Demographic patterns of exposure and transmission for a rural Canadian community outbreak of COVID-19, 2020

Kaitlin Patterson¹*, Mathieu Chalifoux², Rita Gad², Shannon Leblanc², Paige Paulsen², Louise Boudreau³, Theresa Mazerolle⁴, Mariane Pâquet²

Abstract

Background: A coronavirus disease 2019 (COVID-19) community outbreak was declared October 5–December 3, 2020, in the Restigouche region of New Brunswick, Canada. This article describes the epidemiological characteristics of the outbreak and assesses factors associated with its transmission in rural communities, informing public health measures and programming.

Methods: A provincial line list was developed from case and contact interviews. Descriptive epidemiological methods were used to characterize the outbreak. Incidence rates among contacts, and by gender for the regional population were estimated.

Results: There were 83 laboratory-confirmed cases of COVID-19 identified during the observation period. The case ages ranged from 10–89 years of age (median age group was 40–59 years of age) and 51.2% of the cases were male. Symptom onset dates ranged from September 27–October 27, 2020, with 83% of cases being symptomatic. A cluster of early cases at a social event led to multiple workplace outbreaks, though the majority of cases were linked to household transmission. Complex and overlapping social networks resulted in multiple exposure events and that obscured transmission pathways. The incidence rate among men was higher than women, men were significantly more likely to have transmission exposure at their workplace than women, and men were the most common index cases within a household. No transmission in school settings among children was documented despite multiple exposures.

Conclusion: This investigation highlighted the gendered nature and complexity of a COVID-19 outbreak in a rural Canadian community. Targeted action at workplaces and strategic messaging towards men are likely required to increase awareness and adherence to public health measures to reduce transmission in these settings.

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Affiliations

¹ Canadian Field Epidemiology Program, Public Health Agency of Canada, Ottawa, ON

² New Brunswick Department of Health, Fredericton, NB

³ Vitalité Health Network, Bathurst, NB

⁴ Vitalité Health Network, Richibucto, NB

*Correspondence:

kaitlin.patterson@phac-aspc.gc.ca



Introduction

The Restigouche region is located in north-central part of New Brunswick and has a population of 30,955 residents over a land mass of 8,580 km² (1). With a population density of 3.6 people per km², and no urban centres with a population over 30,000 people, Restigouche is considered to be a rural region (1). Between January 1 and October 4, 2020, the Restigouche region reported only 98 cases and relatively low community transmission rates of coronavirus disease 2019 (COVID-19). Here we describe a community outbreak within the Restigouche region where multiple chains of transmission resulted in 83 cases of COVID-19 identified between October 5 and November 4, 2020. The outbreak was declared on October 9, 2020, following the identification of an initial cluster of seven cases following a social gathering.

There is a paucity of reporting on rural COVID-19 outbreaks with complex overlapping social networks in the published literature. Because many rural and remote areas have limited capacity to manage and treat COVID-19, essential services may be rapidly paralyzed as individuals are implicated in outbreaks as either cases or contacts. Therefore, evidence is needed to inform targeted public health measures and programming for outbreak prevention and management in these rural communities. The objectives of this outbreak analysis are to describe the outbreak, to assess factors that led to spread and transmission and to inform recommendations for public health measures and programming in rural communities.

Methods

Public health nurses from both of New Brunswick's health networks (*Réseau de santé Vitalité* and Horizon Health Network) led data collection through case investigations and contact tracing interviews. The New Brunswick Department of Health also requested the assistance of the Canadian Field Epidemiology Program to provide epidemiological support to the investigation team, and the investigation was completed collaboratively between these agencies.

Sources of data included detailed case and contact interviews, a provincial case and contact line, and documentation of public health measures implemented during the outbreak (e.g. web pages, press releases, internal government documents).

Outbreak cases were defined as those with a laboratoryconfirmed case using polymerase chain reaction (PCR) tests with nucleic acid detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), were a resident and/or visitor to the Restigouche region, whose episode date occurred from September 27, 2020, to November 5, 2020 (inclusive), and their source of acquisition was not travel-associated. Each case was assigned an episode date for analysis using either the date of symptom onset, or for asymptomatic cases the date of their positive laboratory specimen collection. The outbreak was declared over on December 3, 2020 (28 days or two COVID-19 incubation periods) from the last confirmed case on November 4, 2020 (2).

