Clinical Infectious Diseases

MAJOR ARTICLE

Characteristics Associated With Household Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Ontario, Canada: A Cohort Study

Lauren A. Paul,[1] Nick Daneman,[1,2,3,4,5,6] Kevin A. Brown,[1,3,7] James Johnson,[8] Trevor van Ingen,[9] Eugene Joh,[1] Sarah E. Wilson,[1,3,7] and Sarah A. Buchan[1,3,7]

[1]Health Protection, Public Health Ontario, Toronto, Ontario, Canada; [2]Sunnybrook Research Institute, Sunnybrook Health Sciences Centre, Toronto, Ontario, Canada; [3]ICES, Toronto, Ontario, Canada; [4]Division of Infectious Diseases, Sunnybrook Health Sciences Centre, Toronto, Ontario, Canada; [5]Department of Medicine, University of Toronto, Toronto, Ontario, Canada; [6]Institute of Health Policy, Management, and Evaluation, University of Toronto, Toronto, Ontario, Canada; [7]Dalla Lana School of Public Health, University of Toronto, Toronto, Ontario, Canada; [8]Environmental and Occupational Health, Public Health Ontario, Toronto, Ontario, Canada; and [9]Knowledge Services, Public Health Ontario, Toronto, Ontario, Canada

Background. Within-household transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection has been identified as one of the main sources of spread of coronavirus disease 2019 (COVID-19) after lockdown restrictions and self-isolation guidelines are implemented. Secondary attack rates among household contacts are estimated to be 5–10 times higher than among non-household contacts, but it is unclear which individuals are more prone to transmit infection within their households.

Methods. Using address matching, a cohort was assembled of all individuals with laboratory-confirmed COVID-19 residing in private households in Ontario, Canada. Descriptive analyses were performed to compare characteristics of cases in households that experienced secondary transmission versus those that did not. Logistic regression models were fit to determine index case characteristics and neighborhood characteristics associated with transmission.

Results. Between January and July 2020, there were 26 714 individuals with COVID-19 residing in 21 226 households. Longer testing delays (≥5 vs 0 days; odds ratio [OR], 3.02; 95% confidence interval [CI], 2.53–3.60) and male gender (OR, 1.28; 95% CI, 1.18–1.38) were associated with greater odds of household secondary transmission, while being a healthcare worker (OR, .56; 95% CI, .50–.62) was associated with lower odds of transmission. Neighborhoods with larger average family size and a higher proportion of households with multiple persons per room were also associated with greater odds of transmission.

Conclusions. It is important for individuals to get tested for SARS-CoV-2 infection as soon as symptoms appear, and to isolate away from household contacts; this is particularly important in neighborhoods with large family sizes and/or crowded households.

Keywords. COVID-19; SARS-CoV-2; household; transmission.

Transmission and acquisition of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection has become an active area of coronavirus disease 2019 (COVID-19) research since person-to-person transmission was confirmed at the beginning of 2020 [1, 2]. The primary source of acquisition of SARS-CoV-2 infection transitioned from travel-related transmission early in the pandemic, to local transmission as countries implemented restrictions to reduce imported infections. Households, in particular, have been highlighted as an important source of COVID-19 transmission [3–7]. The shift to household transmission has resulted from public health measures, ranging from teleworking to full lockdowns, encouraging individuals to spend time at home where there is increased duration and intensity of contact [4, 5]. However, it is unclear which individuals are more likely to transmit infection within their households.

Existing observational studies of household transmission typically included household contacts identified through contact tracing [4–6, 8–10]. These studies have estimated secondary attack rates in households to be 5 to 10 times higher than in non-household settings [4, 6]. Most of these studies were conducted in Asia, included smaller numbers of households, and/or did not compare with households where no transmission occurred. Many also focused on the characteristics of the acquirers of infection (secondary cases) rather than the characteristics of the transmitters of infection (index cases).

Using address matching, we sought to identify all households with confirmed SARS-CoV-2 infections from Ontario, Canada, between January and July 2020. We were interested in comparing households that experienced secondary transmission versus those that did not, and also sought to determine individual- and neighborhood-level characteristics of index cases associated with household transmission. This work may

Received 3 December 2020; editorial decision 23 February 2021; published online 5 March 2021.

Correspondence: S. A. Buchan, Public Health Ontario, 661 University Avenue, Floor 17, Toronto, ON, M5G 1M1, Canada (sarah.buchan@oahpp.ca).

Clinical Infectious Diseases® 2021;73(10):1840–8

DOI: 10.1093/cid/ciab186

help inform future public health strategies to reduce within-household transmission during the ongoing pandemic.

METHODS

Study Population

We assembled a cohort of all individuals with confirmed COVID-19 [11] reported in Ontario, Canada's most populous province (14.6 million residents), among residents of private households from 1 January 2020 to 28 July 2020. We identified individuals with confirmed COVID-19 using surveillance data from provincial reportable disease systems, which is collected through public health follow-up of cases and entered by local public health units [12]. We obtained ethics approval from Public Health Ontario's Research Ethics Board.

