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Original Article

Transmission dynamics and risk factors for pandemic H1N1-related illness: outbreak investigation in a rural community of British Columbia, Canada

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Objective To characterize the first-wave epidemiologic features of influenza-like illness (ILI) associated with the novel pandemic A/H1N1 [A(H1N1)pdm09] virus.

Methods We used generalized linear mixed models (GLMM) to assess risk factors and non-parametric and/or parametric distributions to estimate attack rates, secondary attack rates (SAR), duration of illness, and serial interval during a laboratory-confirmed community outbreak of A(H1N1)pdm09 clustered around on-reserve residents and households of an elementary school in rural British Columbia, Canada, in late April/early May 2009. ILI details were collected as part of outbreak investigation by community telephone survey in early June 2009.

Results Overall, 92/408 (23%) of participants developed ILI and 36/408 (9%) experienced medically attended ILI (MAILI). The overall SAR in households was 22%: highest among participants 1–4 years of age (yoa) (50%) followed by <1 yoa (38%), 5–8 yoa (20%), 10–19 yoa (13%), 20–49 yoa (20%), and 50–64 yoa (0%). The median serial interval was estimated at 3·5 days (95% CI: 2·1–5·1). In multivariable GLMM analysis, having a chronic condition (OR: 2·58; 95% CI: 1·1–6·04), younger age [1–8 yoa: OR: 4·63; 95% CI: 2·25–9·52; 9–19 yoa: OR: 1·95; 95% CI: 0·97–3·9 (referent: ≥20 yoa)] and receipt of 2008–2009 influenza vaccine (OR: 2·68; 95% CI: 1·37–5·25) were associated with increased risk of ILI. Median duration of illness was 9 days, longer among those with chronic conditions (21 days). Median time to seeking care after developing illness was 4·5 days. On-reserve participants had higher chronic conditions, household density, ILI, MAILI, and SAR.

Conclusions During a community outbreak of A(H1N1)pdm09-related illness, we identified substantial clinical ILI attack rates exceeding 20% with secondary household attack rates as high as 50% in young children. The serial interval was short suggesting a narrow period to prevent transmission.

Keywords Aboriginal, human influenza, H1N1 pandemic, risk factors, serial interval, transmission.

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Introduction

During the last week of April 2009, a laboratory-confirmed outbreak of pandemic A/H1N1 [A(H1N1)pdm09] influenza was reported in an elementary school in a rural community of British Columbia (BC), Canada. The school includes students of Aboriginal and non-Aboriginal backgrounds drawn from the local town and surrounding First Nations reserves. Because A(H1N1)pdm09 had recently emerged in mid-April as a novel virus and in order to characterize its transmission, clinical profile, risk factors, and impact, an outbreak investigation was organized by public health authorities through household telephone survey between May 15 and June 5, 2009.

Initial findings from this investigation have previously been published.[1] Of note, this outbreak investigation provided first detection of an association between prior 2008–2009 trivalent influenza vaccine (TIV) receipt and A(H1N1)pdm09 risk that was subsequently confirmed in at least four other studies conducted during the summer, 2009 in Canada.[2] In this paper, we report additional epidemiologic features of influenza-like illness (ILI) experience during this outbreak including characteristics such as medical care, risk factors, and duration of illness both

on- and off-reserve. As a further main objective, we evaluate transmission patterns such as the household secondary attack rate (SAR) and serial interval (SI: interval between the index and secondary case), both of which are relevant in planning for and responding to novel influenza virus emergence.

Materials and Methods

Outbreak investigation

As previously described,[1] an elementary school (school A) in a rural BC community identified a >10% absenteeism rate owing to respiratory illness among students. Local health authorities were notified on April 28, 2009, and nasopharyngeal specimens confirmed A(H1N1)pdm09 as the cause on May 3, 2009. The school was closed on May 1, 2009 and re-opened May 11, 2009.

