Seasonality of influenza and coseasonality with avian influenza in Bangladesh, 2010–19: a retrospective, time-series analysis

Isha Berry, Mahbubur Rahman, Meerjady Sabrina Flora, Tahmina Shirin, A S M Alamgir, Manjur Hossain Khan, Rubaid Anwar, Mona Lisa, Fahmida Chowdhury, Md Ainul Islam, Muzzafar Osmani, Stacie Dunkle, Eric Brum, Amy L Greer, Shaun K Morris, Punam Mangtani, David N Fisman

Summary

Background Seasonal and avian influenza viruses circulate among human and poultry populations in Bangladesh. However, the epidemiology of influenza is not well defined in this setting. We aimed to characterise influenza seasonality, examine regional heterogeneity in transmission, and evaluate coseasonality between circulating influenza viruses in Bangladesh.

Methods In this retrospective, time-series study, we used data collected between January, 2010, and December, 2019, from 32 hospital-based influenza surveillance sites across Bangladesh. We estimated influenza peak timing and intensity in ten regions using negative binomial harmonic regression models, and applied meta-analytic methods to determine whether seasonality differed across regions. Using live bird market surveillance data in Dhaka, Bangladesh, we estimated avian influenza seasonality and examined coseasonality between human and avian influenza viruses.

Findings Over the 10-year study period, we included 8790 human influenza cases and identified a distinct influenza season, with an annual peak in June to July each year (peak calendar week 27·6–28·6). Epidemic timing varied by region (I²=93·9%; p<0·0001), with metropolitan regions peaking earlier and epidemic spread following a spatial diffusion pattern based on geographical proximity. Comparatively, avian influenza displayed weak seasonality, with moderate year-round transmission and a small peak in April (peak calendar week 14·9, 95% CI 13·2–17·0), which was out of phase with influenza peaks in humans.

Interpretation In Bangladesh, influenza prevention and control activities could be timed with annual seasonality, and regional heterogeneity should be considered in health resource planning. Year-round avian influenza transmission poses a risk for viral spillover, and targeted efforts will be crucial for mitigating potential reassortment and future pandemic threats.

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Introduction

The epidemiology of influenza is well defined in many temperate regions, with annual seasonal epidemics occurring during the winter months.1 However, influenza seasonality is not as well characterised in tropical and subtropical climate regions globally. Key parameters of interest include periodicity (ie, epidemic frequency), phase angle (ie, epidemic peak timing), and amplitude (ie, seasonal strength), which can be used to measure the peak timing and intensity of annual or semi-annual influenza seasons.2 Robust data on influenza seasonality are also crucial for supporting guidance on prevention and control efforts, such as optimal vaccine timing, particularly since treatment for influenza infection remains suboptimal and is costly to national health-care systems.3

In Bangladesh, the burden of influenza is moderately high, with an estimated annual incidence of 458 cases per 100 000 people and six to 11 influenza-associated deaths per 100 000 people across all age groups.4 Bangladesh does not have a national influenza immunisation policy and vaccine uptake remains low; however, vaccine campaigns have been recommended for specific high-risk subgroups including Hajj pilgrims.5 Previous studies have reported a distinct seasonal influenza pattern in Bangladesh,6 but long-term trends and subnational heterogeneity in seasonality have not been examined. A better understanding of regional influenza transmission patterns in Bangladesh could be used to bolster the development of immunisation policies, direct appropriate health resource planning and facility preparedness, and support diagnostic and treatment approaches.

Examining influenza seasonality not only in humans, but also in animals such as poultry and swine, is important for understanding zoonotic risk.6 In Bangladesh, sporadic avian influenza outbreaks in poultry have been reported since 2007 and avian influenza are endemic in live bird markets.9 In Bangladesh, more than 90% of poultry products are marketed through live bird markets and products are marketed through live bird markets and...
Evidence before this study
We searched PubMed with no language restrictions for studies published from database inception to Dec 7, 2021, that reported on the seasonality of influenza or avian influenza in humans or poultry in Bangladesh. Using the search terms "(influenza OR avian influenza OR bird flu) AND (seasonality OR coseasonality) AND (Bangladesh)", we identified 63 studies, of which 27 contained information on influenza seasonality or burden in Bangladesh. Several studies reported on the burden of human influenza and cocirculation with other respiratory viruses in Bangladesh, including COVID-19 and respiratory syncytial virus. Five studies examined human influenza seasonality across multiple countries in south and southeast Asia, and three were single-site studies in Bangladesh. In general, these studies noted diversity in national influenza epidemic timing across south Asia, with epidemic peaks in Bangladesh occurring broadly between May and September. In addition to seasonality, two studies reported on correlation or associations between environmental factors and influenza epidemics. Six studies reported on avian influenza burden and seasonality in domestic and wild poultry. Only one study examined influenza seasonality in humans in Bangladesh at the subnational level and coseasonality with avian influenza, but this study covered a short time span and relied on passive avian influenza surveillance. All studies used descriptive statistics to examine seasonality, which do not robustly account for non-stationarity over time and cannot capture multiyear trends. To our knowledge, no robust long-term studies of influenza and avian influenza seasonality and coseasonality exist for Bangladesh.