Identification of Private Households

Private households were defined as any residences not identified as congregate in nature, such as homeless shelters or long-term-care homes. Individual houses and apartments/suites within multiunit dwellings (eg, apartment buildings) were considered private households. Details about the address-matching algorithm used to identify private households are provided in the Supplementary Methods.

Outcomes

The primary outcome of interest was any secondary transmission within a household, defined as cases that occurred 1–14 days after the index case of the household [8, 10, 13]. We used each case's symptom-onset date as the date of comparison, or their specimen collection date if symptom-onset date was unavailable, and excluded the rare cases (0.5%) that lacked information on both dates. We excluded households with multiple index cases (ie, 2 or more cases occurring on the earliest case date of the household) from the cohort as they would present challenges for estimating the predictive value of individual-level index case characteristics. We also considered household transmission to older adults (≥60 years) as a secondary outcome of interest.

Individual- and Neighborhood-Level Characteristics

We considered a variety of individual- and neighborhood-level covariates in our analyses that were hypothesized to influence household transmission. At the individual level, we obtained information on each case's age, gender, and health-region of residence (Supplementary Table 1). Furthermore, we included covariates for case month (January–July), employment as a healthcare worker, high risk status (≥60 years of age, immunocompromised, had cardiovascular-related health issues, or had chronic obstructive pulmonary disease [COPD]), and association with a COVID-19 outbreak outside the home (eg, association with a workplace or long-term-care home outbreak) [11].

We also considered 3 delay metrics for each case: (1) the delay between the case's symptom onset and when his/her specimen was collected by a healthcare provider (testing delay), (2) the delay between specimen collection and report of a positive test result to the local health unit (reporting delay), and (3) the delay between test report and when the health unit began entering the case into a reportable disease system for provincial notification (data entry delay). For the testing delay metric, we additionally separated out cases who were missing symptom-onset date (thus, specimen collection date was used) and did not have any COVID-19 symptoms flagged in provincial disease reporting systems. We excluded cases who were missing symptom-onset date but had COVID-19 symptoms flagged from all analyses.

We did not have any information on the total number of residents of each household. However, we were able to adjust for several characteristics related to the average size and composition of households at the neighborhood level. These included characteristics such as the average family size, proportion of households with multiple persons per room, proportion of multifamily households, and urban/rural status (see Supplementary Definitions and Table 2 for all characteristics included). Characteristics were derived from 2016 Canadian census records, which had a 98.4% response rate [14]. The Canadian census is a mandatory questionnaire that collects extensive information from each of the 15.4 million dwellings across Canada, with all dwellings reporting household composition, and a 25% sample completing a more detailed long-form questionnaire [14]. We linked neighborhood characteristics at the aggregate dissemination area level, which divides the country into areas with populations between 5000 and 15 000 persons, on average.

Statistical Analysis

We applied logistic regression models to obtain both unadjusted and adjusted odds ratios (ORs) and 95% confidence intervals (CIs) for the associations between covariates and the odds of secondary transmission within households. We also carried out descriptive analyses to compare the characteristics of index cases, secondary cases, and cases that were not involved in household transmission. We examined the direction of transmission by age group and assessed the distribution of the number of days between symptom-onset dates for index cases and secondary cases (serial interval).

In sensitivity analyses we adjusted the definition of household transmission to be (1) cases that occurred 2–14 days after the index case (more specific) or (2) cases that occurred 1–28 days after the index case (more sensitive). We also restricted the analysis to households with an index case date on or after 29 May 2020; testing approaches expanded as of 29 May, which may have improved the ability to identify secondary transmission [15].

RESULTS

As of 28 July 2020, there were 38 984 individuals with confirmed COVID-19 reported in Ontario. After removing cases based on our inclusion criteria, we were left with 26 714 cases residing in private households, of which 7993 cases were from households with secondary transmission (Figure 1). Of the 3067 index cases from households with secondary transmission, the median number of secondary cases in the same household was 1 (interquartile range [IQR] = 1 case). The mean age of the cohort was 44.2 years and 53% were female.

The median serial interval from index case to secondary case was 4 days (IQR = 5 days) (Supplementary Figure 1). For the