Investigation methods included descriptive epidemiology (e.g. frequency tables, epidemiological curves) using the available data collection tools, and additional case interviews to inform the extent of the outbreak and development of the social network diagrams. To examine potential transmission settings, we defined cluster events/locations where three or more cases were epidemiologically linked.

When multiple exposure settings were identified, a setting of most likely transmission was assigned for each case (family/ household, social interaction and/or workplace), from likeliest to least likely. To ascertain most likely exposure settings, we examined the infectious period of cases present at each setting based on symptom onset date (if symptomatic) or specimen collection date (if asymptomatic) and risk of exposure. Cases who were secondary cases within their household (as defined by symptom onset date or testing date) were categorized as household exposure.

All cases were interviewed to identify how the case may have been exposed (backwards contact tracing) and any contacts the case may have exposed (forward contact tracing). At the outset of the outbreak, there were no public health recommendations for people in the community to wear a mask and no vaccine was available. Individuals that had close contact (i.e. less than two meters away for 15 or more minutes) with cases during their infectious period were classified as contacts, as per recommendations outlined by the Canadian government at the time of this outbreak. We calculated the secondary attack rate among contacts by dividing the number of known contacts that subsequently became cases by the total number of identified contacts.

We calculated the regional incidence rates overall and by age and gender. Gender, as part of the case investigation form, was defined as the socially constructed roles, behaviours, expressions and identities of girls, women, boys, men and gender diverse people (options for this variable were male, female, another gender or unknown). For the overall incidence rate, we divided the total number of laboratory-confirmed cases by the number of Restigouche residents according to the 2016 census (1). Then we divided the number of laboratory-confirmed cases by age/ gender by their respective resident populations according to the census.

Cross tabulations (chi-squared or Fisher's exact for categorical or binary variables) and t-tests (for continuous variables) were used

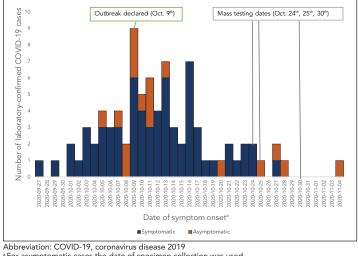
to examine differences in severity outcomes, number of contacts, exposures and testing delays by age and gender. Descriptive statistics were conducted using STATA, the charts were produced using excel and the social network diagram was produced in R.

Results

Case and testing demographics

A total of 83 laboratory-confirmed cases were associated with the community outbreak in Restigouche region between September 27, 2020, and November 5, 2020 (Figure 1) and 5,312 tests were conducted. None of the cases was genetically sequenced. Additionally, during the outbreak, three mass testing days were offered for asymptomatic individuals in Restigouche region (1,985 tests were conducted October 24, 25 and 30 during this mass testing). Slightly more females (58%) were tested than males (42%), and the majority (65%) of the tests were conducted among 40-79 year-olds.

Figure 1: Number of confirmed outbreak cases of COVID-19 in Restigouche region, New Brunswick by date of symptom onset^a (n=83), between September 27 and November 5, 2020



^a For asymptomatic cases the date of specimen collection was used

The overall test positivity rate was 1.70% (2.76% excluding the mass testing) during the outbreak period. Among the laboratory confirmed cases, the highest proportion of cases was among 40-49 year-olds (38%), and 52% of cases were male (Table 1). Overall, males had a higher incidence rate than females (Figure 2). None of the cases reported identifying as "another gender" or "unknown".

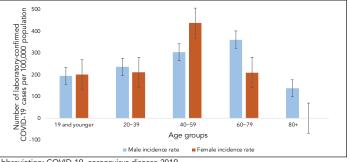
Table 1: Descriptive data on confirmed COVID-19 cases in Restigouche region, New Brunswick between September 27 and November 5, 2020

