.1.5 in Wastewater of Aircraft Flying from China to Denmark, 2023

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We analyzed wastewater samples from 14 aircraft arriving in Denmark directly from China during January 9–February 12, 2023. Wastewater from 11 aircraft was SARS-CoV-2–positive by PCR; 6 predominantly contained BQ.1 and XBB.1 subvariants. Wastewater-based surveillance can contribute to public health monitoring of SARS-CoV-2 and other emerging infectious agents.

Relaxation of China's zero-COVID policy in December 2022 led the European Centre for Disease Prevention and Control to recommend several nonpharmaceutical interventions to curb COVID-19 spread and monitor any emerging SARS-CoV-2 variants; those interventions included wastewater-based surveillance (1). We report results of subsequent wastewater surveillance of aircraft arriving at Copenhagen Airport in Copenhagen, Denmark, directly from Beijing or Shanghai, China.

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During weeks 2–6 of 2023 (January 9–February 12), a total of 14 aircraft arrived at Copenhagen Airport from China. A service truck extracted waste from the aircraft by using vacuum pressure, after which a rinsing program was performed, and the disinfectant Idu-Flight (Brenntag Nordic A/S, <https://www.brenntag.com>) was added to the waste tank. Wastewater samples were collected as grab samples from the service truck and immediately transported to Statens Serum Institut in Copenhagen for analysis.

The pH value of the sample material ranged from 9–10 because of the addition of Idu-Flight. Idu-Flight contains the active ingredients glutaraldehyde and benzalkonium chloride; the disinfectant is expected to negatively affect the stability of virus particles and hinder amplification of RNA sequences. We adjusted the samples to pH 7.5–8.5 by using HCl and homogenized them by vigorous vortexing. We split the 14 samples into a total of 43 aliquots and then centrifuged those at either 4,000 × g or 10,000 × g for 10 min to pellet solid material. For the first aliquot from aircraft AC1, we analyzed 10 mL of sample material without any centrifugation; for all other samples, we analyzed 10 mL of supernatant after centrifugation. We purified viruses by using NanoTrap Microbiome A particles (Ceres Nanosciences Inc., <https://www.ceresnano.com>) and RNA by using Maxwell RSC Cartridges (Promega Corporation, <https://www.promega.com>). We performed quantitative reverse transcription PCR (qRT-PCR) in technical triplicate by using the GoTaq Enviro kit (Promega) and the US Centers for Disease Control and Prevention N2 primer/probe for SARS-CoV-2 detection (Table; Appendix Table, <https://wwwnc.cdc.gov/EID/article/29/12/23-0717-App1.pdf>).

Of the 43 qRT-PCR reactions, 31 (72%) were positive for SARS-CoV-2, representing 11 aircraft. We conducted whole-genome sequencing of samples from those 11 aircraft by using the Illumina MiSeq platform (<https://www.illumina.com>) according to the ARTIC protocol; we generated 2 × 150-bp paired-end reads by using the ARTIC 4.1 primer scheme (2). Wastewater raw reads are available from the European Nucleotide Archive (<https://www.ebi.ac.uk/ena>; accession no. PRJEB66221). We trimmed reads by using Trim Galore with default settings (3; <https://zenodo.org/record/5127899>). We removed human sequence reads by using the BWA-MEM alignment algorithm with default settings (H. Li, unpub. data, <http://arxiv.org/abs/1303.3997>) and the human genome reference build GRCh38. We then used BWA-MEM with default settings to map SARS-CoV-2 reads to the SARS-CoV-2 wild-type reference genome (GenBank accession no. MN908947.3). We performed