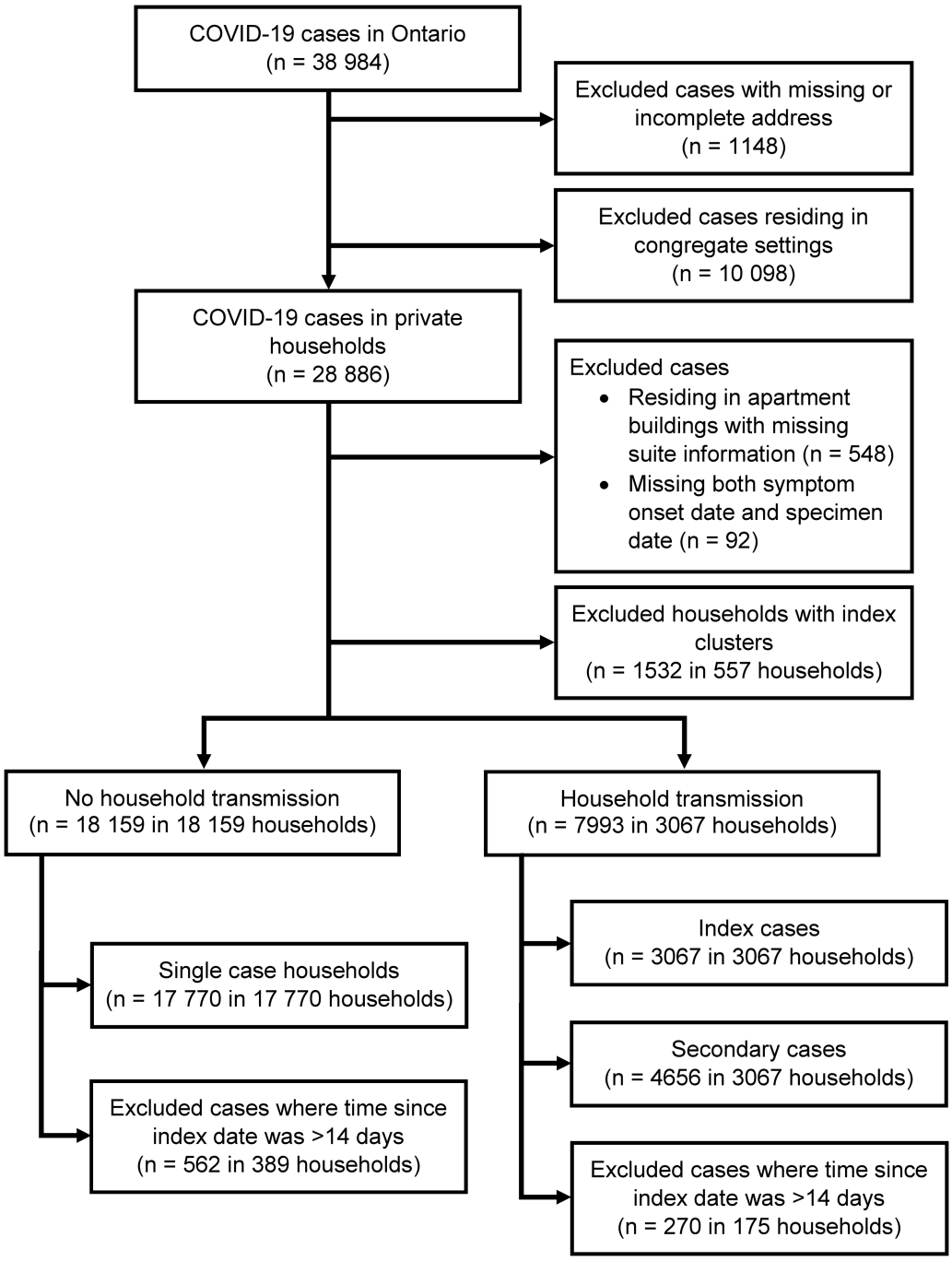

Figure 1. Flow diagram of study cohort. Abbreviation: COVID-19, coronavirus disease 2019.

direction of transmission from index cases to secondary cases, individuals in the 20- to 59-year age group were both the most frequent transmitters and acquirers of SARS-CoV-2 infections within households (Supplementary Figure 2). Transmissions to secondary cases in different age groups than the index case were less frequent.

Individual-Level Characteristics

Compared with index cases with no household transmission, index cases with household transmission had a higher proportion of healthcare workers or cases associated with a COVID-19 outbreak (Table 1). However, they had a lower proportion of males and had median testing delays that were twice as long as index cases without household transmission. There was no difference in median reporting delay or data entry delay for the 2 groups. We also compared the characteristics of index cases and secondary cases and found that secondary cases had shorter median testing delays than index cases (Supplementary Table 2).

From adjusted logistic models, we observed increased odds of any household transmission with longer testing delays for the index case compared with 0-day (ie, tested on the same day as symptom onset) testing delays (ORs: 1-day delay = 2.02, 2-day delay = 1.96, 3-day delay = 2.36, 4-day delay = 2.64, ≥5-day delay = 3.02) (Figure 2, Supplementary Table 3). Individuals with no symptoms flagged in provincial reportable diseases systems had lower odds of any household transmission (.48; 95% CI, .38–.61). This trend was similar in models for household transmission to older adults. Conversely, there were no notable trends for increased odds of household transmission with reporting delays or data entry delays.

Male index cases had higher odds of any household transmission (1.28; 95% CI, 1.18–1.38) or transmission to older adults (1.19; 95% CI, 1.02–1.38) compared with female index cases (Table 2). We also observed increased odds if the index case was high risk (1.14; 95% CI, .97–1.34), while decreased odds were observed if the index case was a healthcare worker (.56; 95% CI, .50–.62) or was associated with an outbreak (.61; 95% CI, .55–.68). Older (≥60 years) and younger (20–49 years) index cases had lower odds of any household transmission compared with the 50- to 59-year reference group. There were also some trends for decreased odds of transmission from May to July.

