



Community-based COVID-19 outbreak of the B.1.1.7 (Alpha) variant of concern in Newfoundland, February to March 2021

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Abstract

Background: From March 2020 to January 2021, Newfoundland and Labrador experienced 408 coronavirus disease 2019 (COVID-19) cases (incidence 78 per 100,000). In February and March 2021, a community outbreak of the B.1.1.7 (Alpha) variant occurred in the Eastern Regional Health Authority. This article describes the epidemiology of this variant of concern outbreak, identifies settings that likely contributed to spread and informs recommendations for public health measures (PHMs).

Methods: Provincial surveillance data were linked with case interview data and a school class roster. Descriptive epidemiological methods were used to characterize the outbreak. Secondary attack rates (SAR) were calculated for households and classrooms.

Results: This outbreak involved 577 laboratory-confirmed and 38 probable cases. Whole genome sequencing determined cases were B.1.1.7. The median age was 31 years and the highest proportion of cases were in the 15 to 19-year age group (29%); 293 (51%) were female and 140 (24%) were asymptomatic upon identification. Early cases were linked to a high school, sports activities, a restaurant and social gatherings. As the outbreak progressed, cases were associated with household transmission, a daycare, healthcare settings and a workplace. The unadjusted SAR estimate among laboratory-confirmed cases was 24.4% for households and 19.3% for classroom exposures. When adjusted for other potential exposures, SAR estimates were 19.9% for households and 11.3% for classrooms.

Conclusion: This outbreak demonstrated how B.1.1.7 spread rapidly through a community with previously low COVID-19 transmission and few preventative PHMs in place. Implementation and compliance with school and community-based PHMs is critical for preventing transmission during outbreaks.

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Keywords: COVID-19, Canada, variant of concern, outbreak, emerging infectious diseases, household transmission, school transmission, secondary attack rates, public health measures

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Introduction

Coronavirus disease 2019 (COVID-19) is a respiratory disease caused by severe acute respiratory coronavirus 2 (SARS-CoV-2). Variant of concern (VOC) refers to a SARS-CoV-2 lineage characterized by significant genetic mutations that affect its spread, severity, detection, prevention or treatment (1).

The B.1.1.7 (Alpha) VOC was first identified in England in September 2020. The first cases in Canada (Ontario) were identified in December 2020 (2). The B.1.1.7 variant was associated with significantly increased rates of transmission (3,4)



and increased disease severity (5,6) compared to non-VOC SARS-CoV-2.

One of the first community outbreaks of B.1.1.7 in Canada occurred in February 2021 among residents of Newfoundland and Labrador (NL's largest health authority, Eastern Regional Health Authority (Eastern Health), when Canadian health authorities had little experience with the prevention and control of VOCs. Evidence was accumulating about the effectiveness of personal public health measures (PHMs) such as handwashing, mask wearing and physical distancing, and societal PHMs such as quarantine (7).

Newfoundland and Labrador had observed only 408 cases of COVID-19 across the province from March 2020 to January 2021 (incidence: 78 per 100,000) (1). The outbreak of 577 laboratory-confirmed cases in the Eastern Health region occurred primarily in a census metropolitan area of 206,000 population (8) and did not extend into other parts of the province.

The outbreak was identified when a restaurant worker, with no known exposures, became symptomatic on February 4, 2021, and tested positive the following day. On February 6, patrons were advised to seek testing if they had attended the restaurant during the index case's incubation period (9). Mass testing within surrounding communities identified cases and clusters linked to other potential transmission settings.

This outbreak investigation aimed to describe the epidemiology, identify settings that likely contributed to spread and inform recommendations for PHMs. Evaluating the effectiveness of PHMs in various settings was out of scope.

Methods

Eastern Health led data collection and case finding via case interviews and contact tracing. Data sources included case and contact data from the provincial COVID-19 surveillance system, detailed case interview information, a school class roster and documentation of PHMs (e.g. web pages, press releases, and internal government documents).

