Big Data and Information Analytics

https://www.aimspress.com/journal/BDIA

BDIA, 10: 53–69.
DOI:10.3934/bdia.2026003
Received: 17 December 2025
Accepted: 29 December 2025
Published: 21 January 2026

Research article

Changes in the age distribution of confirmed influenza cases in Alberta, Canada

DaiHai He[1,*], Jonathan Dushoff[2,3], Alice P. Y. Chiu[1], Mark B. Loeb[3,4], Kevin Fonseca[5] and David J. D. Earn[3,6]

[1] Department of Applied Mathematics, Hong Kong Polytechnic University, Hung Hom, Kowloon, Hong Kong, China

[2] Department of Biology, McMaster University, Ontario, Hamilton, Canada

[3] M. G. DeGroote Institute for Infectious Disease Research, McMaster University, Ontario, Hamilton, Canada

[4] Department of Clinical Epidemiology and Biostatistics, McMaster University, Ontario, Hamilton, Canada

[5] Department of Microbiology & Infectious Diseases, University of Calgary, Alberta, Canada

[6] Department of Mathematics and Statistics, McMaster University, Ontario, Hamilton, Canada

* **Correspondence:** Email: daihai.he@polyu.edu.hk; Tel: +8522766 7864; Fax: +85223629045.

Abstract: The age-incidence pattern during an influenza pandemic tends to be characterized by a relatively high proportion of severe cases in young adults. After a pandemic, the age pattern of those infected with the pandemic strain shifts toward that of seasonal strains, likely due to population immunity, and possibly viral evolution as well. We study age-incidence patterns of three influenza subtypes in Alberta, Canada from January 2009 to March 2015, a period that includes the 2009 pandemic. We find a consistent age drift toward older populations from A/H1N1pdm (pandemic strain) cases. Unexpectedly, we also find similar shifts toward the elderly for confirmed cases of seasonal influenza A/H3N2 and influenza B. The school term schedule also has clear effects on the age structure of reported cases. At the national level, we show the weekly reports for influenza from 2009 to 2025 and the season *vs.* age group *vs.* subtype patterns from 2015 to 2024. We find that A/H3N2 was the first subtype to return in Canada after the COVID-19 pandemic, followed by A/H1N1. We also highlight that A/H1N1 severely impacted the age 65+ group in the 2023–24 season.

Keywords: influenza; age group; 2009 influenza pandemic; COVID-19 pandemic

1. Introduction

Both seasonal and pandemic influenza cause substantial morbidity and mortality and thus pose a considerable burden to human society [1]. The age distributions of influenza mortality and reported cases are skewed toward the very young and the elderly in typical seasons, but can have a peak in young adults during pandemics [2, 3]. In the years following a pandemic, influenza morbidity and mortality patterns can be expected to return to seasonal norms due to the accumulation of immunity in younger persons [4], and possibly also due to viral evolution; this pattern was reported for the 1918, 1957, and 1968 influenza pandemics and more recently for the 2009 influenza pandemic [5, 6]. Using network-based mathematical modeling techniques, Bansal et al. [7] found that schoolchildren experienced the highest attack rates in the 1918, 1957, and 1968 pandemics, with the burden shifting to adults after these pandemics, and they predicted a similar shift would follow the 2009 pandemic.

Here we use a detailed data set of laboratory influenza confirmations from the Canadian province of Alberta (population size $\approx$ 3.6 million in 2011) to study the age distributions of confirmed cases of three distinct influenza subtypes. Our primary objective is to determine whether the burden of the A/H1N1pdm strain in Alberta shifted toward older age groups after the 2009 pandemic (as expected, and as reported for other locations previously [5, 6]). We also investigate age distribution changes for H3N2 and influenza B cases.

2. Methods

2.1. Surveillance data

We analyze daily laboratory-confirmed respiratory infection data from the Provincial Public Health Laboratory of Alberta (ProvLab). All samples submitted to regional laboratories for respiratory virus testing were processed by ProvLab. Due to high demand arising from pandemic concerns from 30 Oct until 30 Nov 2009, respiratory virus testing was restricted to patients awaiting hospital admission, hospitalized patients, specimens from outbreak investigations, special requests made by public health officials, and specimens noted by the sentinel physician network (The Alberta Recording and Research Network (TARRANT)) during that period. Before and after this time, there were no restrictions on testing.

The data analyzed cover the period from January 2009 to March 2015. Variables included the sample date, geographical region, age and gender of the patient, and influenza type and subtype (A/H1N1pdm, A/H3N2 or influenza B). We use collection dates for 2009 samples and confirmation dates for later samples.

Population estimates for each age class were obtained from the 2011 Alberta census [8].

We also obtained national data for Canada from 2009 to 2025 from FluNet [9] and FluWatch [10].

2.2. Statistical analysis

Following Bolotin et al. [11], we compared patient ages for each subtype in different time periods using the Wilcoxon rank sum test (Figure A.2). Statistical analyses were conducted using R (version 3.3.3) [12]. Significance tests were 2-sided, with the α-level for statistical significance set at 0.05.

3. Results

Between January 2009 and March 2015, ProvLab conducted influenza respiratory virus tests on approximately 152,900 specimens. In Figure 1, we show the weekly confirmations of the three circulating influenza subtypes (A/H1N1pdm, A/H3N2 and Influenza B) and the total specimens processed. Two waves of A/H1N1pdm occurred in 2009, which was followed by a gap of about a year with very few cases in any of the three subtypes. There were larger outbreaks in 2013–2015, with A/H3N2 dominating in 2013 and 2015.

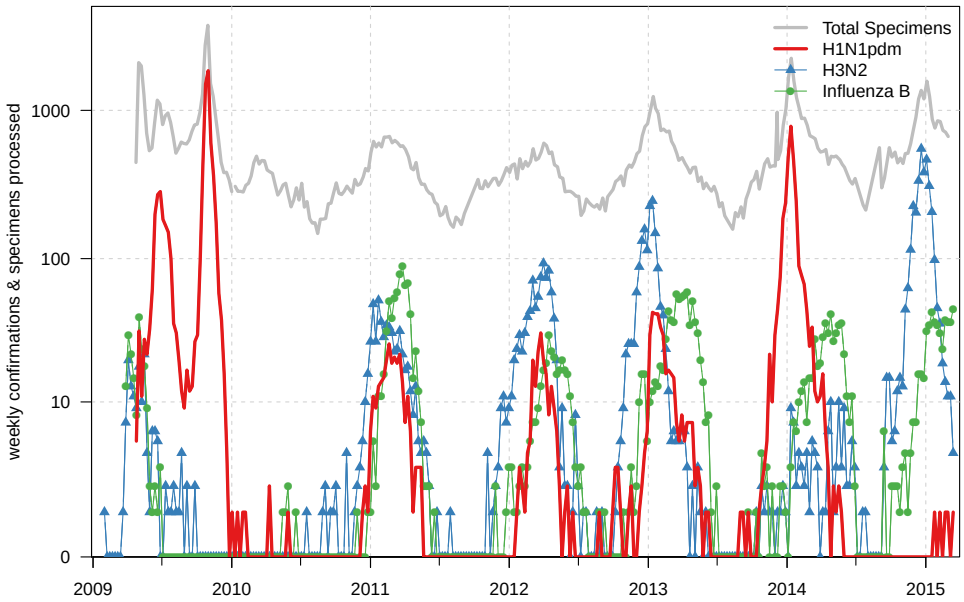

Figure 1. Weekly total confirmations of the three subtypes and total tests (specimens processed) from January 2009 to March 2015. Note the log scaling on the y axis.