Neighborhood-Level Characteristics

The strongest associations observed for household transmission were in neighborhoods with larger average family size (1.88 per person increase; 95% CI, 1.70–2.09) or with a higher proportion of households with multiple persons per room (1.25 per 10% increase; 95% CI, 1.13–1.38) (Table 2). We also observed increased odds for neighborhoods with a higher proportion of multifamily households; this was a particularly strong predictor of transmission to older adults (1.63 per 10% increase; 95% CI, 1.17–2.26). Additionally, odds of transmission were higher for neighborhoods with a higher proportion of individuals in the 65-years-and-older age group; individuals below the low income cutoff; individuals with less than high school education; unsuitable housing; recent immigrants; non-White, non-Indigenous groups; and apartments with 5 or more floors. Odds were lower for more remote areas compared with large urban areas.

Sensitivity Analysis

We compared the estimates from our primary outcome model with those produced in our 3 sensitivity analyses and found that our associations were robust (Supplementary Table 4). Notably, longer testing delays continued to display strong trends towards increased odds of household transmission. Larger average family size and a higher proportion of households with multiple persons per room also continued to exhibit the strongest associations at the neighborhood level.

DISCUSSION

In this retrospective study of 26 714 individuals with confirmed COVID-19 residing in 21 226 private households, we found that longer testing delays and male gender were associated with greater odds of household secondary transmission.

Table 1. Characteristics of Index Cases of Households With No Household Transmission Compared With Index Cases of Households With Household Transmission

	Index Cases With No Household Transmission (n = 18 159)	Index Cases With Household Transmission (n = 3067)
Gender, n (%)		
Female	9890 (54.5)	1464 (47.7)
Male	8214 (45.2)	1595 (52.0)
Age, median [IQR], years	45 [31, 58]	46 [31, 57]
Age group, n (%)		
<10 years	164 (0.9)	26 (0.8)
10–19 years	536 (3.0)	127 (4.1)
20–29 years	3387 (18.7)	523 (17.1)
30–39 years	3169 (17.5)	481 (15.7)

Table 1. Continued

	Index Cases With No Household Transmission (n = 18 159)	Index Cases With Household Transmission (n = 3067)
40–49 years	3256 (17.9)	571 (18.6)
50–59 years	3711 (20.4)	726 (23.7)
60–69 years	2271 (12.5)	404 (13.2)
70–79 years	972 (5.4)	138 (4.5)
≥80 years	692 (3.8)	70 (2.3)
High risk (≥60 years, immunocompromised, cardiovascular, COPD), n (%)	5066 (27.9)	844 (27.5)
Outbreak-associated,[a] n (%)	4901 (27.0)	540 (17.6)
Healthcare worker, n (%)	4916 (27.1)	517 (16.9)
Month reported, n (%)		
January	1 (0.0)	1 (0.0)
February	8 (0.0)	3 (0.1)
March	2009 (11.1)	312 (10.2)
April	6374 (35.1)	945 (30.8)
May	4978 (27.4)	989 (32.2)
June	2931 (16.1)	528 (17.2)
July	1858 (10.2)	289 (9.4)
Region, n (%)		
Toronto	6292 (34.6)	1025 (33.4)
Central East	5891 (32.4)	1236 (40.3)
Central West	2445 (13.5)	343 (11.2)
Eastern	1569 (8.6)	231 (7.5)
Northern	199 (1.1)	32 (1.0)
South West	1763 (9.7)	200 (6.5)
Testing delay,[b] median [IQR], days	2 [0, 6]	4 [2, 8]
Testing delay distribution,[b] n (%)		
No symptoms[c]	2883 (16.2)	131 (4.3)
<0 days[d]	963 (5.4)	60 (2.0)
0 days	1745 (9.8)	164 (5.4)
1 day	1955 (11.0)	349 (11.5)
2 days	1958 (11.0)	341 (11.2)
3 days	1560 (8.8)	327 (10.8)
4 days	1230 (6.9)	276 (9.1)
≥5 days	5529 (31.0)	1390 (45.8)
Reporting delay, median [IQR], days	2 [1, 3]	2 [1, 3]
Reporting delay distribution, n (%)		
<0 days	312 (1.7)	43 (1.4)
0 days	1165 (6.4)	200 (6.5)
1 day	5931 (32.8)	1038 (34.0)
2 days	5276 (29.2)	926 (30.3)
3 days	2414 (13.4)	390 (12.8)
4 days	1010 (5.6)	188 (6.2)
≥5 days	1966 (10.9)	271 (8.9)
Data entry delay, median [IQR], days	0 [0, 1]	0 [0, 1]
Data entry delay distribution, n (%)		
<0 days	1065 (5.9)	173 (5.6)
0 days	11 050 (60.9)	1852 (60.4)
1 day	3699 (20.4)	696 (22.7)
2 days	824 (4.5)	132 (4.3)
3 days	457 (2.5)	80 (2.6)
4 days	286 (1.6)	32 (1.0)
≥5 days	778 (4.3)	102 (3.3)

Abbreviations: COPD, chronic obstructive pulmonary disease; COVID-19, coronavirus disease 2019; IQR, interquartile range.