The provincial definition of a laboratory-confirmed case (9) was a person with confirmation of infection with SARS-CoV-2 documented by:

- Detection of at least one specific gene target by a validated laboratory-based nucleic acid amplification test-based assay (e.g. real-time polymerase chain reaction or nucleic acid sequencing) performed at a community, hospital or reference laboratory (National Microbiology Laboratory or a provincial public health laboratory)

OR

- The detection of at least one specific gene target by a validated point-of-care nucleic acid amplification test that has been deemed acceptable to provide a final result (i.e. does not require confirmatory testing)

OR

- Seroconversion or diagnostic rise (at least fourfold or greater from baseline) in viral-specific antibody titre in serum or plasma using a validated laboratory-based serological assay for SARS-CoV-2

Outbreak cases resided in the Eastern Health region, met the provincial definition of a laboratory-confirmed case (9), had an episode date of February 1, 2021, to March 31, 2021 (inclusive), did not have an out-of-province travel history in the 14 days prior to the episode date, were not linked to a travel-associated case, and whose viral lineage was B.1.1.7 or not typed. Lineage assignments were determined in a subset of cases with sufficient viral load using pangolin v.2.2.2 (10), following whole genome sequencing on the Oxford Nanopore Technology GridION platform using a 1,200-base pair tiled amplicon scheme (11).

Cases with a positive lab test were interviewed by a public health nurse using a standardized form to identify potential exposures and contacts. The episode date for each case was the date of symptom onset or of specimen collection (if asymptomatic). Contacts were identified through case interviews as individuals who had close interactions with cases during the communicability period, starting 72 hours before the episode date.

Social network diagrams were used to explore connections between cases and identify clusters, defined as four or more cases epidemiologically linked to a setting where there was reasonable evidence of transmission (i.e. likely exposure to a case during their period of communicability).

Secondary attack rates (SAR) were calculated for households and school classrooms. The first laboratory-confirmed case in each household or classroom was considered the primary case, and any subsequent case was secondary if their onset occurred one to 14 days after the episode date of the primary case (or the last classroom exposure). Co-primary cases whose onset dates were the same as other primary cases were not considered secondary cases and were excluded from the SAR analysis. Household contacts of cases were identified in the provincial surveillance system. Classroom contacts were identified by the class roster, assuming perfect attendance. The SARs were calculated as the number of secondary cases divided by the number of contacts and represent the proportion of contacts who became cases. The unadjusted classroom SAR was calculated for all secondary cases in a classroom, and adjusted classroom SARs excluded school-associated cases who were secondary within their household or linked to other clusters.



An acquisition setting was assigned for each case, based on a hierarchy. Secondary cases in households were assumed to have acquired COVID-19 in their home, due to high proximity and duration of household contact compared to other settings. All other cases were categorized by their linkage to a cluster and its setting. No attempt was made to further distinguish the acquisition setting of cases linked to multiple clusters.

Public health measures were immediately implemented for containment, with incremental school closures and subsequently a province-wide lockdown beginning on February 12, including closure of all nonessential businesses and facilities, restrictions on gathering in groups over five, and restricted visitation to long-term care homes and assisted living facilities (12,13).

Analyses were completed in R/R Studio, using data accessed April 18, 2021 (14).

Results

There were 577 laboratory-confirmed and 38 probable cases in this outbreak. Of the confirmed cases, 183 (32%) were identified as B.1.1.7; the remainder were locally acquired and assumed B.1.1.7 as there had been no known community transmission prior to the outbreak. The median age was 31 years and the highest proportion of cases were in the 15 to 19-year age group (29%); 293 (51%) were female and 140 (24%) were asymptomatic upon identification (Table 1). The last episode date was March 28, 2021 (Figure 1).