Methods
Influenza surveillance datasets
Human influenza data were obtained from two sentinel surveillance systems: the hospital-based influenza surveillance (HBIS) and the national influenza surveillance (NISB), which span the country’s eight divisions. Standardised surveillance protocols for case recruitment and testing have been described elsewhere.5,8

Briefly, on one or two randomly selected days each week, surveillance physicians enrolled patients with influenza-like illness (defined as measured fever ≥38°C and cough with onset in the previous 10 days) from hospital outpatient departments. Additionally, patients with severe acute respiratory infection (SARI; defined as subjective or measured fever ≥38°C and cough with onset in the previous 10 days and requiring hospitalisation) were enrolled from inpatient departments. Nasopharyngeal or oropharyngeal swabs were collected from each patient. Samples were tested at the laboratories of the Institute of Epidemiology, Disease Control and Research, Bangladesh (icddrb) by real-time RT-PCR to identify influenza and, if positive, types and subtypes. Over the study period, 32 hospitals across the country contributed to the influenza surveillance network; however, the number of hospitals participating and the testing efforts varied over time (appendix pp 2–3).
Avian influenza data were obtained from environmental surveillance operated by the UN Food and Agriculture Organization and the Bangladesh Department of Livestock Services in live bird markets in North and South Dhaka City Corporations (DCC). Routine, active, market-level avian influenza surveillance commenced in January, 2016, and here we report on data available from January, 2010, to December, 2019. Detailed live bird market sampling and surveillance protocols have been described previously. Briefly, each month, environmental surveillance officers collected samples from around 110 live bird markets across DCC. Within each live bird market, three work areas were sampled—poultry arrival, poultry slaughtering and processing, and consumer exposure and sales—and area-specific swabs were pooled. All pooled samples were tested for influenza at the Bangladesh Livestock Research Institute by RT-PCR; if a sample pool was positive, it was further subtyped.

Our analyses focus on the study period January, 2010, to December, 2019 (inclusive), for seasonal influenza and January, 2016, to December, 2019 (inclusive), for avian influenza, given the improvement in surveillance quality after the A(H1N1)pdm09 influenza pandemic in 2009 and before the large-scale impacts of the COVID-19 pandemic in 2020.

This study received ethics approval from the University of Toronto (protocol number 38902), the Institute of Epidemiology Disease Control and Research (IRB/2019/11), and the London School of Hygiene & Tropical Medicine (reference I7661). At the time of surveillance enrolment, participants or legal guardians provided written informed consent for data collection; the present study used deidentified data obtained from these surveillance databases.

**Statistical analysis**

Influenza data across all regions were aggregated by month and year, and the number of samples tested (or live bird markets sampled), number of positive results, and the influenza types and subtypes were described. To examine regional variation in human influenza seasonal characteristics, we grouped the HBIS and NISB surveillance sites into ten regions by geography, as follows: the eight administrative divisions of Bangladesh with Chattogram divided into north and south regions, and DCC as its own region (appendix p 2). Avian influenza surveillance data were missing for six consecutive months in DCC, and human influenza data were missing for three consecutive months in Mymensingh and Chattogram North regions (appendix p 4). A Poisson regression imputation method accounting for monthly and annual trends was used to impute data for missing months in each region; imputed datasets were used for all harmonic regression analyses.