To characterize clinical and epidemiologic features of A(H1N1)pdm09 illness and spread in the community, a telephone survey of households with at least one child enrolled in any of the community schools was conducted May 15 through June 5, 2009. Among consenting households, an adult respondent provided information about household characteristics and illness among all household members. Household information included the number of household members and sleeping rooms, self-identification as Aboriginal/non-Aboriginal, and among Aboriginal participants residency on-/off-reserve. Individual-level information included age, flu-like symptoms and related dates of onset, days spent in bed, health care visits, comorbidity (corresponding to high-risk categories specified by the National Advisory Committee on Immunization), and receipt of 2008–2009 and/or 2007–2008 TIV.[3]

To validate clinical case definitions, households with at least one member reporting ILI (fever and cough plus ≥1 of headache, general aches, sore throat, and/or prostration since April 1, 2009) were subsequently invited to provide blood specimens from both symptomatic and asymptomatic household members. Antibody response to A(H1N1)pdm09 was measured by the hemagglutination inhibition and micro-neutralization assays according to procedures described earlier.[1] As previously described,[1] serology and RT-PCR testing indicated that the outbreak was mainly confined to households of the initially affected school A and among Aboriginal people who lived on-reserve in the surrounding community. Thus, analysis of A(H1N1)pdm09 clinical and epidemiologic features was restricted to elementary school and on-reserve participants.[1]

Data analysis

Descriptive features including the proportion with ILI and medically attended ILI (MAILI) as well as the distribution by age, comorbidity, Aboriginality, household density, and vaccination status for school A, on-reserve participants, and both combined were derived. The SAR was defined as the proportion of household members who developed symptoms after the index case within a household. We present SAR by age, Aboriginality, and 2008–2009 TIV receipt. Among those with ILI, the duration of illness was estimated using information on the date of symptom onset and resolution as reported by participants. Individuals who still had symptoms at the time of interview were treated as right censored, that is, illness had not ended yet.

We fit non-parametric Kaplan–Meier distribution to the data to estimate median duration. For comparison, we also fit log-logistic distribution. Based on the information collected during interviews, we used generalized linear mixed models (GLMM) for binary outcomes to compute risk factors for transmission while accounting for within household clustering and adjusting for other covariates.

The SI is the duration between onset of symptoms in an index and a secondary case.[4,5] SI was estimated using data from infector/infectee pairs in the households where a single infector could be identified and date of onset was known for both. For these analyses, we considered two scenarios where both index and secondary case had ILI (no. of pairs = 15) and where index case was laboratory-confirmed and the secondary case had ILI (no. of pairs = 6). We assumed that transmission was possible only if the delay between symptom onset of the index case (infector) and of the secondary case (infectee) in the household was ≥1 day. Thus, according to this assumption, it is not possible for both the index and secondary case to start symptoms on the same day. We fit Weibull, gamma, log-normal, and log-logistic parametric models to the number of days, and the Weibull model achieved the lowest Akaike information criterion (AIC) of these distributions. From the Weibull distribution, we computed median serial interval and its 95% confidence interval (CI).

This survey was conducted as a public health authorized outbreak investigation, and research ethics board review was not required. However, ethics review and approval were obtained prior to blood collection.

Results

Participant characteristics

Outbreak details, including predominant involvement of school A and Aboriginal on-reserve residents and related epidemic curves of ILI, are available in prior publication.[1]

The overall analysis of epidemiologic characteristics based on the telephone survey included 408 participants, 253 from school A and 191 participants who lived on- reserve including 36 who were also part of the school A population.

Overall, characteristics of the school A and on-reserve participants were similar with some exceptions. The school A-associated participants were slightly younger than the on-reserve participants (median age 13 versus 18 years, respectively). A higher proportion of on-reserve versus school A participants had an underlying chronic condition (14% versus 5%) and received 2008–2009 TIV (38% versus 21%) as is recognized from other community surveys comparing Aboriginal to non-Aboriginal populations.[6,7] There was suggestion of greater crowding among on-reserve households. The proportion of participants living in households in the fourth quartile of density was greater among those living on-reserve (39%) compared to school A participants overall (25%) (Table 1). Mean and median household size for the school A population were 4·1 and 4·0 (range: 1–10), whereas for the on-reserve population, it was 4·7 and 5 (range: 1–8), respectively. Mean (SD) and median number of people per room were 1·38 (0·37) and 1·33 for school A and 1·47 (0·66) and 1·33 for on-reserve participants.