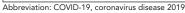
Characteristics	Number of confirmed cases	
	n	%
Age (years)	83	100
19 and younger	10	12.1
20–39	13	15.7
40–59	32	38.6
60–79	27	32.5
80 and older	1	1.2
Gender		
Male	43	51.8
Female	40	48.2
Symptoms at time of interview		
Asymptomatic	14	16.9
Symptomatic	69	83.1
Severity ^a		
Hospitalizations	5	6.0
Intensive care unit admissions	3	3.6
Mechanical ventilation	2	2.4
Deceased	2	2.4
Testing delay among symptomatic cases		
Range in time to testing after symptom onset (days)	0–12	N/A
Mean time to testing after symptom onset (days)	2.78	N/A
Median time to testing after symptom onset (days)	3	N/A
Contacts ^b		
Range in number of contacts	0-34	N/A
Mean number of contacts	6.43	N/A
Median number of contacts	4.5	N/A

Abbreviations: COVID-19, coronavirus disease 2019; N/A, not applicable Severity categories are not mutually exclusive. A total of five cases were hospitalized, among those five, three were admitted to the intensive care unit, among those three, two required mechanical ventilation and both of those cases died

^b These numbers exclude cases 19 years of age and under due to the large influence of the number of school contacts

Figure 2: Incidence rate of COVID-19 confirmed cases by age and gender in the Restigouche region, New Brunswick identified between September 27 and November 5, 2020





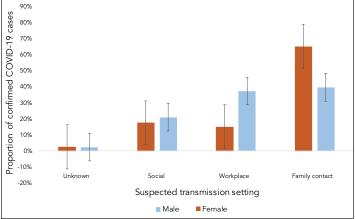
An initial cluster of seven cases was identified following a social gathering; no masking or physical distancing was reported among individuals attending the event. Symptom onset date and contact tracing were used to identify the probable source case (earliest symptom onset date with laboratory-confirmed COVID-19). None of the early cases had any travel exposure history or contact with known cases outside of the community. Because Restigouche region is on the border of New Brunswick and Québec, and as the Québec regions (Gaspésie-Îles-de-la-Madeleine and Bas Saint Laurent) bordering New Brunswick were experiencing community transmission and several outbreaks in the weeks leading up to this outbreak (3), the most likely introduction was as a result of interprovincial travel. As part of the "Atlantic Bubble", New Brunswick borders were controlled for interprovincial travel outside the Atlantic Provinces (4); however, residents on both sides of the Québec/New Brunswick border were exempt from travel restrictions if they were travelling for essential reasons (e.g. work, school and emergency services) (5). There was a series of indoor and outdoor events/ gatherings held in the weeks prior to the identification of the outbreak that were mentioned during case investigations that did not fall within standard exposure periods (e.g. more than 14 days prior to episode onset). However, these events had both Québec and New Brunswick residents in attendance and may mean that some early cases were undetected.

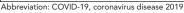
The mean number of contacts per case was 6.43, with a total of 470 contacts of adult cases identified. Both men and women had similar mean numbers of reported contacts (6.25 and 6.61, respectively), but the median number of contacts for men was higher (6 versus 4). Of these contacts, 39 subsequently tested positive, resulting in a secondary attack rate of approximately 8.2% among identified case contacts. The remaining cases were not identified through contact tracing prior to testing positive for COVID-19. Forty-two were linked to cases through backwards contact tracing.

Among laboratory confirmed cases, men aged 20–39 years sought testing significantly longer after symptom onset (3.57 days after symptom onset) than women (1.2 days after symptom onset) (p>0.05). Additionally, cases aged 60 years or older (4.64 days after symptom onset) sought testing significantly (p>0.01) longer after symptom onset than cases younger than 60 years of age (2.63 days after symptom onset). Men and women had similar proportions of asymptomatic cases at time of testing, hospitalizations, admissions to intensive care units, mechanical ventilations, and deaths.

Among cases younger than 19 years of age, 210 contacts were identified and isolated (mean number of contacts per case was 23.33, significantly higher than cases older than 19 years of age). There were no secondary cases identified and no transmission observed in schools, school buses or child/youth-related activities. All adolescent cases were linked to household contacts (none were the primary case of the household) and resulted in no secondary transmission to non-household contacts, despite exposing contacts during their infectious periods. Among all cases, there were significant differences in exposure by gender (**Figure 3**). Women were most likely to be exposed by family and/or household members (67% vs. 40% p>0.05) whereas men were more likely to be exposed at their workplace or through social interactions (60% vs 37% p>0.05).