We used harmonic regression models to estimate the timing and strength of the influenza peak in each region. In each a priori specified model, we adjusted for linear and quadratic terms and included an offset term for the number of monthly samples tested to control for temporal trends and surveillance changes over time (eg, changes in surveillance effort or size of population under surveillance [which was unknown]). We examined both Poisson and negative binomial models; mean and variance estimates and model goodness-of-fit statistics suggested over-dispersion of influenza case counts (appendix p 7). Therefore, we fitted negative binomial generalised linear models with harmonic terms to time series from each region separately, as follows:

\[
Y(t) = \text{nbinomial}(\lambda_t) \\
\ln(\lambda_t) = \beta_0 + \beta_1 \sin\left(\frac{2\pi t}{12}\right) + \beta_2 \cos\left(\frac{2\pi t}{12}\right) + \beta_3 t + \beta_4 t^2 + \ln(n_r) + \varepsilon
\]

where \(Y(t)\) is the monthly count of combined influenza A and B positive samples, \(t\) is the running index for month beginning January, 2010, and \(\ln(n_r)\) is the log-transformed monthly number of samples tested (ie, offset term). The harmonic sine and cosine terms correspond to a 12-month period of oscillation, as supported by preliminary examination using wavelet analysis and autocorrelation functions (appendix pp 5–6). The coefficients from each regional harmonic regression model were used to calculate the amplitude and phase angle of the influenza season. The amplitude was calculated as \(\sqrt{\beta_1^2 + \beta_2^2}\). We present exponentiated amplitude estimates, which reflect the ratio between the annual influenza peak and mean, where smaller values indicate weaker seasonality and larger values indicate stronger seasonality. The phase angle was calculated as \(-\arctan(\beta_2/\beta_1)\), which was then converted from radians to weeks using standardised methods as described by Naumova and colleagues.

We calculated 95% CIs for seasonal estimates using a seasonal block bootstrap with 1000 replicates, to preserve the autocorrelation structure of the time series.

Subsequently, we pooled region-specific estimates of amplitude and peak timing using a random-effects meta-analytic model to calculate national estimates. Between-region heterogeneity of seasonal estimates were examined using Cochran’s Q and P statistics. Given evidence of heterogeneity, we constructed a meta-regression model to examine whether spatial variability in seasonal characteristics was explained by distance from DCC (distance in km; calculated as the regional mean of the distances from the centroids of each hospital’s district to the centroid of DCC). Meta-regression models were weighted by the inverse of the variance of region-specific seasonal estimates. As a sensitivity analysis, pooled estimates were also calculated using a negative binomial generalised linear mixed model with trend and harmonic terms as fixed effects and random intercepts for region to jointly fit to all ten regions. In addition to seasonal parameters, we also estimated indicators of seasonal onset and end for each
region, defined as the first month in which model-based estimates of influenza activity exceed (ie, onset) and fall below (ie, end) the mean annual influenza positivity.

To examine coseasonality between human and avian influenza, we restricted the HBIS and NISB surveillance sites to the DCC region for the period 2016–19 to align with the live bird market surveillance. Correlation between monthly counts of avian influenza-positive live bird markets and influenza-positive patients was assessed visually using wavelet coherence analysis, which displays correlation between non-stationary time series. Negative binomial harmonic regression models were then used to estimate the peak timing and amplitude of influenza in humans and avian influenza in live bird markets in DCC for this period, with 95% CIs calculated for each using seasonal block bootstrapping. Coseasonality in epidemic peak timing was examined by calculating the difference in phase angle between the human and avian influenza estimates.

In sensitivity analyses, we used the original surveillance datasets with missing values and conducted zero-inflated negative binomial harmonic regression models to account for the excess zeros. All analyses were done in Stata version 16.0 and R version 4.1.0; spatial analyses were done in QGIS version 3.12.

Results

Between January, 2010, and December, 2019, 60 906 samples were tested, with 8790 (14⋅4%) positive for influenza (table 1). Most positive cases were influenza A (62⋅3%), and influenza B accounted for about a third of cases (37⋅9%). The largest proportion of influenza A cases were the pandemic A(H1N1)pdm09 strain, followed by A(H3) strains. The proportion of influenza-positive cases remained fairly consistent over time (ie, 2010–19), but there were differences in circulating influenza types by year, with 2015 being influenza A dominant (93⋅9%) and 2016 being influenza B dominant (57⋅4%; table 1).

Despite changes in surveillance sites within the study period (appendix p 3), testing generally increased over time. There was a consistent annual peak in influenza positivity each year (figure 1), and wavelet analysis and autocorrelation functions indicated a significant 12-month oscillatory period (appendix pp 5–6).