Table 1. Distribution of ILI and MAILI among school A, on-reserve, and both combined, rural community of British Columbia, Canada, April–May 2009

	School A ***n* = 253**			**On-reserve** ***n* = 191**			**Combined** ***n* = 408**		
	Overall ***n* (%)***	**ILI** ***n* (%)****	**MAILI** ***n* (%)****	**Overall** ***n* (%)***	**ILI** ***n* (%)****	**MAILI** ***n* (%)****	**Overall** ***n* (%)***	**ILI** ***n* (%)****	**MAILI** ***n* (%)****
Overall attack rate		66 (26)	25 (10)		44 (23)	25 (13)		92 (23)	36 (9)
Age category (years)									
1–8	67 (26)	32 (48)	14 (21)	42 (22)	16 (38)	14 (33)	96 (24)	37 (39)	18 (19)
9–19	86 (34)	22 (26)	7 (8)	58 (30)	12 (21)	5 (9)	135 (33)	29 (21)	9 (7)
20–49	89 (35)	11 (12)	3 (3)	65 (34)	10 (15)	3 (5)	144 (35)	20 (14)	6 (4)
50–64	10 (4)	1 (10)	1 (10)	19 (10)	6 (32)	3 (16)	25 (6)	6 (24)	3 (12)
>64	1 (0)	0 (0)	0 (0)	7 (4)	0 (0)	0 (0)	8 (2)	0 (0)	0 (0)
Median (range)	13 (1–66)			18 (1–86)			15 (1–86)		
Sex									
Female	132 (53)	33 (25)	13 (10)	106 (56)	28 (26)	17 (16)	217 (54)	50 (23)	22 (10)
Male	118 (47)	32 (27)	12 (10)	83 (44)	15 (18)	8 (10)	186 (46)	40 (22)	14 (8)
Chronic conditions									
No	240 (95)	62 (26)	23 (10)	164 (86)	34 (21)	20 (12)	368 (90)	78 (21)	29 (8)
Yes	13 (5)	4 (31)	2 (15)	27 (14)	10 (37)	5 (19)	40 (10)	14 (35)	7 (18)
2008–2009 vaccination status									
No	208 (82)	47 (23)	13 (6)	125 (65)	20 (16)	9 (7)	318 (78)	63 (20)	18 (6)
Yes	45 (18)	19 (42)	12 (27)	66 (35)	24 (36)	16 (24)	90 (22)	29 (32)	18 (20)
2007–08 vaccination status									
No	197 (79)	42 (22)	11 (6)	115 (61)	16 (14)	7 (6)	299 (75)	56 (19)	16 (5)
Yes	53 (21)	24 (45)	14 (26)	72 (38)	26 (36)	17 (24)	100 (25)	34 (34)	19 (19)
Aboriginal people									
No	180 (77)	43 (24)	8 (4)	–	–	–	180 (46)	43 (24)	8 (4)
Yes, off-reserve	18 (8)	2 (11)	1 (6)	–	–	–	18 (5)	2 (11)	1 (6)
Yes, on-reserve	36 (15)	18 (50)	14 (39)	–	44 (23)	25 (13)	191 (49)	44 (23)	25 (13)
Household density									
1st quartile	49 (21)	10 (20)	3 (6)	49 (26)	13 (27)	5 (10)	94 (24)	22 (23)	7 (7)
2nd quartile	102 (44)	23 (23)	2 (2)	33 (17)	7 (21)	4 (12)	135 (35)	30 (22)	6 (4)
3rd quartile	22 (10)	3 (14)	2 (9)	35 (18)	2 (6)	2 (6)	51 (13)	5 (10)	4 (8)
4th quartile	58 (25)	24 (41)	17 (29)	74 (39)	22 (30)	14 (19)	106 (27)	29 (27)	18 (17)
Travel outside BC									
None	211 (84)	54 (26)	21 (10)	176 (92)	42 (24)	25 (14)	354 (87)	78 (22)	32 (9)
Mexico	3 (1)	1 (33)	1 (33)	0 (0)	0	0	3 (1)	1 (33)	1 (33)
Other N. America	37 (15)	11 (30)	3 (8)	15 (8)	2 (13)	0 (0)	49 (12)	13 (27)	3 (6)
Outside N. America	0	0	0	0	0	0	0	0	0