Figure 3: Transmission settings for COVID-19 outbreak in Restigouche region, New Brunswick by gender, identified between September 27 and November 5, 2020

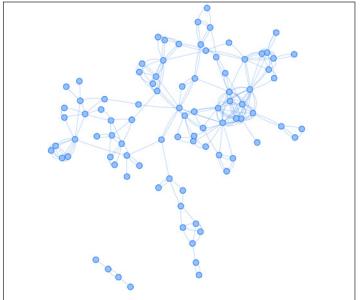




Clusters

Through case interviews, contact tracing and analysis of the local line list, we were able to link all cases to two main transmission chains (**Figure 4**). Additionally, we identified a total of seven clusters of three or more confirmed cases associated with settings, events or locations where transmission may have occurred. A social event likely preceded the majority of transmission chains identified during the community outbreak.

Figure 4: Network analysis of Restigouche region, New Brunswick COVID-19 cases between September 27 and November 5, 2020^{a,b}



Abbreviation: COVID-19, coronavirus disease 2019

^b Due to privacy considerations, the sequence of cases and clusters are not identified in this figure

Each node represents a case

We also identified clusters among social outings with overnight stays and at several workplaces. Finally, we identified one family cluster we were unable to connect with other chains of transmission (Figure 4).

Discussion

Introduction of COVID-19 into Restigouche region most likely occurred through travel for essential reasons across the New Brunswick-Québec borders, given the strict provincial border quarantine measures and absence of evidence of ongoing community transmission prior to the outbreak. The leading hypotheses are linked to a series of indoor and outdoor events/ gatherings held in the weeks prior to the identification of the outbreak. These events had both Québec and New Brunswick residents in attendance. Interprovincial spread of COVID-19 cases due to land travel has been difficult to track throughout Canada, as each case is reported to the public health unit of their residence. Alternatively, it is possible COVID-19 was circulating undetected within the community from another source of introduction, and it was only identified upon reaching a critical threshold, resulting in rapid spread (6). However, undetected widespread community transmission in this case is unlikely, given the relatively short duration and small number of cases linked to this outbreak.

Globally, men have a higher proportion of COVID-19 case counts than women, and experience more severe illness and higher mortality (7). In this outbreak, we also found that the incidence rate among men was significantly higher than among women and that men were more likely to be the index case in workplaces and households, despite fewer men getting tested. Research of other health outcomes has found that male gender expectations within communities and work environments can drive various high-risk behaviours (e.g. poor health seeking behaviours and drinking and driving) (8). Emerging evidence on COVID-19 has found that women are more likely than men to follow government recommendations, take health precautions (e.g. mask-wearing, physical distancing, handwashing and staying at home) and encourage others to take health precautions (9,10). Decreasing adherence to public health measures for COVID-19, such as staying at home, physical distancing and reducing contacts, has been observed over time regardless of gender (11). We also observed that older adults had longer delays in testing and had more contacts than younger adults. Often, older adults delayed seeking care because they underestimated the seriousness of their condition and attributed severity of symptoms as inevitable due to their age (12). Alternatively, older adults may have delayed seeking care because they had issues accessing transportation or don't know where to seek help (12).

Perception of risk of COVID-19 exposure may be underestimated in areas with low community transmission and case numbers. Several case contacts identified through backwards contact tracing were not initially reported as contacts as they did not meet the "two metres/15-minute interaction" criteria to be classified as a contact during the outbreak time period. This lack of reporting may have been as a result of a reluctance to disclose those interactions, or because individuals underestimated the time or overestimated the distance of their interactions (13). Another possibility is that transmission occurred despite those adhering to the two metres/15-minute interaction rule; however, most cases in this outbreak were linked to close contact with a known case. In backward contact tracing studies, an over dispersion effect has been observed, where the likelihood of transmission varies by case, and that certain events and individuals lead to a large number of secondary cases (14). It is possible that not all exposures to cases and/or events were captured.

Complex social networks that led to multiple exposures and transmissions throughout the region were identified. Other rural outbreaks of COVID-19 have been similarly characterized, and alternative approaches have been used to classify exposures and households where these networks occur (15). Modelling has demonstrated that full lockdowns for 14 days in these tightly connected communities can reduce significantly both the extent of the outbreak and the length, potentially reducing cases by 95% (16).