The number of surveillance sites varied by region, as did the sampling intensity, with the greatest mean annual number of tests done in the Rajshahi region.
In this study, we applied time-series methods to multiyear laboratory-confirmed influenza surveillance data to examine regional epidemic timing and intensity in Bangladesh. We identified a distinct annual seasonal pattern, with influenza activity peaking between June and July each year. Our results suggest that influenza epidemics are spatially structured, beginning earlier in central Bangladesh and spreading radially to neighbouring

(n=1037.7 tests per year; table 2) and the least in Mymensingh (238·3 tests per year). The mean annual influenza positive proportion was similar across regions (table 2). Seasonal estimates indicated that influenza was concentrated in the monsoon season in all regions, with influenza peaking in mid-June in DCC (peak calendar week 24·3–25·3). In Rajshahi (29·4, 28·9–30·0; table 2). Influenza showed strong annual periodicity across regions, with the strongest seasonality (ie, greatest amplitude) in Chattogram south districts (amplitude 4·82, 95% CI 3·99–5·93) and moderate seasonality in Mymensingh (2·66, 2·29–3·33; table 2). When pooled across the region-specific estimates, there was significant heterogeneity in both influenza peak timing (pooled peak calendar week 27·6, 95% CI 26·7–28·6; I²=93·9%; p<0·0001) and seasonality (pooled amplitude 3·74, 95% CI 3·25–4·30; I²=88·4%; p<0·0001; table 2). Across Bangladesh, DCC had the earliest epidemic timing, with epidemic spread generally following a spatial diffusion pattern based on geographical proximity and peaking latest in the western part of the country (figure 2A). In exploratory meta-regression, greater distance from DCC, measured in km, was associated with later epidemic peak timing, although this was not statistically significant (coefficient 0·01, 95% CI 0·00–0·02; p=0·071; figure 2B). We found no association between influenza amplitude and distance from DCC (p=0·299). Estimates of seasonal onset and end, as well as the proportion of influenza activity during seasonal, interseasonal, and peak periods are included in the appendix (p 8).

In terms of avian influenza, 4359 live bird market samples were tested between January, 2016, and December, 2019. 2274 (52·2%) live bird market samples were positive for avian influenza, but the proportion of positive markets decreased over time with 818 (65·4%) positive in 2016 down to 397 (32·1%) positive in 2019 (table 1). Subtypes identified in live bird markets included A(H5) and A(H9), with A(H5) being predominant but both subtypes circulating each year (table 1). There was moderate year-round avian influenza circulation (figure 3; appendix p 5), which contrasts with the distinct annual peak observed in human influenza positivity in DCC. Seasonal estimates for DCC indicated a small avian influenza peak in early April (peak calendar week 14·9, 95% CI 13·2–17·0); however, there was very weak seasonality (amplitude 1·17, 95% CI 1·13–1·22; table 3). The corresponding epidemic peak timing for human influenza in DCC during this period was mid June (peak calendar week 24·4, 95% CI 23·4–25·5), with intense seasonality (amplitude 7·64, 95% CI 5·75–13·1; table 3). Peak timing of avian influenza in live bird markets was out of phase with peak timing of influenza in humans, with a phase difference of 9·4 weeks (95% CI 8·6–10·2; table 3). Correlation between avian influenza in live bird markets and influenza cases in humans was not significant over time (appendix p 7). Results for peak timing and amplitude from region-specific zero-inflated models and pooled estimates from mixed-effects models remained robust in sensitivity analyses (appendix p 9).

Discussion
In this study, we applied time-series methods to multiyear laboratory-confirmed influenza surveillance data to examine regional epidemic timing and intensity in Bangladesh. We identified a distinct annual seasonal pattern, with influenza activity peaking between June and July each year. Our results suggest that influenza epidemics are spatially structured, beginning earlier in central Bangladesh and spreading radially to neighbouring
regions over the following months. We also characterised avian influenza seasonality in live bird markets and found a weak seasonal pattern, with a small peak in April. Although seasonal influenza and avian influenza peaks do not coincide, evidence of year-round avian influenza circulation increases the possibilities for co-circulation of influenza viruses, co-infections in a population that is known to have high exposure to live poultry on a regular basis, and viral reassortments, which could generate novel influenza strains with pandemic potential.