ILI, influenza-like illness = fever/cough plus one of headache, general aches, sore throat, prostration since April 1, 2009; MAILI, medically attended ILI.

*Column percent showing overall distribution.

**Row percent: *n/N*

Illness profile

The overall ILI rate was comparable among school A versus on-reserve participants (26% versus 23%); however, more on-reserve participants sought care for their illness (25/66 = 38% versus 25/44 = 57%) (Table 1). The ILI rate decreased with age: higher in children 1–8 years of age (yoa) among school A (48%), on-reserve (38%), and overall (39%) participants and falling to ∼10% in working-age adults in school A. There were few elderly participants (n = 8). Those with chronic conditions also had higher frequency of ILI overall (35% versus 21%) and in school A (31% versus 26%) and among on-reserve participants (37% versus 21%). The rate of MAILI was also higher among those with comorbidity (18% versus 8%). Those in the 4th quartile of household density also had higher ILI and MAILI overall and in both groups. Among school A participants, those living on-reserve had higher ILI (50% versus 11%, 24%) and MAILI (39% versus 6%, 4%) than those off-reserve or non-Aboriginal participants. Those who received 2008–2009 TIV also had higher ILI (32% versus 20%) and MAILI (20% versus 6%) rates overall evident in both school A and on-reserve participants.

The median interval between onset of symptoms and seeking medical care for ILI was 5·0 days (95% CI: 4·0 – 8·0). This interval was significantly longer for on-reserve compared to school A participants (8·0, 95% CI: 8·0–9·0 versus 4·5, 95% CI: 3·0–6·0 days). A comparable but small proportion sought care within 48 hours of onset of symptom onset [3/15 (20%) versus 3/16 (19%)]. None was prescribed antivirals and none was hospitalized.

Duration of illness

Median duration of illness was 9 days (95% CI: 6–10) (Figure 1). Of 92 individuals with ILI, 34 (37%) reported mild, 40 (43%) moderate, and 18 (20%) severe illness. Median duration of illness varied by self-reported severity of illness: mild 4 days (95% CI: 3–7), moderate 8 days (5–14), and severe 14 days (9- not estimated owing to censoring); P = 0·001. Median duration of illness among the age group 9–19 years [6 days (3–8)] was significantly shorter than among those >19 years (10 days (9- unestimated, P = 0·01), but not significantly different from those <9 years [7 days (5–14), P = 0·3]. Those with comorbidity also had longer duration of illness [21 days (4- unestimated)] than those without [9 days (6–10) (P = 0·05)]. On-reserve participants also had slightly longer duration of illness compared to non-Aboriginal people [9 days (7–14) versus 7 days (4–12)]; P = 0·18.

Risk factors

In multivariable GLMM analysis among school A and on-reserve households combined, younger age (1–8 yoa: OR = 5·2, 95% CI: 2·61–10·36; 9–19 yoa: OR = 1·87, 95% CI: 0·95–3·69 compared to ≥20 yoa), presence of comorbidity (OR = 2·65, 95% CI: 1·16–6·05), and receipt of 2008–2009 TIV (OR = 2·38, 95% CI: 1·26–4·5) were associated with increased risk of A(H1N1)pdm09-related illness (Table 2). Sample size did not support estimates by specific comorbidity.