In Figure 2, we show patient age versus sample date for each confirmed case of each circulating subtype (each gray dot represents one confirmation). At two times in 2009 (indicated by red arrows), the number of A/H1N1pdm cases identified in schoolchildren declined abruptly. These two shifts are associated with summer school closure in the last week in June 2009 and the implementation of testing restrictions in November 2009. School closure slowed down transmission among schoolchildren, pushing the mean age toward adults [13]. Testing restrictions seem to have had a disproportionate effect on the testing of children, perhaps because they are more likely to be tested in the absence of severe illness under ordinary circumstances.

Figure 3 shows the patient age distribution for the three influenza subtypes, the time series of total confirmations for each subtype, and total tests from January 2009 to March 2015. We show the age-standardized distribution (in units of confirmations per 10,000 census inhabitants) for the three subtypes. For A/H1N1pdm, we further divided the year 2009 into two periods: first wave (April 2009 to August 2009) and second wave (September 2009 to August 2010; most of these cases were reported before January 2010). A vaccination campaign was implemented in December 2009 and January 2010 [14]. We omit the 2014/15 flu season for A/H1N1pdm since only five confirmations

were reported. For H3N2 (panel b) and influenza B (panel c), we show the age distributions for 2009/10 (January 2009 to August 2010), and flu seasons (September to August) for 2010/11, 2011/12, 2012/13, 2013/14, and 2014/15 (up to March 2015).

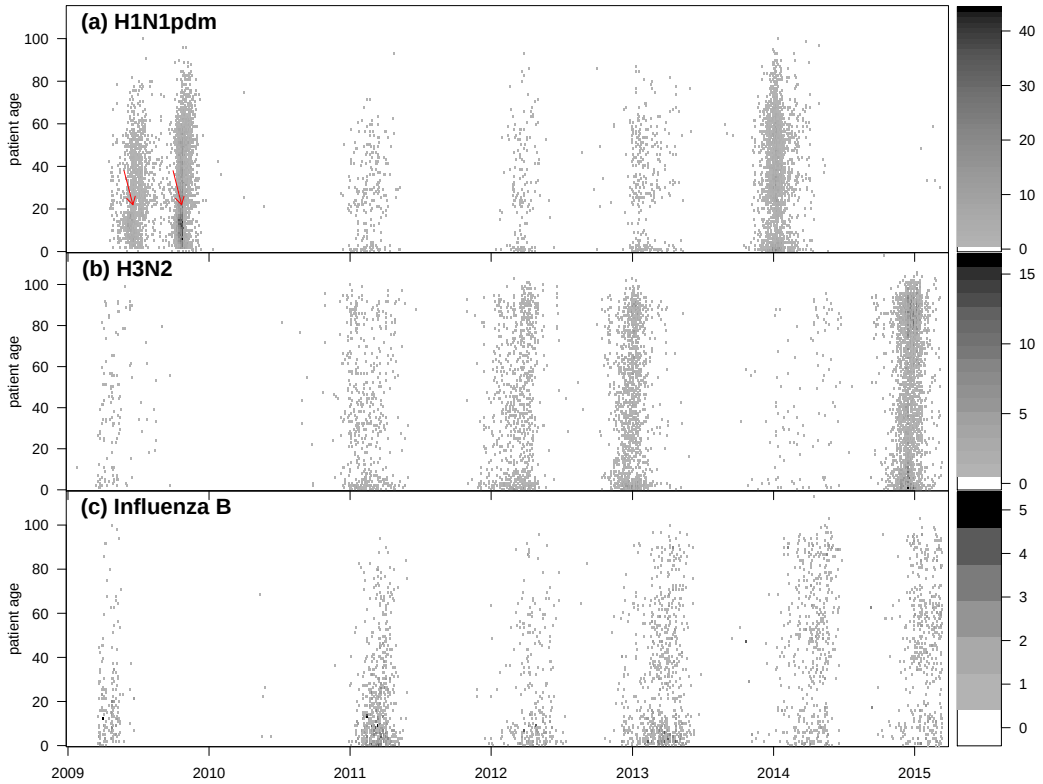

Figure 2. Scatter plots of all laboratory confirmations. Grey dots show patient age versus specimen date from January 2009 to March 2015 in Alberta, Canada; each dot represents one laboratory confirmation. Cases are classified into three types: A/H1N1pdm (panel a), A/H3N2 (panel b), and influenza B (panel c). The sudden changes in June and November 2009 (indicated with red arrows) were most likely due to summer school closure and implementation of testing restrictions [13].

The temporal changes in the age distribution of influenza confirmations shown in Figure 3 show the expected pattern for A/H1N1pdm, namely a shift toward older age classes after the pandemic. Unexpectedly, substantial age shifts were also observed for A/H3N2 and influenza B in 2013/14 and 2014/15.

A violin plot of patient age for each strain in each flu season is shown in Figure 4, along with sample size (grey dots) and the confidence interval for the estimated median (vertical lines). The changes in the full age distributions for the various subtypes are more evident in these plots.

A/H1N1pdm cases among schoolchildren were high in 2009 but low thereafter. All three subtypes show high rates in preschool. This is presumably due, at least in part, to the fact that this age group has less pre-existing immunity, and is thus more likely to be infected or to have more serious infections. It is also possible that these individuals are more likely to be tested.

