Court file No CV-22-006282-0000

ONTARIO
SUPERIOR COURT OF JUSTICE

B E T W E E N:

RANDY HILLIER

Applicant

-and-

HIS MAJESTY THE KING IN RIGHT OF THE PROVINCE OF ONTARIO

Respondent

AFFIDAVIT OF MATTHEW HODGE
(Affirmed November 18, 2022)

I, MATTHEW HODGE, of the City of Toronto in the Province of Ontario, **AFFIRM**:

I. BACKGROUND

1. I am a licensed medical practitioner who practices Public Health & Preventive Medicine ("**PHPM**") and Emergency Medicine in Ontario. I joined Public Health Ontario ("**PHO**") in October 2020 and was the co-lead for Epidemiology & Surveillance activities within the Incident Management System ("**IMS**") structure of the Health Protection division of PHO from November, 2020 until April 9, 2021. The global COVID-19 pandemic (the "**Pandemic**") constitutes a public health emergency, so many organizations, including PHO, established IMS structures to redeploy staff and prioritize activities. In my role within the IMS, I was responsible for strategic input and work on data management, analyses and reporting. Throughout the pandemic, I continued

practicing emergency medicine at the Scarborough General site of the Scarborough Health Network. My work there includes caring for patients with COVID-19 infections since March 2020.

2. I graduated with an MD (1996) and PhD (Epidemiology & Biostatistics, 1995) from McGill University and completed PHPM specialty training at the University of Toronto in 2000. Over the past twenty-two years, my practice has included multiple roles in public health, including Associate Medical Officer of Health, City of Hamilton (2005-2007), United Nations agencies (WHO: 1999-2001, UNICEF: 2001-2002, UNFPA: 2008-2010), Cancer Care Ontario (2010-2011), two positions with the Ontario Ministry of Health and Long-Term Care (2003-2004, 2015-2016), and a wide range of consulting work. I also completed Harvard's Masters in Health Care Management in 2011.

3. Following the province's declaration of an emergency in response to the Pandemic on March 17, 2020, I worked for six months assisting Peel Public Health's Pandemic response. My work there included guiding the implementation of the provincial Case & Contact Management system.

4. I also worked as a consultant with PHO from April 2021 to early 2022 providing expert witness testimony in litigation relating to provincial public health measures. In this capacity, I provided an expert report and was cross-examined in both *Ontario v. Adamson Barbecue Limited and Skelly* (Superior Court of Justice File No CV2020-652216) and *Ontario v. Trinity Bible Chapel* et al (Superior Court of Justice File No CV-2100000095). In this proceeding, I have been retained directly by the Ministry of the Attorney General to provide this report.

5. Since January 10, 2022, I have been employed 4 days a week by the Ontario Ministry of the Solicitor General as a Provincial Medical Officer in the Death Analytics for Safety and Health (DASH) Unit within the Office of the Chief Coroner and the Ontario Forensic Pathology Service.

I have attached as **Exhibit "A"** a copy of a job posting for this position which describes my duties. The terms of my employment allow me to take on outside work for a limited number of hours per week and I have been retained to provide evidence in this matter on that basis. It is not related to my duties and employment as a Provincial Medical Officer.

6. My *curriculum vitae* is attached to this affidavit as **Exhibit "B"**.

7. Public health is a distinct medical specialty recognized as such by the Royal College of Physicians and Surgeons of Canada (RCPSC). The RCPSC establishes the requirements for the 5-year specialist training in Public Health & Preventive Medicine comprising clinical training, Masters-level course work and placements in public health organizations which not all doctors practice or have training in. I attach as **Exhibit "C"** a page from the website of the Public Health Physicians of Canada providing its definition of public health's scope of practice. It notes that "While other physicians concentrate on diagnosing and treating individual patients, Public Health Physicians see entire communities as their patients" and that "Governments, communities and organizations rely on Public Health Physicians' unique training and expertise to inform fair public health policies, evaluate data, develop programs to prevent illness and injuries, and respond in times of emergencies such as outbreaks and natural disasters."