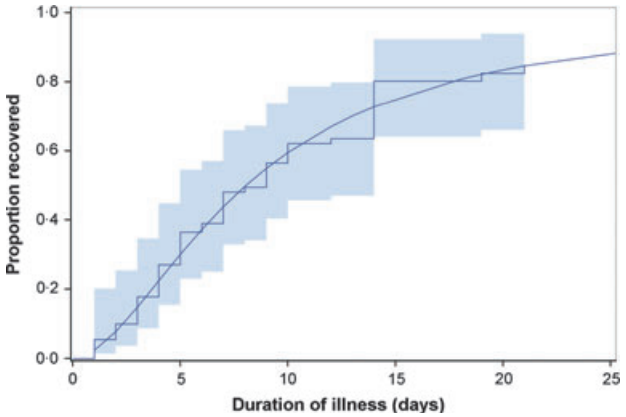

Figure 1. Estimated proportion of people recovered from ILI by number of days after symptom onset. Step line presents non-parametric distribution, and solid smooth line presents log-logistic model-based estimates. Shaded area is 95% confidence band around non-parametric estimate. We found that 50% of people recovered within 9 days (95% CI: 6–10).

Among school A participants, younger age (1–8 yoa: OR = 9·33, 95% CI: 3·82–22·82; 9–19 yoa: OR = 2·76 95% CI: 1·14–6·17 compared to ≥20 yoa) and having received 2008–2009 TIV (OR = 4·53, 95% CI: 1·86–10·99) were each independently associated with A(H1N1)pdm09-related illness (Table S1). Among on-reserve participants, younger age (1–8 yoa: OR = 4·63, 95% CI: 1·63–13·18; 9–19 yoa: OR = 1·84, 95% CI: 0·65–5·23 compared to ≥20 yoa), presence of comorbidity (OR = 3·40, 95% CI: 1·12–10·30), and receipt of 2008–2009 TIV (OR = 2·78, 95% CI: 1·90–6·41) were each associated with A(H1N1)pdm09-related illness (Table S2).

Secondary cases

Overall, the SAR was 49/339 (22%). The SAR among school A households was 32/119 (27%); excluding on-reserve households, this was 19/94 (20%). The SAR among on-reserve households was 23/94 (24%). The SAR among school A households that were also on-reserve was 13/25 (52%). The SAR was higher overall among younger age groups: <1 yoa: 38%, 1–4 yoa 50%, 5–9 yoa: 20%, 10–19 yoa: 13%, 20–49 yoa: 20%, and 50–64 yoa (0%) (Table 3). Among school A participants, respective proportions were 53%, 57%, 26%, 12%, 0%, and 0%, and for school A, excluding on-reserve participants were 46%, 40%, 15%, 12%, 0%, 0%.

Table 2. Risk factors for A(H1N1)pdm09-related Illness in both school A and on-reserve participants*

	Crude	Multivariable model** ILI = 83, non-ILI = 281	Multivariable model*** ILI = 87, non-ILI = 284	Multivariable model† ILI = 90, non-ILI = 300
Covariates	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
Age (years)				
1–8	3·69 (1·96–6·96)	4·63 (2·25–9·52)	4·79 (2·38–9·65)	5·2 (2·61–10·36)
9–19	1·41 (0·74–2·67)	1·95 (0·97–3·9)	1·85 (0·94–3·65)	1·87 (0·95–3·69)
≥20	1	1	1	
Chronic conditions				
No	1	1	1	1
Yes	2·2 (1·02–4·74)	2·58 (1·1–6·04)	2·47 (1·06–5·73)	2·65 (1·16–6·05)
Received 2008–2009 TIV				
No	1	1	1	1
Yes	2·06 (1·14–3·71)	2·68 (1·37–5·25)	2·61 (1·34–5·09)	2·38 (1·26–4·5)
Aboriginal people††				
No	1	1	1	
On-reserve Aboriginal people	0·96 (0·55–1·67)	0·74 (0·4–1·4)	0·71 (0·39–1·3)	Not included
Household density				
1st–3rd	1	1		
4th quartile	1·34 (0·73–2·46)	1·17 (0·6–2·28)	Not included	Not included

*Estimates based on generalized linear mixed models.
**With Aboriginal people residing on-reserve and household density.
***With Aboriginal people residing on-reserve.
†Without Aboriginal people residing on-reserve and household density.
††Off-reserve Aboriginal people were excluded from analysis owing to sparse data.