[a]Cases associated with a public health declared outbreak outside the home.

[b]269 cases were excluded who had COVID-19 symptoms flagged in provincial reportable disease systems but were missing symptom-onset date.

[c]Cases with no symptoms were defined as cases who were missing symptom-onset date (thus, specimen collection date was used) and did not have any COVID-19 symptoms flagged in provincial reportable disease systems.

[d]Cases with a testing delay of <0 days were those who were tested prior to the onset of their symptoms.

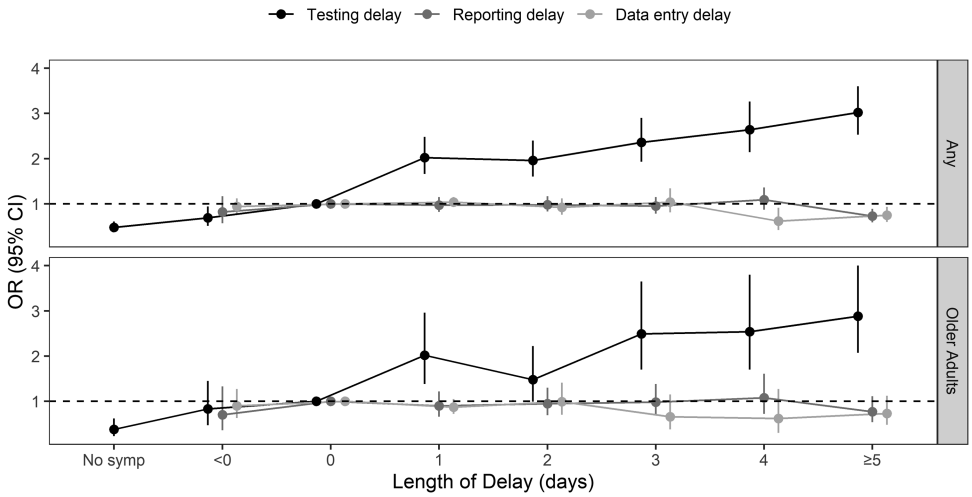

Figure 2. Adjusted ORs and 95% CIs for the associations between index case delay metrics and odds of household transmission. A total of 269 cases were excluded from the testing delay models that had COVID-19 symptoms flagged in provincial reportable disease systems but were missing symptom-onset date. Cases with no symptoms were defined as cases who were missing symptom-onset date (thus, specimen collection date was used) and did not have any COVID-19 symptoms flagged in provincial reportable disease systems. Cases with a testing delay of <0 days were those who were tested prior to the onset of their symptoms. Horizontal dashed line at OR = 1 indicates no association. Abbreviations: CI, confidence interval; COVID-19, coronavirus disease 2019; No symp, no symptoms; OR, odds ratio.

Additionally, neighborhoods with larger average family size and a higher proportion of households with multiple persons per room were associated with greater odds of household transmission.

Previous studies of household transmission have considered secondary attack rates, defined as the proportion of household members of confirmed cases who acquire infection. The majority of these studies were conducted in Asia, as well as some in Europe and the United States [4–6, 8–10]. Madewell et al [4], Lei et al [6], and Curmei et al [5] conducted meta-analyses of previous studies and found pooled household secondary attack rates of 19% (95% CI, 15–23%), 27% (21–32%), and 30% (18–43%), respectively.

We identified only 2 other studies that considered the impact of testing delays on household transmission; Xin et al [16] and Wang et al [13] examined the time from illness onset to laboratory confirmation. They reported hazard ratios for household transmission of 2.32 (95% CI, .89–6.10) (<7-day delays vs ≥7-day delays) calculated from 106 households and 2.35 (95% CI, .63–8.77) (<3-day delays vs ≥3-day delays) calculated from 124 households, respectively. It has been estimated that infectivity peaks 3–5 days after symptom onset [17, 18], which underlines the importance of rapid testing and self-isolation as soon as symptoms appear. Our other finding of lower odds of household transmission among individuals with no symptoms is in line with estimates of lower secondary attack rates

Table 2. Adjusted Odds Ratios and 95% Confidence Intervals for the Associations Between Index Case Characteristics and Odds of Household Transmission

	Any Household Transmission	Household Transmission to Older Adults (Aged ≥60 Years)
Individual-level characteristics		
Gender		
Female	Ref	Ref
Male	1.28 (1.18–1.38)	1.19 (1.02–1.38)
Age group		
<10 years	.87 (.57–1.34)	.18 (.02–1.27)
10–19 years	1.20 (.97–1.49)	.65 (.37–1.17)
20–29 years	.78 (.69–.89)	.60 (.45–.80)
30–39 years	.80 (.71–.91)	.72 (.55–.94)
40–49 years	.90 (.80–1.02)	.66 (.50–.86)
50–59 years	Ref	Ref
60–69 years	.93 (.81–1.06)	2.15 (1.72–2.69)
70–79 years	.78 (.64–.95)	2.67 (2.04–3.49)
≥80 years	.58 (.45–.76)	2.07 (1.49–2.88)