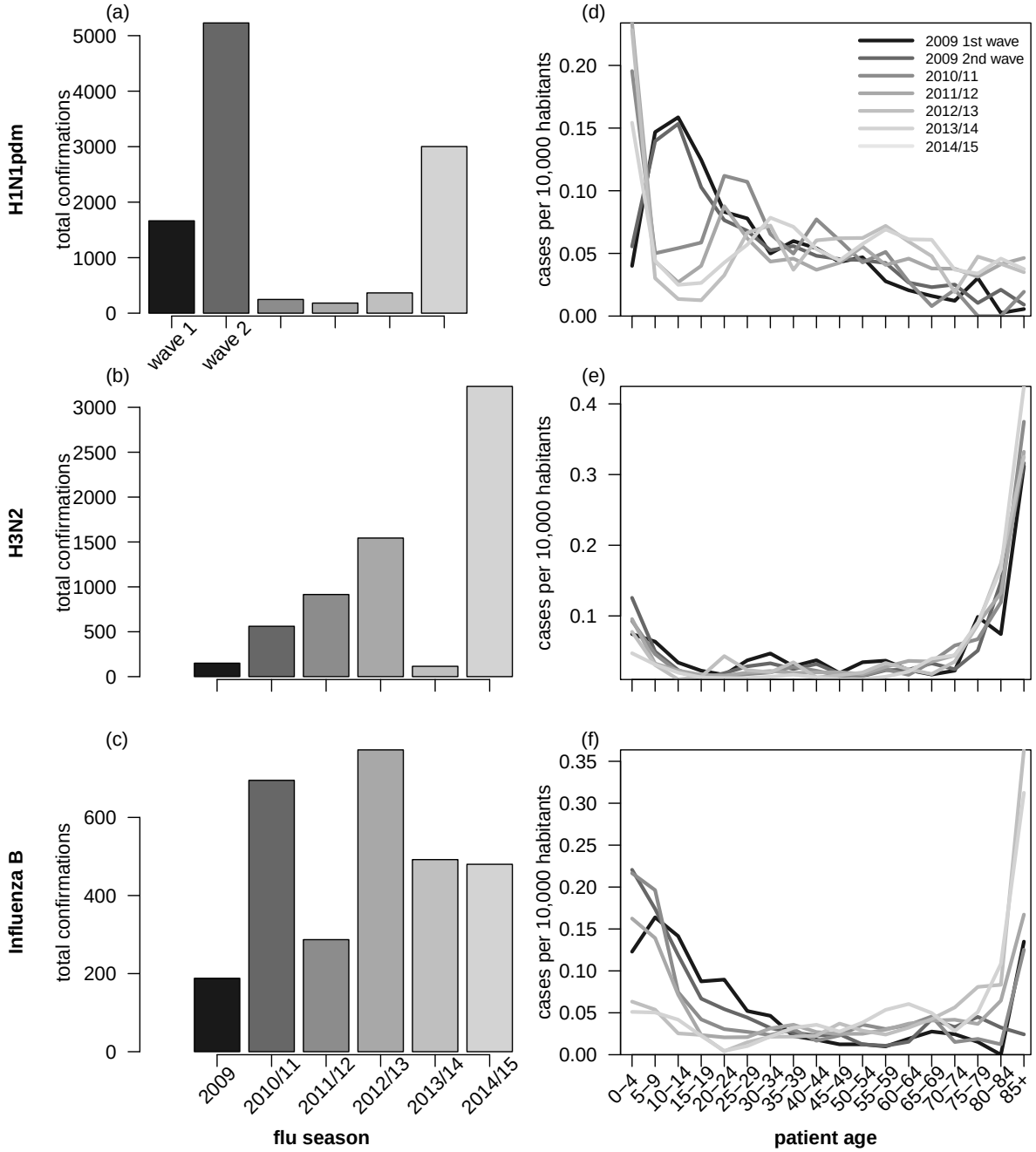

Figure 3. Number of confirmations and normalized age profile for each subtype in different time periods. To obtain the population-standardized age profile, we aggregate cases into 18 five-year age bins, normalize using age-specific population estimates from 2011 Alberta census data (see Figure A.1), and then normalize the age profile for each season to facilitate comparison of relative risk across age bins by season. The age profiles are shown for six different flu seasons. For A/H1N1pdm in panels (a,d), the year of 2009 is further divided into two waves, while 2014/15 is omitted because of insufficient data (only five cases were confirmed).

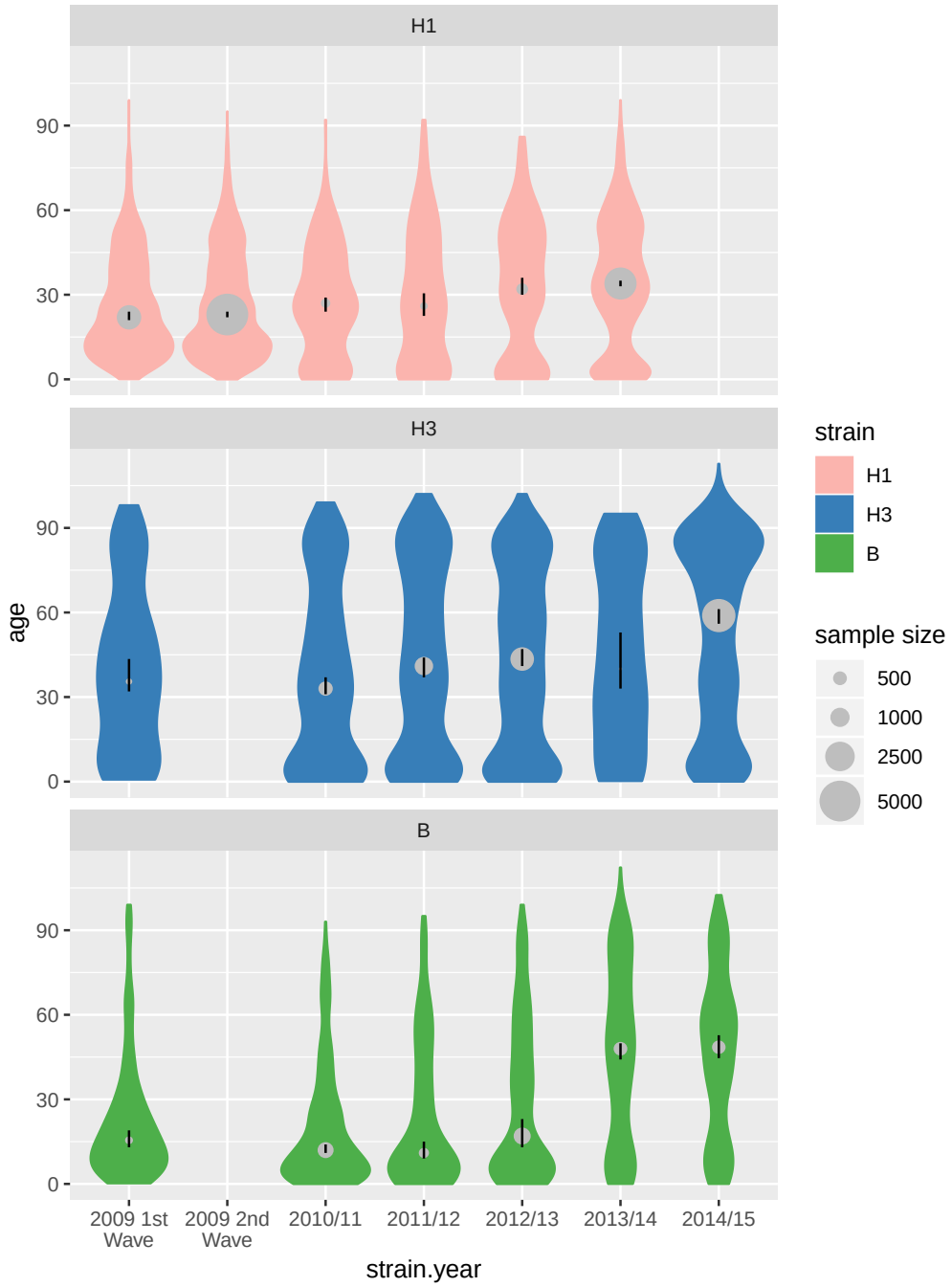

Figure 4. Violin plot of patient ages of each strain in each influenza season. Sizes/positions of red dots indicate the sample size/median of patient ages. Bars indicate the 95% confidence intervals of the medians. H1 in 2014/15 is omitted due to insufficient sample size (only five samples).

A/H3N2 and influenza B were most commonly confirmed in the typical at-risk groups: preschool and primary school (< 10 years) and the elderly (> 85 years). Comparing these two subtypes, A/H3N2 had relatively more confirmations in the elderly. A/H1N1pdm was more common in young adults and adults than the other two subtypes.