8. I have been asked to provide an expert opinion answering the questions relevant to this court proceeding that are set out below. My signed Acknowledgment of Expert's Duty is attached to this Affidavit as **Exhibit "D"**. Where I have relied on a document or data in forming my opinion, I have set out the citation to that document or data in the footnotes. Where I have relied on information provided to me by others, I have stated the source of that information and I believe it to be true.

II. OVERVIEW

9. I have been asked to answer the following questions in this expert affidavit:

a. What are the harms caused by COVID-19 disease?

b. How is COVID-19 disease transmitted?

c. What are the risk factors for transmission?

d. Why are measures to limit COVID transmission needed in Ontario?

e. Why do limits on outdoor gatherings and mobility contribute to reducing COVID-19 transmission and harms from COVID-19?

f. Do you agree or disagree with the affidavits of Dr. Warren and Dr. Kettner provided in this proceeding?

10. My answers are detailed below. I make three preliminary observations. First, my opinions are informed by the realities of public health practice in Ontario, including the need to prepare advice and make decisions with imperfect information, and the challenge of minimizing adverse effects of measures that establish limits on human behaviour. Ontario's Health Plan for an Influenza Pandemic, ("OHPIP"), attached as **Exhibit "E"** explicitly recognizes this reality of incomplete information, noting that 'the OHPIP severity model includes an initial stage before severity is known when the limited availability of surveillance data does not allow for confident identification of severity. The severity may not be clearly known until after an influenza pandemic is over'. [1] For COVID-19, the emergence of multiple clinically-significant variants with increased transmissibility and, for some variants, increased severity of illness, has added additional uncertainty.

11. Second, public health measures in Ontario must take into account the precautionary principle. The OHPIP states 'The MOHLTC does not await scientific certainty before taking

[1] See **Exhibit "E" at 10-14:** Ontario Ministry of Health and Long-Term Care, "Ontario's Health Plan for an Influenza Pandemic", (March 2013), online <https://www.health.gov.on.ca/en/pro/programs/emb/pan_flu/docs/ch_01.pdf >.

action to protect health'[2]. The application of the precautionary principle is particularly relevant during the early stages of a pandemic when scientific evidence on the severity of a novel virus is limited or, for COVID-19, as new variants are identified whose transmissibility and severity are incompletely understood at the time that government must make decisions to protect Ontarians from infection, illness and death.[3]

12. Third, my opinions are informed by the burden model, which recognizes that it is generally appropriate to implement more restrictive public health measures when an infectious disease imposes a higher burden. This notion of burden can be understood as a function of the prevalence of the disease (i.e. number of cases in a population), the exposure risk (i.e. the probability that one infected person will infect others), and the consequences of infection, such as hospitalization and death.

13. When Ontario enacted more stringent public health measures in the three waves of COVID-19 (spring 2020, winter 2020-21 and spring 2021) before vaccination was widely available, the combination of increasing community prevalence of COVID-19 and growing numbers of new cases, raised concerns about hospital and ICU occupancy. Accordingly, in my opinion it was a reasonable public health measure to limit gatherings temporarily while community spread of COVID-19 posed this potential (wave 1) or real (waves 2 & 3) burden on Ontario's health care system. Furthermore, the emergence of variants of concern ("VOC"), with initial uncertainty about their transmissibility and severity, borne out by evidence of higher transmissibility (alpha & delta variants) and more severe illness (alpha variant) prompted a more stringent public health response

[2] *Ibid*, at p. 11.
[3] For an example in the context of influenza, see *Ibid*, at p. 11.

III. WHAT ARE THE HARMS CAUSED BY COVID-19?

14. COVID-19 illness is caused by a coronavirus that infects the respiratory system. Infection causes symptoms of upper respiratory tract infection including cough, fever and sore throat. COVID-19 infection also appears to cause a characteristic loss of taste and smell for many infected people. Based on Ontario's COVID-19 experience through mid-2021, 5% of people with COVID-19 required hospital-based care, typically for oxygen at a minimum and often, ICU-level care. Complications leading to ICU admission or death may include respiratory failure, acute respiratory distress syndrome , sepsis and septic shock, thromboembolism, and/or multiorgan failure, including injury of the heart, liver or kidneys.[4] As of June 24, 2021 in Ontario, 543,571 people had been diagnosed with COVID-19, and 9,101 (approximately 1.7%) had died of COVID-19.[5] Both in mid-June 2021 and since, the number of cumulative cases of COVID-19 in Ontario is certainly higher than the number of recorded cases since some individuals who acquire COVID-19 are not tested and diagnosed. This was particularly the case during the early months of the COVID-19 pandemic.