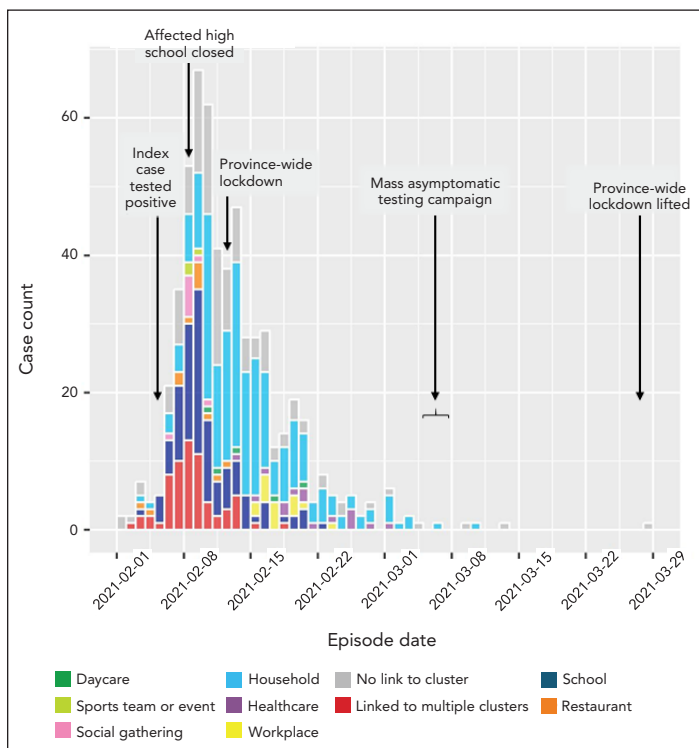
Table 1: Percent positivity by age group for COVID-19 testing performed from February 1 to March 31, 2021, during a COVID-19 B.1.1.7 variant of concern community outbreak in Newfoundland, Canada

Population tested, age (years)	Percent positivity (%)
Younger than 10	1.1
10–14	2.1
15–19	4.1
20–29	0.6
30–39	0.7
40–49	1.6
50–59	1.0
60 and older	0.7
All	1.2

Abbreviation: COVID-19, coronavirus disease 2019

There were 15 hospitalizations, seven intensive care unit admissions and two deaths associated with this outbreak. Most hospitalized cases were females (67%); none were younger than 40 years (Table 2). The two deaths occurred in males who were 75 years or older. One breakthrough case was identified following two doses of a messenger ribonucleic acid (mRNA) vaccine.

Figure 1: Epidemiologic curve for a COVID-19 B.1.1.7 variant of concern community outbreak in Newfoundland, Canada, 2021^a



Abbreviation: COVID-19, coronavirus disease 2019
^a By acquisition setting

Table 2: Demographics, symptoms and outcomes of laboratory-confirmed cases for a COVID-19 B.1.1.7 variant of concern community outbreak in Newfoundland, Canada, February 1 to March 31, 2021, (n=577)

Case characteristic		Count	Percent (%)
Age group (years)	Younger than 10	35	6
	10–14	51	9
	15–19	166	29
	20–29	30	5
	30–39	51	9
	40–49	125	22
	50–59	63	11
	60 and older	56	10
Sex	Female	293	51
Symptom status at time of identification	Asymptomatic	63	11
	Presymptomatic	77	13
	Symptomatic	437	76
Severe outcome(s)	Hospitalized	15	3
	Admitted to intensive care unit	7	1
	Death linked to COVID-19	2	Fewer than 1
	Not reported	561	97
Total		577	100

Abbreviation: COVID-19, coronavirus disease 2019



Provincially, the cumulative number of COVID-19 tests increased by 55% from February 1 (n=142,398) to March 31 (n=221,205), as contacts and community members were encouraged to be tested following exposure, sometimes multiple times during the incubation period. The maximum daily percent positivity was 5.3%. Youth aged 15 to 19 years had the highest percent positivity (4.1%) during the outbreak period (Table 1).