The strong, annual seasonality of human influenza epidemics identified in our 10-year study aligns with results from shorter-term studies in Bangladesh. Unlike some tropical and subtropical regions in Asia, which report biannual peaks, we identified a single, consistent epidemic influenza peak during the summer monsoon season. This contrasts with seasonality in neighbouring countries, including India, which reports semi-annual peaks in January to February and June to July, and Thailand, which reports peaks in February and June to August. Compared with winter-time environmental drivers of influenza activity reported in temperate settings (eg, low absolute humidity and low temperature), the correlation between annual influenza peaks and the monsoon season in this subtropical setting suggests that distinct drivers are at play. Although not examined here, further work could explore whether these differences are due to other environmental factors (eg, precipitation) or reflect changes in population behaviour during the monsoon season that mirror the behaviours of populations in temperate settings during winter months. Additionally, despite being geographically located in the northern hemisphere, influenza epidemic timing in Bangladesh aligns with calendar peaks of southern hemisphere countries. These geographical differences in influenza seasonality have implications for not only vaccine timing but also potentially for vaccine composition. Furthermore, studies have noted changes in influenza seasonality during the COVID-19 pandemic both in Bangladesh and in general; however, continued surveillance is needed to examine whether these changes will result in sustained seasonal shifts in the post-pandemic years. Analyses using phase–phase and phase–amplitude synchronisation could also be done to provide more nuanced understanding of disease synchronisation over time, including by influenza strain.

A novel finding in our study was the significant heterogeneity in influenza epidemic peak timing by

![Figure 2](image-url)
region within Bangladesh. Similar regional heterogeneity in influenza seasonality has been reported in countries such as Brazil, China, and the USA.2,4,25 We identified a spatial diffusion pattern, with regions further from DCC reporting later influenza epidemic peaks. The exception was the region we defined as Chattogram south districts, which also peaked in June despite being a greater distance away from DCC. This finding could be due to Chattogram having the second most populous metropolitan centre (Chittagong City Corporation) in Bangladesh and strong travel links between these two densely populated urban centres.8 Further work examining epidemic timing by regional demographic factors, such as population size and density, could help explain these patterns. The epidemiology of influenza and other respiratory viruses, such as respiratory syncytial virus, in the USA displays similar trends with highly synchronised epidemics beginning in large population centres and spreading radially to other regions.25,26 Transmission dynamic modelling studies have also identified that population mobility (eg, due to religious festivals such as Eid al-Fitr) plays an important role in the epidemic spread of influenza in Bangladesh,27 as well as for other seasonal diseases such as malaria and chikungunya.28,29 Therefore, regional heterogeneity could be an important consideration in the future development of national immunisation policies (eg, permitting staggered vaccine delivery), and might be a useful assessment in other subtropical global regions.

In contrast to influenza seasonality in humans, we found that avian influenza in live bird markets showed weak seasonality, with moderate year-round transmission. Although our findings suggest that avian influenza has a modest yearly peak in April, which does not coincide with the June influenza epidemic peak in humans, there does continue to be transmission throughout the year, with over 40% of markets reporting avian influenza positive samples in June. This finding contrasts with previous studies, which have reported distinct avian influenza seasons out of phase with human influenza.8 One reason for this difference could be that previous studies have reported seasonality based on passively reported poultry outbreaks,10 whereas we measured seasonal characteristics using active surveillance in live bird markets. Although not the focus of our study, this work highlights the importance of active surveillance in live bird markets13 to better understand avian influenza transmission dynamics. We observed a reduction in avian influenza positive markets over the study period, which could be due to ongoing intervention efforts. Avian influenza circulation continues to have important implications for viral reassortment and pandemic risk, particularly given that research has shown that in DCC over 50% of the population visits live bird markets, and almost 75% of people have regular exposure to live poultry.12

Our study has some limitations. Although the availability and robustness of human influenza surveillance data has

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**Table 3:** Seasonality and coseasonality estimates for influenza from hospital-based sentinel surveillance and avian influenza from live bird market surveillance in Dhaka City Corporation, 2016–19

| Seasonality                          | Estimate \* | 95% CI          |
|--------------------------------------|-------------|-----------------|
| **Seasonal influenza in humans**     |             |                 |
| Peak timing, calendar week           | 24.4        | 23.4–25.5       |
| Amplitude                            | 7.64        | 5.75–13.1       |
| **Avian influenza in live bird markets** |             |                 |
| Peak timing, calendar week           | 14.9        | 13.2–17.0       |
| Amplitude                            | 1.17        | 1.13–1.22       |
| **Interval difference**              |             |                 |
| Peak timing, weeks                   | 9.4         | 8.6–10.2        |