Serial interval

The estimated median SI using both index and secondary case pairs with ILI was 3·4 days (95% CI: 2·1–5·13) (Figure 2). When we used a laboratory-confirmed index case, the median SI was 4·21 days (1·6–9·78). The maximum interval between onset dates of primary and secondary cases was 10 days; in further sensitivity analysis based only on primary–secondary case intervals of ≤7 days, the SI was estimated at 2·8 days.

Discussion

In this paper, we report findings from one of the earliest outbreak investigations in Canada to characterize A(H1N1)pdm09-related illness during the first weeks of the first pandemic wave. We capitalized on a discrete, intense but community-wide outbreak involving households associated with a first affected school and on-reserve Aboriginal people to estimate epidemiologic characteristics uniquely across age groups and among on- and off-reserve participants. Overall, we identified illness that was mostly mild and self-limited with no hospitalizations or antiviral prescriptions. Young children, those with chronic diseases, and those who previously received the 2008–2009 seasonal influenza vaccine were more likely overall to report A(H1N1)pdm09-related illness. Participants on-reserve were more likely to report comorbidity and greater household crowding; they also reported higher ILI, MAILI, and SARs. Overall, the median interval between symptom onset and care seeking was about 5 days, and median time to recovery was 9 days, both also longer among on-reserve participants. A similarly low proportion (20%) of on-/off-reserve participants sought care within 48 hours; access to health care services in the region is generally considered comparable both on-/off-reserve. We identified a very short median SI of about 3 days, suggesting a brief period to intervene in prevention and control.

Most of the individuals in this community had self-limited febrile respiratory illness. The median duration of self-reported illness of 9 days was slightly longer but within the range of estimates from other studies in the United States (5 and 6 days from New York School outbreak)[8,9] 6 days in the US Air Force Academy outbreak,[10] Canada (7 days from Ontario)[11], and Germany (9 days in a household transmission study).[12] These estimates of illness duration are also comparable to previous estimates for seasonal influenza: Ng *et al.*[13] reported a median duration for seasonal influenza in 2007 and 2008 of 9 days among those who received oseltamivir and 11 days among those who did not, although others have reported no difference in

Table 3. Secondary attack rates among on-reserve and school A households, and both combined rural community of British Columbia, Canada, April–May 2009

Covariates	School A and on-reserve combined		School A		On-reserve	
	n/N	SAR (95% CI)	*n/N*	SAR (95% CI)	*n/N*	SAR (95% CI)
Overall	42/339	22 (16–28)	32/119	27 (19–35)	23/94	24 (16–33)
Aboriginal people						
No	18/83	22 (13–31)	18/83	22 (13–31)	–	–
Yes, off-reserve	0/5	0	0/5	0	–	–
Yes, on-reserve	23/94	24 (16–33)	13/25	52 (32–72)	–	–
Age category (years)						
<1	10/26	38 (20–57)	9/17	53 (29–77)	4/13	31 (5–56)
1–4	9/18	50 (27–73)	8/14	57 (31–83)	5/8	63 (28–97)
5–8	11/54	20 (10–31)	9/34	26 (11–42)	7/28	25 (9–41)
9–19	10/77	13 (5–21)	6/51	12 (3–21)	5/34	15 (3–27)
20–49	2/10	20 (0–45)	0/3	0	2/8	25 (0–56)
50–64	0/3	0	0/0	0	0/3	0
Received 2008-09 TIV						
No	24/136	18 (11–24)	19/94	20 (12–28)	7/50	14 (4–24)
Yes	18/52	35 (22–48)	13/25	52 (32–72)	16/44	36 (22–51)

SAR, secondary attack rate; CI, confidence interval; On-reserve, aboriginal people residing on-reserve.