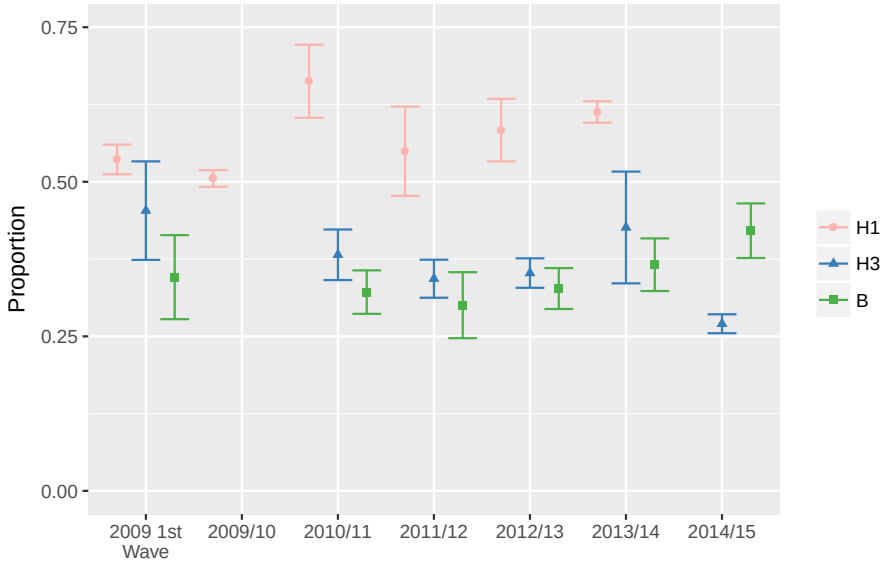

Figure 5. Proportions of confirmations in 18–60 age range and binomial 95% confidence intervals for each subtype or type in each flu season. We omit A/H1N1pdm in 2014/15 since there were only five confirmed cases (aged 48, 33, 58, 33, and 30).

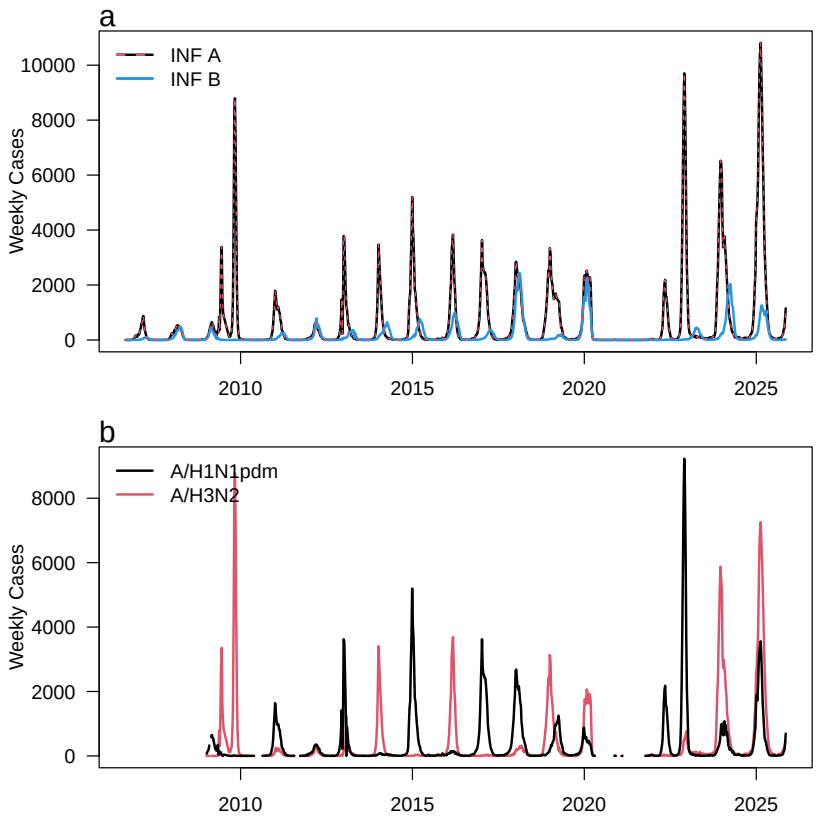

Figure 6. FluNet of World health Organization data of long-term influenza weekly cases in Canada at the country level from 2009 to 2025.

Figure 5 illustrates these effects by showing proportions of confirmations in the 18–60 age range (and binomial 95% confidence intervals) for each subtype or type in each flu season. The proportion in the 18–60 age range was higher for A/H1N1pdm than for A/H3N2 or B. A/H1N1pdm displays an increased proportion in the 18–60 age group after the pandemic, as expected, whereas for A/H3N2 this proportion gradually decreased.

The unexpected trends in age distributions of confirmations for A/H3N2 and B might have resulted from changes in patterns of testing (which could have occurred due to real or perceived severity of an influenza outbreak). There was a strong correlation between number of confirmations and median age of A/H3N2-positive samples ($\rho = 0.93$, $p < 0.01$). This correlation was weak for A/H1N1pdm ($\rho = -0.33$) and influenza B ($\rho = 0.044$).

In the following, we show the long-term weekly influenza cases from 2009 till 2024 in Canada at the country level. We also show the subtype/age-group/flu-season plot from 2015 till 2024.

In Figure 6, we show weekly Influenza cases from 2009 to Sep 2025 in Canada (country level). This figure covers two pandemics: the 2009 swine flu pandemic and the COVID-19 pandemic. The 2009 pandemic caused a major wave of A/H1N1pdm, followed by a three-year low level of A/H1N1pdm. The A/H3N2 subtype showed a brief biennial cycle period between 2011–2018. The COVID-19 pandemic stopped the transmission of influenza for two years 2020–2021, followed by a resurgence of A/H3N2 in 2022/23, then a resurgence of A/H1N1 in 2023/24.

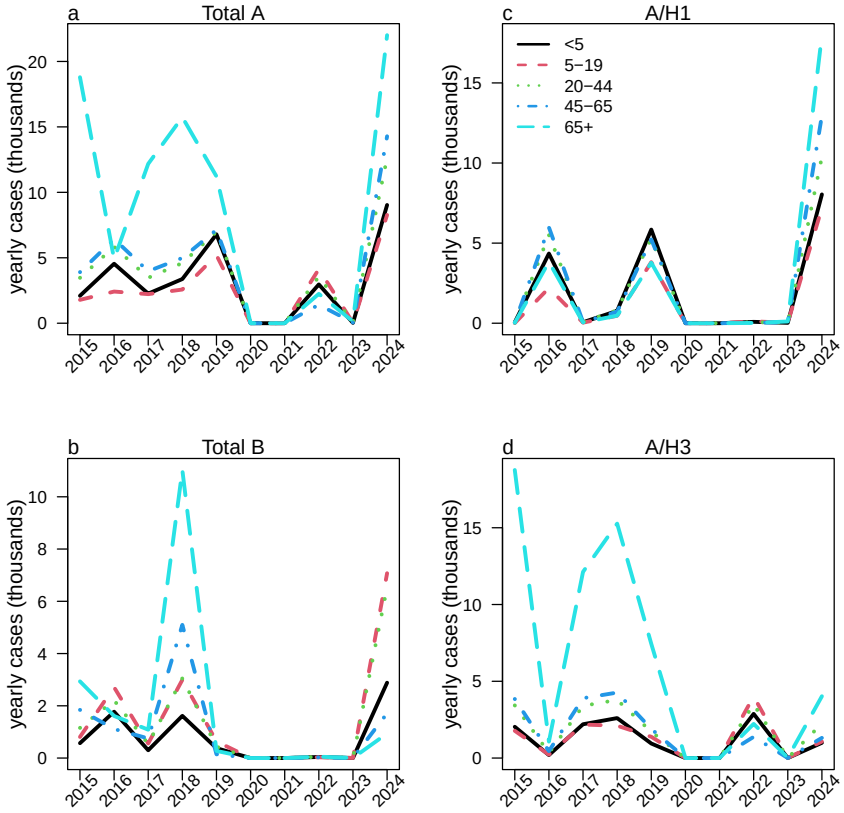

Figure 7. Subtype-age group-flu season plot on data from FluWatch of Canada at the country level from 2015 to 2024.