Table 2. Continued

	Any Household Transmission	Household Transmission to Older Adults (Aged ≥60 Years)
High risk (≥60 years, immunocompromised, cardiovascular, COPD)		
No	Ref	Ref
Yes	1.14 (.97–1.34)	1.17 (.84–1.64)
Outbreak-associated[a]		
No	Ref	Ref
Yes	.61 (.55–.68)	.49 (.39–.61)
Healthcare worker		
No	Ref	Ref
Yes	.56 (.50–.62)	.47 (.37–.59)
Month reported		
January	7.91 (.46–136.45)	Insufficient data
February	2.55 (.67–9.77)	4.25 (.86–20.95)
March	1.09 (.95–1.26)	1.48 (1.18–1.86)
April	Ref	Ref
May	1.25 (1.13–1.38)	1.12 (.93–1.36)
June	1.14 (1.01–1.28)	.90 (.70–1.14)
July	1.04 (.90–1.21)	.85 (.62–1.16)
Region		
Toronto	Ref	Ref
Central East	1.04 (.94–1.15)	1.22 (1.01–1.47)
Central West	.91 (.79–1.04)	.87 (.66–1.15)
Eastern	1.08 (.92–1.26)	1.02 (.75–1.39)
Northern	1.28 (.87–1.89)	1.30 (.65–2.61)
South West	.84 (.71–.99)	.77 (.55–1.08)
Neighborhood-level characteristics[b]		
Age group		
0–14 years	.89 (.78–1.02)	.69 (.53–.89)
15–64 years	.93 (.84–1.02)	.84 (.70–1.01)
≥65 years	1.12 (1.02–1.22)	1.34 (1.14–1.58)
Male	.89 (.68–1.16)	.95 (.58–1.56)
Recent immigrants	1.35 (1.21–1.51)	1.13 (.92–1.41)
Non-White, non-Indigenous	1.05 (1.03–1.08)	1.04 (.99–1.09)
Non-White, non-Indigenous groups		
Black	1.05 (1.00–1.11)	.93 (.83–1.04)
East/Southeast Asian	1.02 (.98–1.06)	1.04 (.98–1.10)
Latin American	1.41 (1.19–1.66)	1.18 (.84–1.65)
Middle Eastern	1.06 (.96–1.17)	.83 (.67–1.02)
South Asian	1.04 (1.00–1.08)	1.09 (1.02–1.16)
Below low-income cutoff	1.06 (1.00–1.13)	.94 (.83–1.06)
Labor force participation	.89 (.83–.95)	.87 (.77–.99)
Less than high school education	1.08 (1.02–1.15)	1.02 (.91–1.15)
Unsuitable housing[c]	1.19 (1.11–1.27)	1.02 (.89–1.17)
Households with multiple persons per room[c]	1.25 (1.13–1.38)	1.10 (.90–1.34)
Multifamily households[c]	1.10 (.92–1.31)	1.63 (1.17–2.26)
Average family size[c]	1.88 (1.70–2.09)	1.82 (1.50–2.21)
Households living in apartments with ≥5 floors	1.02 (1.00–1.04)	1.00 (.97–1.04)
Households living in apartments with <5 floors	1.00 (.96–1.04)	.93 (.86–1.01)
Community type[c]		
Large urban	Ref	Ref
Medium/small	.93 (.78–1.10)	.90 (.65–1.25)
Rural	.97 (.79–1.18)	1.05 (.72–1.53)
Remote	.73 (.53–1.01)	1.07 (.64–1.79)

Estimates were adjusted for age group, gender, month reported, health region, and average family size.

Abbreviations: COPD, chronic obstructive pulmonary disease; Ref, reference.

[a]Cases associated with a public health declared outbreak outside the home.

[b]Odds ratios for neighborhood-level characteristics are reported per 10% increase, except for average family size and community type.

[c]Defined in the Supplementary Definitions.

among asymptomatic or mildly symptomatic individuals [4, 19], although it may be that secondary attack rates are underestimated in these groups due to lower testing rates [19]. Our "no symptom" classification may have included some individuals who missed having their symptoms reported in provincial disease systems; however, we would expect these individuals to bias our estimate towards the null.

Considering other individual-level characteristics, 2 studies found similar positive associations with male gender and immunodeficiency [8], and an inverse association with healthcare employment [20]. In addition to healthcare employment, we also found lower odds of household transmission among individuals linked to an outbreak. This may reflect testing practices, where outbreak-linked cases are more quickly identified and isolated. Healthcare workers may also be part of these outbreaks, leading to more rapid identification; additionally, they may have different practices within the household given their heightened awareness of risk of exposure, and may have increased use of personal protective equipment.