The index case was likely not the primary case, given that they had no history of travel or contact with travellers. The suspected primary case was a rotational worker who returned on January 14, followed all applicable provincial guidance, and tested negative on day seven. The rotational worker isolated at home—but not from their household contacts (per public health direction), who were among the earliest outbreak cases according to episode dates and had multiple potential community exposures. The rotational worker was identified as a symptomatic case after their household contacts tested positive, with symptom onset more than 14 days after travelling.

The number of contacts per laboratory-confirmed outbreak case ranged from zero to 189. The median number of contacts was eight prior to implementation of the province-wide lockdown order on February 12; thereafter, cases had a median of three contacts. Among the eight cases who had more than 100 contacts, their ages ranged from five to 17 years.

Twenty-five clusters of four or more confirmed cases were associated with settings, events or locations where transmission may have occurred. Households were the most common acquisition setting (39%), followed by a senior high school (18%) (Table 3 and Figure 1). Approximately 21% of cases were not linked to a known cluster.

Table 3: Acquisition setting for laboratory-confirmed cases of a COVID-19 B.1.1.7 variant of concern community outbreak in Newfoundland, Canada, 2021 (n=577)

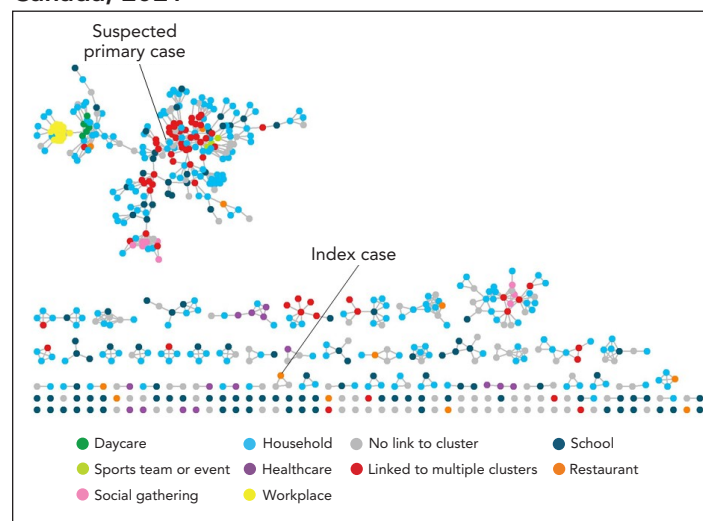
Acquisition setting	Count	%
Household	226	39
No link to cluster	122	21
School	106	18
Linked to multiple clusters	64	11
Healthcare	15	3
Workplace	15	3
Restaurant	12	2
Social gathering	9	2
Daycare	5	1
Sports team or event	3	1
Total laboratory-confirmed cases	577	100

Abbreviation: COVID-19, coronavirus disease 2019

Early cases in the outbreak were linked to school, sports activities/events, a restaurant and social gathering settings. As the outbreak progressed, cases were associated with household transmission, daycare, healthcare settings and a workplace (Figure 1).

A social network diagram (Figure 2) identified one large cluster and 25 smaller clusters of four or more cases. Figure 2 shows the connectivity of cases from contact tracing data and does not incorporate directionality or timing. Cases linked to multiple clusters (n=73) were centrally located among the largest clusters in the social network diagram; 68 (93%) were linked to the school, 44 (60%) to sports-related cluster(s), 36 (49%) to social gathering cluster(s) and 15 (21%) to the restaurant.

Figure 2: Social network diagram of laboratory-confirmed cases (n=577) for a COVID-19 B.1.1.7 variant of concern community outbreak in Newfoundland, Canada, 2021^a