15. The number of reported COVID-19 infections, hospitalizations, and deaths as of June 24, 2021 (Ontario) or June 25, 2021 (Canada, global) are set out in the table below:[6]

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[4] See **Exhibit "F":** World Health Organization, "Coronavirus disease (COVID-19)", (October 12, 2020), online <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/question-and-answers-hub/q-a-detail/coronavirus-disease-covid-19>.

[5] See **Exhibit "G":** Public Health Ontario, "Ontario COVID-19 Data Tool", (June 24, 2021), online < https://www.publichealthontario.ca/en/data-and-analysis/infectious-disease/covid-19-data-surveillance/covid-19-data-tool?tab=summary> (accessed 26 June 2021).

[6] See **Exhibit "E"**, *supra* note 2; **Exhibit "H"**: Government of Canada, "Coronavirus disease 2019 (COVID-19): Epidemiology update", (June 25, 2021), online <https://health-infobase.canada.ca/covid-19/epidemiological-summary-covid-19-cases.html>. **Exhibit "I"**: World Health Organization, "Weekly epidemiological update – April 20, 2021" (April 20, 2021), available online < https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---20-april-2021>.

Table 1: Cases, hospitalizations, and deaths

	Cases	Hospitalizations	Deaths
Ontario[7]	543,571	27,643	9,101
Canada[8]	1,412,226	74,044	26,197
Global[9]	179,686,071	Unavailable	3,899,172

16. By spring 2021, clinically-significant (i.e. causing significantly more frequent or more severe illness in humans) COVID variants were expected to continue to arise due to high rates of viral transmission globally. Between March 2020 and June, 2021, Ontario's context evolved with increases in the prevalence of VOCs. As an example of the impact of VOCs in Ontario, the B117 variant (later designated as the alpha variant) was reported to be more transmissible and cause more severe illness, contributing to an increased percentage of people with COVID-19 who need hospitalization and ICU care, including younger people in their 40s and 50s.[10]

17. At the beginning of each new variant's emergence throughout COVID-19, it was very hard to know with any certainty if the new variant would have different transmissibility and severity of symptoms than previous variants. In broad terms, respiratory viruses infecting humans 'want' to become more transmissible because they cannot survive without human hosts. Lacking the ability to direct their own evolution, viral evolution favours mutations that are more transmissible. As a result of this general biologic principle, COVID variants were expected to arise, expected to be more transmissible and the specifics of when and where they would arise remained unknowable.

[7] See **Exhibit "G"**, *supra* note 5.
[8] See **Exhibit "H"**, *supra* note 6.
[9] See **Exhibit "J":** World Health Organization, "WHO Coronavirus (COVID-19) Dashboard", (June 25, 2021), online <https://covid19.who.int/>.
[10] See **Exhibit "K":** A.R. Tuite et al., "COVID-19 hospitalizations, ICU admissions and deaths associated with the new variants of concern" (2021) Science Briefs of the Ontario COVID-19 Science Advisory Table 1(18), online <https://covid19-sciencetable.ca/wp-content/uploads/2021/03/Science-Brief_VOC-Prognosis_20210329_published4.pdf>.

18. Specifically relevant to early 2021 events at issue in this matter, the delta variant had been identified in late 2020 in India and rapidly overtook other variants to become dominant by mid-2021 in Ontario.[11] Early reports from the UK suggested more than double the rate of hospitalization due to delta variant infection than had been seen with the alpha variant that delta supplanted. In addition, concern about higher transmissibility of delta and uncertainty about vaccine effectiveness against delta meant that even if overall case numbers in Ontario were decreasing, delta variants would make up an increasing proportion of all cases thus raising risks of overwhelming hospitals due to the higher risks of hospitalization due to delta.