In Figure 7, we show the subtype/age-group/flu-season plot for confirmed influenza cases in Canada (country level) for the period 2015–2024. A/H1N1pdm rebounded strongly in 2024 across all age groups. The A/H3N2 rebounded started in 2022, but was biased toward younger age groups; in particular, the 65+ group had relatively few cases compared to 2017–19. Influenza B rebounded in 2024, also with a focus among younger age groups ($\leq$ 45). The mechanism behind this pattern warrants further study.

4. Interpretation

Low post-pandemic A/H1N1pdm confirmation rate in school ages. The low rates of influenza observed in the post-pandemic period among schoolchildren could be associated with high A/H1N1pdm sero-protection among the group. The sero-protection level against A/H1N1pdm for schoolchildren was > 70% [15] in the middle of 2010 in a neighboring province, British Columbia, Canada, which was double the level among young adults (age 20–40). We show this pattern of sero-prevalence across age in Figure A.3 in the Appendix. A large proportion of the sero-protection should be from natural infection following high attack rate among schoolchildren in 2009. Low attack rates from A/H3N2 and B could be due to cross-immunity in the post-pandemic period, or due to these strains taking time to recover from population depletion due to effects of short-term immunity during the pandemic.

Skip of A/H1N1pdm in 2014/15. The A/H1N1pdm strain "skipped" the 2014/15 season with only five confirmed cases; A/H1N1pdm showed similar skips in many European and Asian countries in the 2011/12 season [16]. These skips could be due to high population immunity caused by previous infections with A/H1N1pdm and cross-protection caused by infections with A/H3N2.

Replacement of dominant strains. In addition to changes in patient age of A/H1N1pdm confirmations in Alberta, Canada after the 2009 pandemic, we also found a substantial age shift toward the elderly for A/H3N2 and influenza B in the 2013/14 and 2014/15 flu seasons. We argue that replacements of dominant strains of the A/H3N2 subtype and the B Yamagata lineage could be responsible for the age changes in A/H3N2 and influenza B confirmations. A summary of the dominant strains in Canada, obtained from FluWatch weekly reports of the Public Health Agency of Canada, is shown in Figure 8. The dominant strains of A/H1N1pdm and the B Victoria lineage were the same from 2011 to 2016. On the other hand, A/H3N2 and the B Yamagata lineage dominant strain designations have been updated annually or biennially.

The list of vaccine strains used from 2015 to 2024 is shown in Table A.1. A/H3N2 vaccines have been updated more frequently than those of A/H1N1 or B.

Testing policy changes during pandemic. In our study, the changes in testing policy in November 2009 in Alberta changed the pattern of the patient age (see Section 2.1 Surveillance data and Figure 2; there was a sudden drop in confirmed cases among schoolchildren right after the start of the testing restrictions). Since testing restrictions make more severe cases relatively more likely to be tested, this rapid age shift suggests that a relatively larger proportion of cases found in younger age groups were less severe. Similar policy changes occurred in other countries/regions. For instance, extensive testing early in the pandemic was reported in Hong Kong. Testing policy changes occurred in Ontario and Quebec, Canada. In the United Kingdom, a new surveillance network was introduced to control the pandemic.

season	total tested	A/H1N1	A/H3N2					B/Victoria	B/Yamagata		
			A/California/7/2009	A/Perth/16/2009	A/Victoria/361/2011	A/Texas/50/2012	A/Switzerland/9715293/2013		B/Brisbane/60/08	B/Wisconsin/01/2010	B/Massachusetts/2/2012
2010/2011	920	15.0	**29.0**	–	–	–	–	53.0	**2.4**	–	–
2011/2012	1202	16.0	**17.0**	–	–	–	–	33.0	**34.0**	–	–
2012/2013	1332	16.0	–	**47.0**	–	–	–	8.0	**29.0**	–	–
2013/2014	2468	57.0	–	–	**7.0**	–	–	1.0	–	**35.0**	–
2014/2015	1171	2.0	–	–	**1.0**	**18.0**	–	9.0	–	**70.0**	–
2015/2016	3040	49.0	–	–	–	**8.6**	–	32.7	–	–	**8.8**
2016/2017	2307	2.6	–	–	–	–	**70.5**	5.4	–	–	**21.5**

Figure 8. Total number of samples sequenced and percentages of each subtype confirmed in each influenza season. Data were obtained from FluWatch weekly reports of the Public Health Agency of Canada (PHAC). There were frequent replacements of strains in the H3N2 and B-Yamagata lineages.

Data from all parts of Canada. We show the age change patterns in influenza confirmations from all parts of Canada in Figures A.4 and A.5 and Tables A.2 and A.3 in the Appendix. Although the age groups are crude, we can see similar patterns as in Alberta, Canada. In particular, we can see an age shift of A/H1N1pdm patients toward non-school-age groups in 2011–2014 and an age shift of A/H3N2 patients towards preschool and elderly (age 65+) age groups in severe A/H3N2 epidemics.

For the period from 2015 to 2024, we show the age change pattern in Figures 6 and 7 . We note a change in age patterns for A/H3N2 and B from pre- to post-COVID-19 pandemic. Compared to younger ages, the elderly (age 65+) showed low incidence for influenza B and A/H3N2, but not for A/H1N1, in the post-COVID-pandemic period up to 2024.

Limitations. We lacked direct sero-protection data from Alberta, but we used data from the neighboring British Columbia as a proxy indicator to study the effects of age-shift as a result of high sero-protection among schoolchildren after the 2009 pandemic. Another limitation of our surveillance data is that we do not know the underlying medical conditions of patients with confirmed influenza, which would facilitate more detailed analysis and comparisons with data from the US.

Highlights. We used high-quality influenza confirmation data across a five-year period (2009–2014) in a detailed analysis of age distribution of infections (standardized by population in each class).

In addition to an expected age shift following the pandemic for A/H1N1pdm, we found unexpected shifts toward the elderly in H3N2 and B. We hypothesize that the replacement of the dominant strains of H3N2 and B could play a key role; in particular, the age shift seen in B in 2013 could be associated with the replacement of the dominant influenza B Yamagata strain.

In conclusion, we detected a systematic change in the age distribution of confirmed A/H1N1pdm in

the post-influenza-pandemic era, and a substantial shift in the age distributions of confirmed A/H3N2 and influenza B, in Alberta, Canada. We reported that testing restrictions dramatically affected the mean age of patients with confirmed A/H1N1pdm in 2009. We showed that the age patterns of patients infected with the pandemic subtype A/H1N1pdm are different from the other two subtypes, A/H3N2 and influenza B. It was surprising that the 2013–14 wave of A/H1N1pdm was so severe in Canada and the United States, given that the subtype was antigenically stable and vaccination coverage among the general population was high in North America.

At the national level, we found changes in the age distribution pattern of influenza confirmations before and after the COVID-19 pandemic.

Author contributions statement

D. H, D. J. D. E., J. D., and M. B. L. conceived the study. K. F. assisted with data collection and management. D. H., J. D., D. J. D. E., and A. P. Y. C. analysed the results and wrote the first draft. All authors reviewed the manuscript.

Use of AI tools declaration

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

Acknowledgments

D. H. was supported by the Otto Poon Charitable Foundation. J. D. and D. J. D. E. were supported by NSERC.

Conflict of interest

The authors declare that they have no conflicts of interest.