Abbreviation: COVID-19, coronavirus disease 2019
^a By acquisition setting

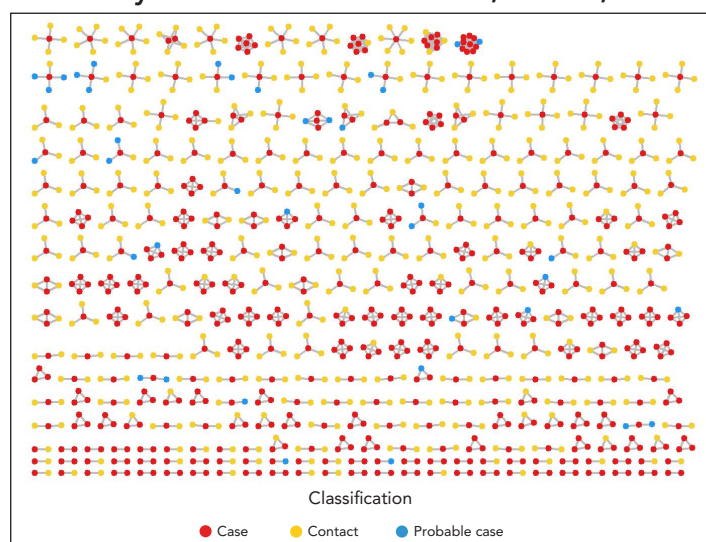
The largest cluster of cases (n=183) was among individuals attending a senior high school, of which 167 (91%) were students and 16 (9%) were teachers or coaches. The number of COVID-19 cases per classroom ranged from zero to 19 (mean: 4.4).

Of all classroom groups in the school (n=298), 161 (54%) were exposed to a student or teacher case during their infectious period. Of the 945 students and teachers on the class list, 845 (89%) were exposed to an infectious student or teacher in their classroom, 17 (2%) were the primary cases in their classes and 163 (17%) became a confirmed case within 14 days following the last date of exposure in the classroom. Including all secondary classroom cases, the unadjusted classroom SAR was 19.3%. The adjusted classroom SAR was 17.8% when excluding those who were secondary cases within their household, and 11.6% when further excluding those linked to other clusters.



There were 308 households of two or more individuals that had at least one laboratory-confirmed outbreak case. Confirmed cases, probable cases and contacts were clustered by household in a social network diagram (Figure 3). The number of close household contacts per laboratory-confirmed outbreak case ranged from zero to 10 (median: 3). Transmission from a laboratory-confirmed primary household case to a laboratory-confirmed secondary household case appeared to have occurred in 119/308 (38.6%) households. The estimated household SAR was 24.4%. The adjusted household SAR was 28.5% when including probable cases and 19.9% when excluding secondary cases who were linked to other cluster types/settings.

Figure 3: Social network diagram of 308 household clusters for a COVID-19 B.1.1.7 variant of concern community outbreak in Newfoundland, Canada, 2021^a



Abbreviation: COVID-19, coronavirus disease 2019

^a By classification

Discussion

Introduction of B.1.1.7 into Newfoundland (the island portion of one of Canada's least populous provinces) likely occurred through travel, given its relative geographic isolation, border quarantine measures and absence of prior evidence of community transmission. It is hypothesized that a rotational worker who returned from work and followed all applicable provincial guidance may have had a false-negative screening test on day seven, and/or may have had a longer incubation period (more than 14 days). Alternatively, it is possible that B.1.1.7 was circulating undetected within the community from an earlier introduction, and was identified upon reaching a susceptible population, resulting in rapid spread (15).

Major contributors to spread were identified as 1) the vulnerability of a highly connected, unvaccinated population including school-aged youth, 2) household transmission within the community and 3) asymptomatic or presymptomatic transmission.

At the time of B.1.1.7 introduction, most adults and all youth were unvaccinated. Less than 2% of the province's population had received one dose at the beginning of the outbreak period (16), while a phased approach to vaccine rollout was underway (17). Although PHMs were in place (e.g. mandatory masking and restrictions on occupancy of indoor settings) (18,19), there were opportunities for community transmission in indoor settings such as restaurants, workplaces and private social gatherings.

Attendees of the senior high school had a high degree of connectedness due to in-person learning, no student or staff cohorting (i.e. students attended multiple classrooms with different teachers and students) and in-person extracurricular activities (e.g. sports tournaments). Non-medical masks (i.e. cloth masks or face coverings) were required in common areas but were not required in classrooms if students were distanced by at least one metre, and no requirements regarding ventilation and indoor air quality were in place for schools.