19. The number of COVID-19 cases and hospitalizations in Ontario increased with each of the first three COVID 'waves', periods marked by rising case loads and concomitant rising pressures on Ontario's health system. Numbers of hospitalizations are relevant to COVID-19 decision-making because Ontario has the lowest rate of hospital beds per 1000 population (1.4) compared to the Canadian average (2.0). Overall, Canada's hospital capacity is among the lowest of the OECD countries, with 20% more in the USA (2.4/1000), 30% more in Italy (2.6/1000) and 55% more in France (3.1/1000).[12] Given that Canada has relatively few beds and Ontario has the fewest in Canada, the threshold above which the burden of COVID-19 infections and illness could push Ontario' acute care system past the point of being able to provide care to patients is logically lower than in other countries or even other Canadian provinces.

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[11] See **Exhibit "L":** Ontario COVID-19 Science Advisory Table, "Graph: Percentage of Cases Caused by Different Variants in Ontario", (September 15, 2022), online <https://covid19-sciencetable.ca/ontario-dashboard/#percentcausedbyvariants>. Also see Initial reports circulated via professional networks indicated higher transmissibility based on India's experience and higher rates of hospitalization (UK) were confirmed in peer-reviewed publications by mid-2021, see **Exhibit "M":** Katherine A. Twohig et al., "Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study", (August 27, 2021), Lancet – Infect Dis 22(1) 35-42, online <https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(21)00475-8/fulltext>.

[12] See **Exhibit "N":** Ontario Hospital Association, "Ontario Hospitals – Leaders in Efficiency", (December 2019), online https://www.oha.com/Documents/Ontario%20Hospitals%20-%20Leaders%20in%20Efficiency.pdf>.

20. Ontario's response to COVID hospitalizations has, by virtue of this lower number of hospital beds compared to other comparable jurisdictions, involved moving substantial numbers of patients from the hospital at which they arrived to one with an available bed, often far from their community[13] and, at a societal level, implementing non-pharmaceutical interventions ("NPIs"). NPIs comprise a bundle of measures, including temporary restrictions on mobility and gatherings, designed to reduce COVID-19 transmission and thus hospitalization and death. NPIs are intended both to mitigate threats to the integrity of health care and to 'minimize serious illness and overall deaths through appropriate management of Ontario's health system.'[14]

21. A health system in which every available bed is occupied by someone infected with COVID-19 has no way to respond to people with heart attacks, hip fractures or strokes, potentially adding to the elevated mortality attributable to COVID-19. Put simply, the harms caused by COVID-19 would be compounded with additional preventable deaths due to heart attacks, hip fractures and other health conditions if there are no beds and, more important, no staff available to care for patients with these conditions. Once overwhelmed, the acute care system would likely face a prolonged recovery period, hence the relevance of the precautionary principle to decision making in these uncertain times to ensure the integrity of the health system.

[13] See **Exhibit "O":** K. Grant & S. Singh, "How COVID-19 exposed long-term health-care issues at Brampton hospitalOntario Health", (June 21, 2021), Globe and Mail, online < https://www.theglobeandmail.com/canada/article-how-the-covid-19-pandemic-exposed-long-term-health-care-issues-at/>. Article cites data noting 3219 transfers between mid-November, 2020 and the end of May, 2021.
[14] See **Exhibit "E"**, *supra* note 1 at p. 10.

IV. HOW IS THE VIRUS TRANSMITTED?

22. COVID-19 is caused by the SARS-CoV-2 virus and its variants (together, "**COVID-19**" or the "**Virus**"), which spreads between people, through respiratory particles of varying sizes, mainly when an infected person is in close contact with another person.[15]

23. COVID-19 can spread from an infected person's mouth or nose in small liquid particles when they cough, sneeze, speak, sing, or breathe heavily. These liquid particles are different sizes, ranging from larger respiratory droplets to smaller aerosols. Notwithstanding the reality that scientific knowledge continues to evolve, a broad consensus that these particles travel further indoors than outdoors and their survival on surfaces appears to be greater indoors than outdoors has emerged. Whether indoors or outdoors, people contract COVID-19 when the Virus enters their mouth, nose, or eyes.[16]