References

1. Earn DJD, Dushoff J, Levin SA, (2002) Ecology and evolution of the flu. *Trends Ecol Evol* 17: 334–340. https://doi.org/10.1016/S0169-5347(02)02502-8
2. Ma J, Dushoff J, Earn DJD, (2011) Age-specific mortality risk from pandemic influenza. *J Theor Biol* 288: 29–34. https://doi.org/10.1016/j.jtbi.2011.08.003
3. Karageorgopoulos DE, Vouloumanou EK, Korbila IP, Kapaskelis A, Falagas ME, (2011) Age distribution of cases of 2009 (H1N1) pandemic influenza in comparison with seasonal influenza. *PLoS One* 6: e21690. https://doi.org/10.1371/journal.pone.0021690
4. Simonsen L, Clarke MJ, Schonberger LB, Arden NH, Cox NJ, Fukuda K, (1998) Pandemic versus epidemic influenza mortality: A pattern of changing age distribution. *J Infect Dis* 178: 53–60. https://doi.org/10.1086/515616

5. Chowell G, Echevarría-Zuno S, Viboud C, Simonsen L, Grajales-Muñiz C, Rascón-Pacheco RA, et al. (2012) Recrudescent wave of pandemic A/H1N1 influenza in Mexico, winter 2011–2012: Age shift and severity. *PLoS Curr Influenza* 4: RRN1306. https://doi.org/10.1371/currents.RRN1306

6. Borja-Aburto VH, Chowell G, Viboud C, Simonsen L, Miller MA, Grajales-Muñiz C, et al. (2012) Epidemiological characterization of a fourth wave of pandemic A/H1N1 influenza in Mexico, winter 2011–2012: Age shift and severity. *Arch Med Res* 43: 563–570. https://doi.org/10.1016/j.arcmed.2012.09.005

7. Bansal S, Pourbohloul B, Hupert N, Grenfell B, Meyers LA, (2010) The shifting demographic landscape of pandemic influenza. *PLoS One* 5: e9360. https://doi.org/10.1371/journal.pone.0009360

8. Alberta Demographic Statistics, 2019. Retrieved December 1, 2025. Available from: https://www.alberta.ca/demographic-statistics.

9. Global Influenza Programme. Retrieved December 1, 2025. Available from: https://www.who.int/tools/flunet.

10. Canadian Respiratory Virus Surveillance Report. Retrieved December 1, 2025. Available from: https://www.canada.ca/en/public-health/services/diseases/flu-influenza/influenza-surveillance/weekly-influenza-reports.html.

11. Bolotin S, Pebody R, White PJ, McMenamin J, Perera L, Nguyen-Van-Tam JS, et al. (2012) A new sentinel surveillance system for severe influenza in England shows a shift in age distribution of hospitalised cases in the post-pandemic period. *PLoS One* 7: e30279. https://doi.org/10.1371/journal.pone.0030279

12. R Core Team, R: A Language and Environment for Statistical Computing, Vienna, Austria: R Foundation for Statistical Computing, 2015. Available from: https://www.R-project.org/.

13. Earn DJD, He D, Loeb MB, Fonseca K, Lee BE, Dushoff J, (2012) Age-specific mortality and hospitalization rates during the 2009 influenza A (H1N1) pandemic in Alberta, Canada. *Ann Intern Med* , 156: 173–181. https://doi.org/10.7326/0003-4819-156-3-201202070-00005

14. He D, Dushoff J, Eftimie R, Earn DJD, (2013) Patterns of spread of influenza A in Canada. *Proc Roy Soc B Biol Sci* 280: 20131174. https://doi.org/10.1098/rspb.2013.1174

15. Skowronski DM, Hottes TS, Janjua NZ, Purych D, Sabaiduc S, Chan T, et al. (2010) Prevalence of seroprotection against the pandemic (H1N1) virus after the 2009 pandemic. *Can Med Assoc J*, 182: 1851–1856. https://doi.org/10.1503/cmaj.100910

16. He D, Lui R, Wang L, Tse CK, Yang L, Stone L, (2015) Global spatio-temporal patterns of influenza in the post-pandemic era. *Sci Rep* 5: 11013. https://doi.org/10.1038/srep11013

Appendices

A.1. Population age structure in Alberta, Canada (2010 survey)

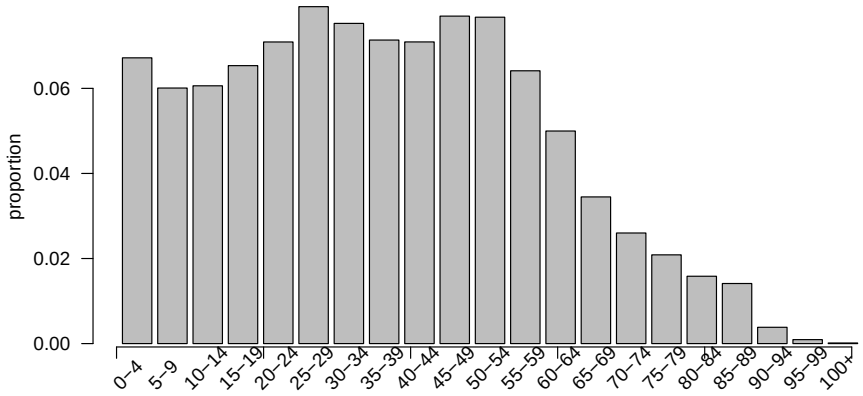

Figure A.1. Population age structure in Alberta, Canada, based on the 2010 census.

A.2. Wilcoxon rank-sum test

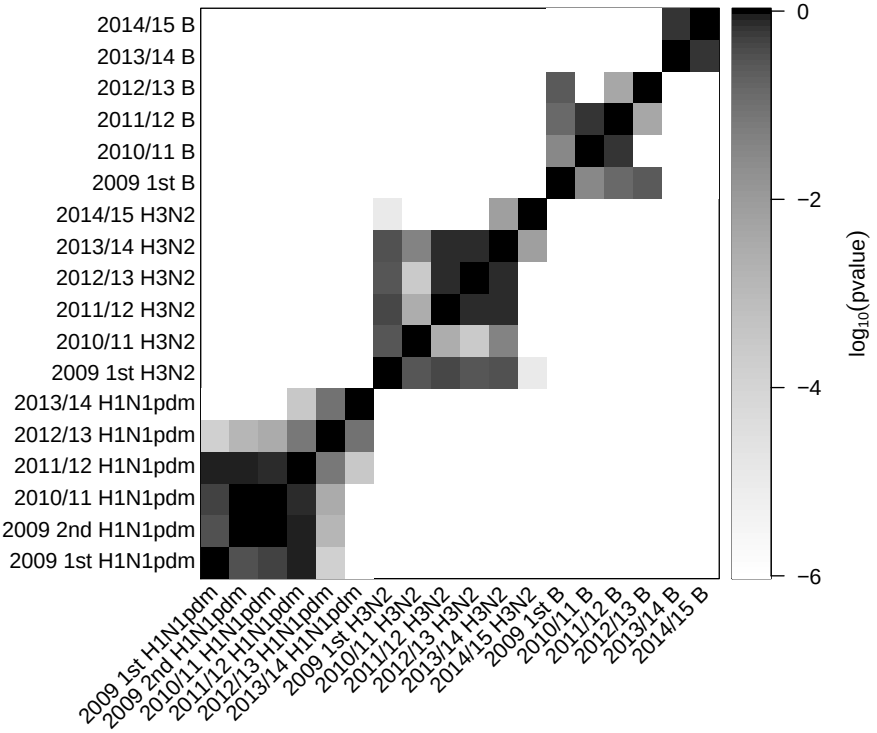

Figure A.2. P-values for Wilcoxon rank-sum test.