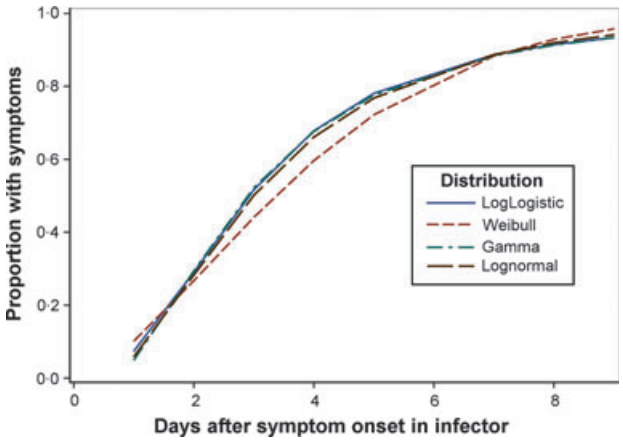

Figure 2. Estimated serial intervals for A(H1N1)pdm09-related illness using Weibull, gamma, lognormal, and log-logistic parametric models.

duration of illness by antiviral use.[9,12] In our study population, antivirals were not prescribed to any patient who sought care. Other studies based on surveillance data may have underestimated the actual duration owing to right censoring and a mix of patients who used antivirals and those who did not.[10,11]

As in our investigation, the preponderance of epidemiological and immunological data support an age-related pattern of A(H1N1)pdm09 risk.[9,13–16] People with comorbidities were more likely to report ILI in our study but whether this reflects a greater tendency to recognize and declare illness (reporting bias) versus a greater risk of acquiring infection is uncertain; comorbidity has also been reported to be associated with higher risk of more severe disease.[17–19] Overall, the targeting of prevention and control measures to people with comorbidities likely has implications for reducing A(H1N1)pdm09-related morbidity and mortality.

The SAR is an important indicator for influenza transmission, assessing the impact of interventions and planning for future pandemics. In our study, the overall SAR was 22%, higher in those age <1 year (38%) and 1–4 years (50%). There is a wide variation in report of SAR from various settings, which is not unexpected. Our estimates are similar to household transmission studies in Germany (26%),[12] Kenya (26%),[20] and the United States (18%).[8] These estimates were slightly lower than other studies in Canada (Sikora C et al: 30%; Papenburg J et al: any ILI: 29%, laboratory-confirmed A(H1N1)pdm09 ILI: 26%, and laboratory-confirmed A(H1N1)pdm09 including asymptomatic infections: 45%)[15,21] and the United States (27·3%).[22] Conversely, our estimates are higher than others reported from Japan (7·6%),[23] UK (17%),[24] and United States (4–13%; 11%; 14·3%).[9,16,25] Many factors affect transmission and hence SAR within households including age, antiviral use, and ascertainment of index and secondary cases or contacts, as well as socio-environmental factors such as climate, crowding, and control behaviors such as the use of masks and hand washing. The initiation of treatment for the index case upon illness onset or the following day was associated with a 42% reduction in secondary

infections in households in a Japanese study.[26] In the study by Morgan *et al.*[16] (SAR: 4–13%), most of the index cases (72%) had received treatment. In the New York school household transmission study (SAR: 11%), about one quarter (26%) of index cases took antiviral treatment and 71% started within 2 days of illness onset.[9] About 7% of the household contacts also received antiviral prophylaxis. In the Suess *et al.*[12] study, SAR among those who did not receive prophylaxis was 26%, very close to our own measured rate. Reduced virus shedding with antiviral treatment for seasonal and A(H1N1)pdm09 viruses has been reported.[13,27,28] Thus, differences in SAR may also in part be attributed to variation in antiviral use. The pattern we found of higher SAR among children than adults (highest in 0–4 and lowest in ≥50 years) is also consistent with other studies.[9,15,16] A higher SAR among children may be explained by differences in cross-protective innate or acquired immunity as well as contact and hygiene patterns.[22,29]