Madewell et al [4] and Lopez Bernal et al [10] further reported inverse relationships between household size and secondary attack rates. These findings are in contrast to our result of higher odds of household transmission among neighborhoods with larger average family size. Madewell et al acknowledged that household crowding may play a more important role in transmission risk than household size; Lewis et al [8] found a relative risk of 2.1 (95% CI, 1.5–2.8) for transmission in households with more than 2 persons per bedroom compared with 1–2 persons per bedroom. Our findings of higher odds of household transmission among neighborhoods with a higher proportion of multiple persons per room and multifamily households may support this hypothesis, and our association with average family size may be capturing aspects of household crowding at the neighborhood level (eg, neighborhoods with larger average family size tended to have a higher proportion of multiple persons per room). Madewell et al also reported a pooled proportion of households with any secondary transmission of 33% (95% CI, 7–58%), while we found only 14% of our households experienced secondary transmission. As we did not have information on total household size, our study includes some single-resident households that had zero probability of household transmission. This would decrease the number of cases associated with household transmission in comparison to studies that excluded single-resident households, and may have also diluted our model estimates.

Our study has some limitations that merit discussion. First, we did not have information on the total number of individuals residing in each household; thus, we were unable to calculate the proportion of household contacts infected to generate secondary attack rates. As a result, we could only conservatively estimate the proportion of households with transmission, and may have underestimated the magnitude of associations between individual characteristics and household transmission. However, we were able to control for neighborhood-level characteristics of household composition including average family size and proportion of households with multiple persons per room or multifamily households, which would partially correct for this caveat. Our finding of high transmission and acquisition of SARS-CoV-2 infection between individuals in the same age group therefore likely reflects the inherent age structures of households in Ontario. Second, we may have misclassified some index cases if a previously infected individual within the household was untested (eg, asymptomatic or symptomatic but did not seek testing) and misclassified some secondary cases if their infection was acquired outside the household. We may also have missed secondary cases within a household who were untested. Third, we only considered 1 index case per household and considered all subsequent cases within a 14-day period to be secondary cases (ie, did not account for tertiary transmission). Finally, because addresses in this dataset are entered manually as a free-text field, some algorithm misclassification is expected due to incorrectly entered addresses or different street and city naming conventions. This type of misclassification would be expected to decrease our pool of multiple-case households.

Our study also has several strengths. To our knowledge, this study contains the largest number of private households with at least 1 confirmed case of COVID-19. Most previous studies included a subset of confirmed COVID-19 cases and used contact tracing to monitor household members for infection and/or symptoms [4]. Thus, these studies were only able to include a smaller number of households (individual studies reporting on <6000 households) compared with the 21 226 households we were able to identify through address matching of all individuals with confirmed COVID-19 in Ontario. We did not find any other studies that used address matching to comprehensively identify all households with SARS-CoV-2 infections in a region, with the exception of 1 study from Israel that used a municipal database of residents to identify household members of cases [21]. Additionally, we considered a large set of individual- and neighborhood-level characteristics of index cases. We were able to compare these characteristics between households where secondary transmission did and did not occur, which yielded important insights into factors that may help reduce secondary transmission in households.

Conclusions

Household transmission plays a key role in local spread of SARS-CoV-2 infection. Our work suggests that it is important for individuals to get tested for COVID-19 as soon as symptoms appear. Ideally, individuals should be tested on the day of symptom onset, as even a 1-day delay was associated with increased odds of secondary transmission. Additionally, if cases are living with other individuals, it may also be important to

try to isolate in a room alone or outside the home, if possible. Examples of strategies that may be implemented by public health officials to reduce household transmission and mitigate the ongoing spread of COVID-19 are public health messaging about early testing (eg, social media campaigns, communication with cases during public health follow-up) or the creation and/or promotion of voluntary isolation facilities for individuals unable to isolate at home. Future research should focus on the magnitude of the role of children and youth in household transmission, particularly as lockdown restrictions are lifted and individuals return to regular activities such as work, school, and daycare.

Supplementary Data

Supplementary materials are available at *Clinical Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

Notes

Author contributions. L. A. P. performed the analysis and drafted the manuscript. S. A. B., N. D., and K. A. B. conceptualized the study. S. A. B., N. D., K. A. B., and L. A. P. developed the methodology. S. A. B., K. A. B., and L. A. P. verified the underlying data. J. J. and T. v. I. contributed to the analysis. S. A. B., N. D., K. A. B., J. J., T. v. I., E. J., and S. E. W. reviewed the manuscript.

Acknowledgments. The authors thank Garima Aryal for her contributions to the address-matching work.

Financial support. This work did not have a direct funding source but was supported by Public Health Ontario.