A.3. Sero-prevalence against A/H1N1pdm after the 2009 pandemic

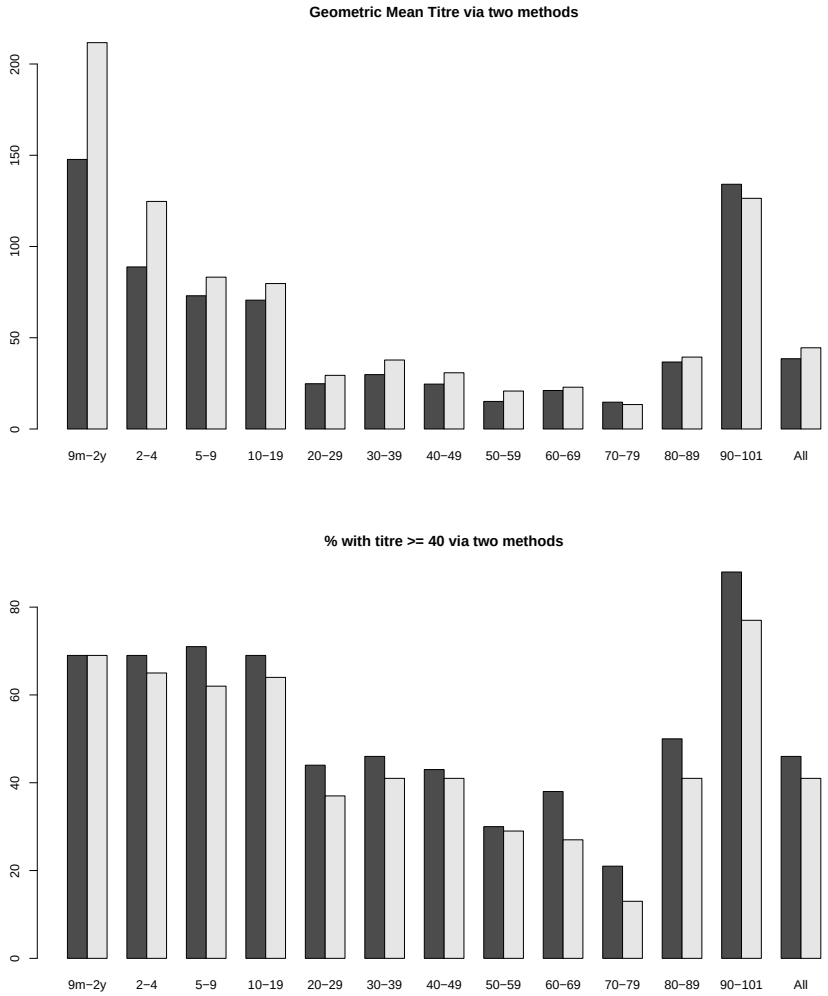

Figure A.3. Data are from [15]. These distributions show the prevalence of seroprotection against the A/H1N1pdm virus six months after the 2009 pandemic in British Columbia, Canada.

A.4. Data from all parts of Canada

In the main text, we showed the lab confirmations from Alberta, Canada in fine time increments (daily) and age scales. We also obtained the lab confirmations in crude age scale from all parts of Canada from FluWatch Canada (https://www.canada.ca/en/public-health.html). We show the age distribution of A/H1N1pdm and H3N2 in the last five flu seasons in Figure A.4. Even though the age group is crude, we can still see an age shift of the A/H1N1pdm group toward age groups other than school age (age 5–19) in 2011–2014 and an age shift of A/H3N2 group toward preschool age and elderly (age 65+) in some years (severe epidemic years) while being relatively uniform across all ages

in other years. These detailed age pattern changes might not be reflected in the annual mean or median age of patients.

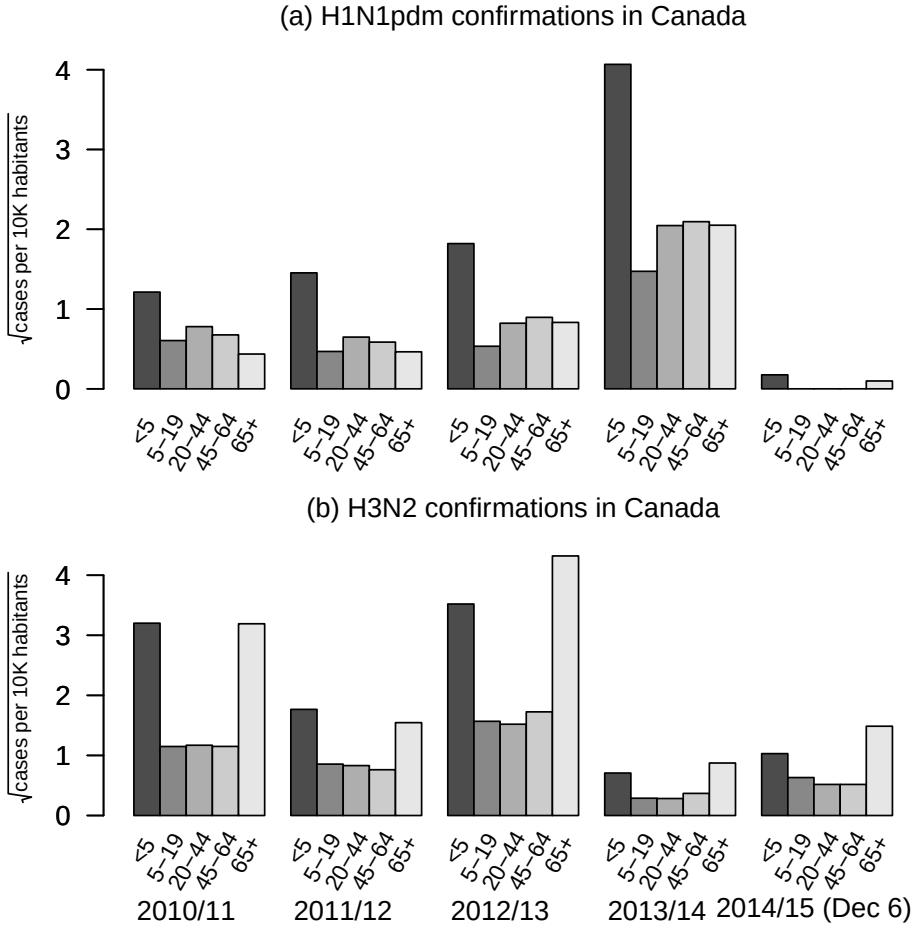

Figure A.4. Age structures of lab confirmations of A/H1N1pdm (panel a) and A/H3N2 (panel b) reported by the participating provinces and territories, Canada, from 2010/11 to 2014/15. Cases of A/H1N1pdm clearly shifted toward the elderly (FluWatch Canada).

We show the raw and age-standardized pattern in Figure A.5 in 2013/14 influenza season. The age pattern is U-shaped with the minimum in the age group 15–19. The risk of being hospitalized due to influenza A was low in the age 15–19 group and very high in < 5 years old in this season (2013/14), and the sole dominate strain is A/H1N1pdm. From Figures A.4 and A.5, we can see that in the age 15–19 group in 2013/14, three-year post the 2009 pandemic, both the lab-confirmed cases and the severity (in terms of hospitalization) were lower than other age groups. This age group had the highest incidence rate in the 2009 pandemic. This might imply that the immunity protection due to infection and immunization in 2009/10 were lasted as long as three years for this age group.