\*Estimates were calculated using negative binomial regression models with harmonic terms adjusted for linear and quadratic trend, and an offset for samples tested (humans) or markets sampled (poultry). 95% CIs were estimated using 1000 block-bootstrapped samples. A Poisson regression imputation method was used to impute data for missing monthly data.
improved since the A(H1N1)pdm09 influenza pandemic in 2009; there was inconsistent reporting over time within the HBIS and NISB surveillance network. The number of regional surveillance sites varied from year to year during the study period, which impacted the number of samples tested. However, we used the monthly number of samples tested in each region as an offset in our harmonic regression models to account for these changes in surveillance efforts. There were also missing data from avian influenza time series for 6 months due to data collection and storage issues. Although we imputed data for missing periods using a Poisson process, the true influenza trends in this period are unknown; however, our results were robust to sensitivity analyses using zero-inflated negative binomial regression models. Longer-term time series would be useful to have more power to detect and verify avian influenza trends. Given variability in human surveillance sampling protocols, we aggregated data to the monthly level in all analyses, which might hide granular variability that could occur at the weekly level. However, fine-scale temporal surveillance data are not usually available and previous studies have found that these are not essential to capture temporal disease transmission patterns. Hospital-based influenza-like illness and SARI surveillance is likely to capture more severe influenza cases, and patients might present later in their course of illness. Although this fact could result in delayed estimates of epidemic peak timing, the effect is probably non-differential across regions given the use of standard case definitions. Additionally, sentinel surveillance only captures a fraction of cases, and can therefore not be used to estimate the burden of disease. Finally, we did not have data to formally explore factors associated with the heterogeneous radial spread of seasonal human influenza from central Bangladesh outwards. There are a wide range of regional, climatic, and environmental (eg, precipitation, temperature, and humidity), and population level (eg, population density) factors that could be examined in meta-regression models to better understand drivers of spatial diffusion. Future work could also include the use of transmission dynamic models and phylogenetic data to further evaluate regional differences and influenza evolutionary dynamics.

Despite these limitations, our study provides robust quantitative estimates for influenza in a subtropical region over a 10-year period at the subnational level. Our findings suggest that influenza epidemics in humans are highly seasonal and peak earlier in metropolitan areas. By contrast, we found that avian influenza in poultry does not show a strong seasonal trend in Bangladesh. Although influenza peaks do not coincide, year-round avian influenza transmission continues to pose a risk for viral reassortment, which suggests that Bangladesh could be a hotspot for emergence of novel influenza strains with pandemic potential. Our results support the need for more quantitative risk assessments of viral reassortment in urban Bangladesh and could be used to inform future timing of sequencing-based surveillance. Additional strategies could also include enhanced SARI surveillance throughout the year for early avian influenza detection or enhanced surveillance for mild infections among humans during periods of higher circulation in poultry.

Contributors
IB, PM, SKM, ALG, MSF, and DNF conceived and designed the study. MR, ASMA, MHK, RA, ML, TS, MAI, FC, SD, EB, MGO, MSF, and IB implemented the study and collected, collated, and verified the data. IB analysed the data and wrote the first draft of the manuscript. IB, MR, PM, SKM, ALG, MSF, and DNF contributed to writing subsequent versions of the manuscript. All authors had access to the data and critically reviewed the manuscript for important intellectual content and approved the final version. IB and DNF had final responsibility for the decision to submit for publication.

Declaration of interests
DNF has received support by a grant from the Canadian Institutes for Health Research (2019 COVID-19 rapid research funding OV4-170360). DNF has served as a legal expert on issues related to COVID-19 epidemiology for the Elementary Teachers Federation of Ontario and the Registered Nurses Association of Ontario. DNF has served on advisory boards related to influenza and SARS-CoV-2 vaccines for Seqirus, Pfizer, AstraZeneca, and Sanofi-Pasteur vaccines. All other authors declare no competing interests.

Data sharing
According to the data policies of the contributing institutions, to protect intellectual property rights, the primary data cannot be made publicly available by the authors. The data can be made available upon reasonable request to the Institutional Data Access Committees of the contributing institutions. Requests for data can be forwarded to Research Administration at icddr,b, Dhaka, Bangladesh (ahmed@icddr.b.org).

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