No transmission in schools or between children was detected in this outbreak, despite children being in contact during their infectious period. At the time of the outbreak, children were required to wear masks, all extracurricular activities were cancelled and most schools were using classroom cohorts to mitigate potential spread. Two hundred and ten individuals were required to isolate for 14 days after their last identified exposure in school settings; no cases were subsequently identified among these contacts. This finding is similar to evidence from the global literature that secondary cases in school environments between children are rare for COVID-19, especially when public health measures, such as masking, are being followed (17,18).

Recommendations/implications for public health

Public health moved quickly to contain the outbreak presented here using enhanced non-pharmaceutical public health measures (including mandatory masking in public placement, workplace assessments, gathering limits) and the closure of nonessential services. As the Canadian population is increasingly vaccinated, and public health measures are reduced, it is likely that undervaccinated populations and areas may experience increased numbers of cases and outbreaks. Early evidence is emerging that in rural areas, COVID-19 vaccine hesitancy is higher and vaccine coverage is lower than in urban areas (19).

In preparing for future outbreaks and emergence of cases the following should be considered, particularly if more transmissible variants are introduced:

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- Public health education about the efficacy of public health measures (e.g. mask wearing and physical distancing) has been effective in increasing voluntary compliance with jurisdictional rules and recommendations (6); however, targeted messaging by gender and age is likely required to increase adherence to public health measures specifically among older men (7). In particular, the identification of trusted messengers (e.g. group leaders, peers, friends, family) has been effective in advocating for public health measures, including vaccination, in targeted groups and rural and remote communities (20).
- Less stringent approaches to managing contacts related to school exposures may be warranted; however, risk will be dependent on community rates of transmission, the nature of the exposure, age demographic of students, rates of vaccination and the variant in circulation.
- Communication of risks related to travel and exposure to individuals who have travelled may be necessary in lowprevalence areas, where risks may be perceived as nonexistent.
- If staffing and resources permit, utilizing both forward and backward contact tracing is preferable, using backward contact tracing has resulted in identifying 2–3 times more cases (21). In rural and/or remote regions often with little to no incidence of COVID-19, identifying the source(s) of infection is critical for controlling spread and prevention strategies in the future (22).
- The number of significant interactions not recognized as such was large in this rural setting. Investigations in these settings may benefit from a broader set of criteria for identifying contacts, including lower thresholds for defining exposure interactions (23). Individuals may perceive a fifteenminute interaction as less time (e.g. "I only stopped in to say hi") (24). Improving the clarity of public health measures and addressing changes to the measures are critical for acceptance and adherence (25). While these changes may not be feasible for public health follow-up due to limited resources, this clarification will support individual's ability to assess risk and make decisions in the context of outbreaks and more transmissible variants.

Limitations

Several limitations warrant discussion. First, because 30% of cases presented as asymptomatic certain dynamics of transmission may have been misclassified. In these cases, we used a combination of exposure information and specimen collection date to assess plausibility. Second, we relied on self-reported exposure information, and we only implemented backward contact tracing in the middle of the outbreak. This may have resulted in missed exposures and or transmission events. Third, we did not have any genomic data to identify whether the outbreak was linked to one or more introductions. At the time of this outbreak investigation, whole genome sequencing was not available in New Brunswick. All whole genome sequencing was conducted through the National Microbiology Laboratory in Winnipeg, Manitoba and because 95% of the cases were linked

epidemiologically, sequencing the outbreak cases was not a high priority.

Conclusion

This investigation highlighted the gendered nature and complexity of a COVID-19 outbreak in a rural Canadian community. Targeted action at workplaces and strategic messaging towards men are likely required to increase awareness and adherence to public health measures to reduce transmission in these settings.

Authors' statement

KAP — Conceptualized, obtained datasets, methodology, analyzed and interpreted data, drafted and revised the manuscript MC — Conceptualized, obtained datasets, methodology, interpreted data, revised the manuscript RRG — Conceptualized, obtained datasets, interpreted data, revised the manuscript SL — Conceptualized, obtained datasets, interpreted data, revised the manuscript PP — Analyzed and interpreted data, and revised the manuscript LB — Conceptualized, collected data, obtained datasets, interpreted data, revised the manuscript TM — Conceptualized, collected data, obtained datasets, interpreted data, revised the manuscript MP — Conceptualized, obtained datasets, methodology, interpreted data, revised the manuscript

Competing interests

None.

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