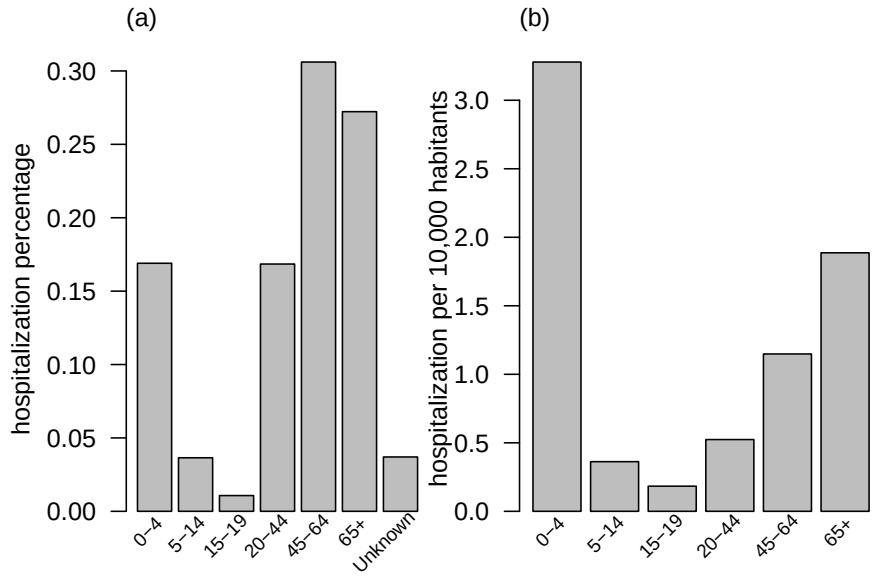

Figure A.5. Age structure of hospitalizations with influenza A reported by the participating provinces and territories in Canada, 2013–14. In the 2013/14 flu season, the dominant strain is A/H1N1pdm. The 15–19 age-group is the least at-risk, and this age group (4 years earlier) was the most infected age group. This might suggest that natural infection is the most effective to prevent hospitalizations. (FluWatch Canada)

Table A.1. List of strains in the recommend vaccine in the Northern Hemisphere. The A/H3N2 vaccine was updated more frequently than other three subtype/lineages, 2015–2025.

A/H3N2	A/District of Columbia/27/2023 (H3N2)–like
	A/Darwin/6/2021 (H3N2)-like
	A/Cambodia/e0826360/2020 (H3N2)-like
	A/Kansas/14/2017(H3N2)
	A/Singapore/INFIMH-16-0019/2016(H3N2)
	A/Hong Kong/4801/2014-like(H3N2)
	A/Switzerland/9715293/2013-like(H3N2)
A/H1N1	A/Wisconsin/67/2022(H1N1)
	A/Wisconsin/588/2019 (H1N1)
	A/Brisbane/02/2018 (H1N1)
	A/Michigan/45/2015(H1N1)
	A/California/7/2009-like(H1N1)
B/Victoria	B/Austria/1359417/2021 (Victoria)
	B/Colorado/06/2017 (Victoria)
	B/Brisbane/60/2008-like(Victoria)
B/Yamagata	B/Phuket/3073/2013(Yamagata)
	B/Massachusetts/2/2012(Yamagata)

Table A.2. Weekly and cumulative numbers of hospitalized cases, ICU admissions and deaths among pandemic A/H1N1pdm 2009 confirmed cases in Canada, April 12, 2009 to April 24, 2010[†].

	1ST WAVE (From Apr.12.2009 to Aug.29.2009 [*])			2ND WAVE (From Aug.30.2009 to Apr.24.2010[*])			TOTAL (From Apr.12.2009 to Apr.24.2010)		
Province/ Territory	Hospitalized cases	ICU admissions	Deaths	Hospitalized cases	ICU admissions	Deaths	Hospitalized cases	ICU admissions	Deaths
BC[1]	49	19	5	1035	149	52	1084	168	57
AB	129	29	7	1147	210	64	1276	239	71
SK	23	12	4	44	40	11	67	52	15
MB	213	43	7	166	18	4	379	61	11
ON	399	69	25	1444	250	103	1843	319	128
QC	572	104	27	2491	361	81	3063	465	108
NB[1]	2	1	0	161	33	8	163	34	8
NS	17	8	1	276	42	6	293	50	7
PE	1	0	0	49	9	0	50	9	0
NL	3	1	0	305	59	18	308	60	18
YT	0	0	0	15	3	3	15	3	3
NT	6	0	0	46	7	1	52	7	1
NU[1]	76	6	1	9	0	0	85	6	1
Canada	1490	292	77	7188	1181	351	8678	1473	428

[*]Based on epidemiological date, hospitalization date, death date, and reporting date. [1]Aggregate counts were reported by these two provinces. [†]Note that due to reporting delays, some provinces and territories reported retrospectively on first and second wave cases.

Table A.3. Descriptive characteristics of laboratory-confirmed Canadian pandemic A/H1N1pdm 2009 hospitalized cases, ICU-admitted cases, and deaths with core information available, reported to PHAC as of April 24, 2010[†]

	(From Apr.12.2009 to Apr.24.2010)			(From Aug.30.2009 to Apr.24.2010[*])			(From Apr.12.2009 to Aug.29.2009 [*])		
	Hospitalized cases(n = 1940)	ICU admissions (n = 292)	Deaths (n = 77)	Hospitalized cases(n = 6737)	ICU admissions (n = 1181)	Deaths (n = 346)	Hospitalized cases(n = 8227)	ICU admissions (n = 1437)	Deaths (n = 423)
Females.%	51.4	57.2	62.3	49.7	49.4	46.8	50.0	51.0	49.6
Aboriginal status[1]	20.1–27.8	16.1–21.9	11.7–17.6	4.6–6.1	5.8–7.6	6.1–8.9	7.4–10.0	7.8–10.4	7.1–10.4
Median age	23.0	37.0	51.0	30.0	47.0	54.0	29.0	46.0	53.0
Underlying medical conditions[2], %	47.5 (653/1374)	60.2 (162/269)	73.3 (55/75)	59.7 (1969/3299)	74.4 (687/924)	85.5 (247/289)	56.1 (2622/4673)	71.2 (849/1193)	83.0 (302/364)
Pregnancy[3], %	27.6 (75/272)	19.7 (15/76)	28.6 (4/14)	18.5 (190/1027)	8.9 (16/180)	0.0 (0/36)	20.4 (265/1299)	12.1 (31/256)	8.0 (4/50)

[1]Since Aboriginal status is not reported by two provinces (which comprise 23% of the Aboriginal population) two methods were used to calculate proportions: One proportion was calculated by including Ontario (ON) and Nova Scotia (NS) cases in the denominator (which is an underestimate of the true proportion); while the other proportion was calculated by excluding ON and NS cases in the denominator (which is an overestimate). [2]Proportion of cases with at least one underlying medical condition (excluding pregnancy) among those for whom the information was available. Note that results may differ slightly compared to the previous weeks due to updates in the national database. [3]Percent of pregnant women among women 15 to 44 years of age. [†] All cases admitted to ICU are included in the hospitalization count; however, not all of the fatal cases included hospitalization before dying.