Potential conflicts of interest. The authors: No reported conflicts of interest. All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

References

1. Chan JFW, Yuan S, Kok KH, et al. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. Lancet **2020**; 395:514–23.
2. Zhou ZM, Zhou HZ, Lin XD, Su ZC, Zhao LS, Chen X. Outbreak of COVID-19 in a family, Wenzhou, China. Epidemiol Infect **2020**; 148:e103.
3. Gan H, Zhang Y, Yuan M, et al. [Epidemiological analysis on 1 052 cases of COVID-19 in epidemic clusters.] Zhonghua Liu Xing Bing Xue Za Zhi **2020**; 41:1004–8.
4. Madewell ZJ, Yang Y, Longini IM, Halloran ME, Dean NE. Household transmission of SARS-CoV-2: a systematic review and meta-analysis of secondary attack rate. medRxiv [Preprint]. August 1, **2020** [cited 2020 Sept 22]. Available from: https://www.medrxiv.org/content/10.1101/2020.07.29.20164590v1.
5. Curmei M, Ilyas A, Evans O, Steinhardt J. Estimating household transmission of SARS-CoV-2. medRxiv [Preprint]. June 27, **2020** [cited 2020 Sept 17]. Available from: https://www.medrxiv.org/content/10.1101/2020.05.23.20111559v2.article-metrics.
6. Lei H, Xu X, Xiao S, Wu X, Shu Y. Household transmission of COVID-19—a systematic review and meta-analysis. J Infect. **2020**; doi:10.1016/j.jinf.2020.08.033.
7. Zhang J, Litvinova M, Liang Y, et al. Changes in contact patterns shape the dynamics of the COVID-19 outbreak in China. Science **2020**; 368:1481–6.
8. Lewis NM, Chu VT, Ye D, et al. Household transmission of SARS-CoV-2 in the United States. Clin Infect Dis **2021**; 73:1805–13.
9. Wei L, Lv Q, Wen Y, et al. Household transmission of COVID-19, Shenzhen, January–February 2020. medRxiv [Preprint]. May 18, **2020** [cited 2020 Sept 28]. Available from: https://www.medrxiv.org/content/10.1101/2020.05.11.20092692v1.
10. Lopez Bernal J, Panagiotopoulos N, Byers C, et al. Transmission dynamics of COVID-19 in household and community settings in the United Kingdom. medRxiv [Preprint]. August 22, **2020** [cited 2020 Sept 25]. Available from: https://www.medrxiv.org/content/10.1101/2020.08.19.20177188v1.
11. Ontario Ministry of Health and Long-Term Care. COVID-19—guidance for the health sector. **2020**. Available at: http://www.health.gov.on.ca/en/pro/programs/publichealth/coronavirus/2019_guidance.aspx. Accessed 10 September 2020.
12. Schwartz KL, Achonu C, Buchan SA, et al. COVID-19 infections among healthcare workers and transmission within households. medRxiv [Preprint]. June 17, **2020** [cited 2020 Oct 1]. Available from: https://www.medrxiv.org/content/10.1101/2020.06.12.20129619v2.
13. Wang Y, Tian H, Zhang L, et al. Reduction of secondary transmission of SARS-CoV-2 in households by face mask use, disinfection and social distancing: a cohort study in Beijing, China. BMJ Glob Heal **2020**; 5:e002794.
14. Statistics Canada. Census data collection—Sampling and Weighting Technical Report, Census of Population, 2016. Available at: https://www12.statcan.gc.ca/census-recensement/2016/ref/98–306/ch1-eng.cfm#a1. Accessed 4 September 2020.
15. Office of the Premier. Ontario opens up COVID-19 testing across the province. **2020**. Available at: https://news.ontario.ca/en/release/57053/ontario-opens-up-covid-19-testing-across-the-province. Accessed 28 August 2020.
16. Xin H, Jiang F, Xue A, et al. Risk factors associated with occurrence of COVID-19 among household persons exposed to patients with confirmed COVID-19 in Qingdao Municipal, China. Transbound Emerg Dis **2020**; doi:10.1111/tbed.13743.
17. Liu T, Liang W, Zhong H, et al. Risk factors associated with COVID-19 infection: a retrospective cohort study based on contacts tracing. Emerg Microbes Infect **2020**; 9:1546–53.
18. Cheng HY, Jian SW, Liu DP, Ng TC, Huang WT, Lin HH; Taiwan COVID-19 Outbreak Investigation Team. Contact tracing assessment of COVID-19 transmission dynamics in Taiwan and risk at different exposure periods before and after symptom onset. JAMA Intern Med **2020**; 180:1156–63.
19. Shah K, Saxena D, Mavalankar D. Secondary attack rate of COVID-19 in household contacts: a systematic review. QJM An Int J Med **2020**; doi:10.1093/qjmed/hcaa232.
20. Arnedo-Pena A, Sabater-Vidal S, Meseguer-Ferrer N, et al. COVID-19 secondary attack rate and risk factors in household contacts in Castellon (Spain): preliminary report. Rev Enf Emerg **2020**; 19:64–70.
21. Dattner I, Goldberg Y, Katriel G, et al. The role of children in the spread of COVID-19: using household data from Bnei Brak, Israel, to estimate the relative susceptibility and infectivity of children. medRxiv [Preprint]. June 5, **2020** [cited 2020 Sept. 30]. Available from: https://www.medrxiv.org/content/10.1101/2020.06.03.20121145v1.