Evidence is conflicted regarding school-based transmission's contribution to community transmission (20–23). Data and modelling show that without robust mitigation measures, school settings with an effective reproduction number above one can contribute to growth of an outbreak (24). The school setting was likely a driver of community transmission; however, the unadjusted classroom SAR of 19.3% decreased to 11.6% when excluding those linked to household exposure or other clusters, suggesting uncertainty about how directly school-associated cases can be linked with classroom transmission given other potential exposures.

The classroom SAR estimates are comparable to a May 2020 high school outbreak in Israel (25), but higher than in-school SAR estimates reported in meta or regional analyses (26–28), reflecting overdispersion in transmission (29). High school outbreaks of this size were unusual in Canada (30,31); however, they have been documented elsewhere when PHMs were not in place or were not followed (25,32). School sports have also been associated with secondary transmission in high and middle school settings in the United States (33).

Although mask-wearing (and other measures) is associated with reduced transmission in schools (34), the masking requirements in place at the school did not appear to curb transmission. Closing the affected school and implementing community-wide restrictions on indoor gatherings were key interventions in containing this outbreak. Improved ventilation could also have contributed to reducing the risk of transmission (35). Subsequent household transmission from school-associated cases in this outbreak is consistent with survey data from the United States that demonstrated increased odds of COVID-19-like illness within households with children in full-time in-person schooling (36).

Household settings accounted for the highest proportion of exposures among laboratory-confirmed cases (39%). Compared to other Canadian estimates for non-VOC COVID-19 household



SARs (e.g. 20.2% in Ontario (37), and 14.7% in the Winnipeg Health Region (38)), the estimated household SAR of 24.4% in this outbreak appears higher, which may reflect increased transmissibility of B.1.1.7. A similar SAR of 25.1% was observed among B.1.1.7 cases in Ontario (37).

In this outbreak, 24% of cases were asymptomatic or presymptomatic (i.e. developed symptoms after testing positive). The younger age groups (zero to nine and 10 to 19 years) had the highest proportion of asymptomatic or presymptomatic infection, which is consistent with evidence that children and adolescents are more commonly asymptomatic or have mild, non-specific symptoms (22,39). Findings from this outbreak support asymptomatic testing as an important case finding intervention in outbreaks among children and youth.

Strengths and limitations

One strength of this investigation is the detailed analysis of potential transmission settings, possible because the outbreak was well contained in an area of low background transmission. There were several limitations to the study. First, the acquisition setting analysis was dependent on case interviews that may have been incomplete due to case volume, or subject to recall bias. Second, there may have been misclassification of COVID-19 lineage, since only 32% of cases were sequenced due to resource limitations. Similar to other jurisdictions (40), all locally acquired outbreak cases were managed thereafter as B.1.1.7. This potential misclassification means that when comparing attack rates in this outbreak to non-VOC outbreaks, the effect of B.1.1.7's increased transmissibility may be underestimated. Third, the analyses mostly excluded probable cases who tested negative, but clinical data suggests these symptomatic individuals who were contacts to laboratory-confirmed household cases were likely true cases (41). The SARs may have been underestimated due to the exclusion of probable cases. Fourth, although hypothesized, the primary case remains unknown.

Conclusion

This outbreak demonstrated how B.1.1.7 spread through an adolescent population and surrounding community with few preventative PHMs in place. Implementation and compliance with school- and community-based PHMs is critical to reduce the number of contacts and prevent transmission, particularly while vaccination coverage is low.

Authors' statement

AN, AM, AC, KP, JS, and KW contributed to conceptualization, analysis and interpretation of data. All authors contributed to drafting and revising the paper.

Competing interests

LG is a member of study teams that received funding from Roche Diagnostics and Seegene Inc. No other competing interests were declared.

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