The spread of an infection is determined by the average number of secondary cases generated by an infectious case. This number is called the basic reproductive number (R_0) when the population is completely susceptible and the effective reproductive number (R) when the population is partially immune. The serial interval is an important parameter as it affects the estimation of R_0.[30] It also determines the rate of growth of an epidemic (R/serial interval): for a given reproductive number (R), an epidemic will grow faster with a shorter serial interval.[31] These two parameters together are also useful in evaluating the impact of interventions employed to control the outbreak. Thus, estimating the serial interval is important in responding to a novel pathogen such as A(H1N1)pdm09 and convergence of estimates from several sources and settings lends credibility to the measure overall.

Our estimate of the A(H1N1)pdm09 serial interval (3·4 days) is comparable to that reported by others using similar methods and laboratory-confirmed index cases from various countries and settings including United States (2·7–4 days),[8,9,16,25,32] Canada (4–5 days[11] and 3·4 days[15]), Mexico (3·2 days),[22] Hong Kong (3·2 days),[33] Australia (2·9 days),[34] and Germany (3 days).[12] These estimates of serial interval are also similar to those of seasonal influenza estimated previously (mean: 3·6 days) and concurrently with A(H1N1)pdm09 activity (3·4 days for H3N2).[5,33]

As discussed in previous publication,[1] there are several limitations warranting cautious interpretation of our results. The study relied upon a non-specific clinical outcome (ILI) for defining A(H1N1)pdm09-related illness. There are many causes of ILI as evidenced by other contributing viruses identified through passive surveillance during the study period (see prior publication).[1] Other respiratory viruses detected from the local community during that period included coronavirus and rhinovirus/enterovirus. We thus attempted to validate the ILI case definition based on A(H1N1)pdm09 sero-positive status and used that to define the study population, but participation in the sero-survey was self-selected and sample size was small. Secondly, we relied on report by one adult for all household members. ILI experience, duration of illness, and TIV history may have been less well known for other household members. Thirdly, sample size was small with large confidence intervals especially for stratified analyses. In comparing school A and on-reserve households, we identified some overlap including 36 of 191 on-reserve participants who also attended school A. To address this, we separately presented estimates for school A participants with and without on-reserve residency but this further reduced sample size, introducing variability.

In summary, during a rural community outbreak of pandemic H1N1-related illness, we identified substantial clinical ILI attack rates >20% with secondary household attack rates as high as 50% in young children on-reserve. Young children and those with comorbidities were at higher risk of illness and those living on-reserve tended also to have higher ILI, MAILI, and SAR. The reasons for this warrant better understanding. Like others, we identified a short serial interval suggesting a narrow period to prevent transmission. These early features of the first wave of the 2009 pandemic should also be considered in preparing for emergence of the next novel influenza virus.

Authors contributions

Naveed Z. Janjua conceived/designed the study, did analysis and interpretation, wrote first draft and did revisions. Danuta M. Skowronski conceived/designed the study, and contributed to analysis, interpretation and revisions. Travis S. Hottes, and Gaston De Serres contributed to concept/design, analysis, interpretation and revisions. William Osei, Evan Adams, Marcus Lem, David Bowering and David M. Patrick, contributed to concept, design and revisions. Patrick Tang, and Martin Petric oversaw laboratory testing and contributed to design and revisions.

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Conflicts of interest

Danuta M. Skowronski was lead investigator to an unrelated study for which influenza vaccine was provided free by Sanofi-Pasteur. Gaston De Serres has received research grants from GlaxoSmithKline and Sanofi-Pasteur for unrelated studies in the past 36 months. All other authors had no conflicts.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. Risk factors for A(H1N1)pdm09-related illness in elementary school population.

Table S2. Risk factors for A(H1N1)pdm09-related illness among on-reserve Aboriginal participants.

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