24. Many people infected with COVID-19 show no symptoms (asymptomatic) or experience several days between when they are infected and when they develop symptoms (presymptomatic). This is particularly challenging for public health practice and policy advice as transmission risk seems to be highest prior to symptoms appearing, meaning that most infected people will unknowingly infect others before they themselves have symptoms.[17] Thus, to reduce COVID-19 transmission and the harms, including hospitalization and death that such transmission can cause, NPIs need to apply to people who do not exhibit COVID-19 symptoms in order to be effective.

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[15] See **Exhibit "P":** Public Health Ontario, "COVID-19 Transmission Through Large Respiratory Droplets and Aerosols…What We Know So Far" (May 2021), online <https://www.publichealthontario.ca/-/media/documents/ncov/covid-wwksf/2021/05/wwksf-transmission-respiratory-aerosols.pdf?la=en>.

[16] See **Exhibit "Q":** World Health Organization, "Coronavirus disease (COVID-19): How is it transmitted?", (December 13, 2020), online <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/question-and-answers-hub/q-a-detail/coronavirus-disease-covid-19-how-is-it-transmitted>.

[17] *Ibid*.

V. WHAT ARE THE RISK FACTORS FOR TRANSMISSION?

25. While transmission risks are probabilistic, they cannot be specified with the accuracy of the probability of different outcomes of a tossed coin or a particular poker hand. What is clear is that transmission risks increase with being in close contact for prolonged periods, higher voice volume, being indoors, inconsistent use of face coverings (such as removing a face covering to talk or shout, eat or drink), improper use of face coverings (e.g. not covering the nose or wearing one that is too loosely fitted), and background infection rates in the community(s) from which a gathering's attendees are drawn.

26. The World Health Organization provides the '3C' framework for assessing risks of COVID-19 transmission: crowded places, close contact, confined spaces. Risks of Virus transmission are increased when two or more of these conditions occur together.[18] In addition, risks increase with increasing degrees of the 3Cs, including:

a. being in close contact for longer periods causes greater risk than shorter periods;[19]

b. higher voice volume likely increases both droplet production and projection;[20]

c. being indoors increases risk, as droplets persist in indoor environments longer than outdoors;[21] and

d. inconsistent or improper use of face coverings, such as removing a face covering to sing or consume food and beverages or leaving the nose uncovered, increases risk.

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[18] See **Exhibit "R"**: World Health Organization, "Avoid the Three Cs", (undated), online <https://www.who.int/images/default-source/wpro/countries/malaysia/infographics/three-3cs/final-avoid-the-3-cs-poster.jpg?sfvrsn=638335c1_2>.
[19] **Exhibit "P"**, *supra* note 15.
[20] See attached **Exhibit "S"**: Valentyn Stadnytskyi et al., "The airborne lifetime of small speech droplets and their potential importance in SARS-CoV-2 transmission", (2020) PNAS 119(22) 11875-11877, online <https://www.pnas.org/content/117/22/11875>.
[21] **Exhibit "P"**, *supra* note 15.

27. The risk from any particular setting is also determined by the likelihood that other persons present are infected with COVID-19. Community prevalence describes the percentage or rate of COVID-19 infection in a population. When community prevalence is elevated, even lower risk activities can contribute to pressures on the integrity of the health system as more infections lead to increased numbers of persons needing hospitalization.

28. After the first wave of COVID-19 in Ontario when COVID-19 spread widely within institutional settings such as long-term care homes ("LTCHs"), transmission risks were highest in non-institutional settings such as workplaces and households. Secondary attack rates (the number of cases among contacts of a case) within households have been estimated to be 5-10 fold higher than in non-institutional , non-household settings.[22] The transmissibility of COVID-19 within households is complex and determined by still poorly understood interactions of density (persons per room), social interaction patterns among household members, use of personal protective equipment within the home, and social and cultural norms determining roles and behaviours within households. As these are not amenable to policy action on the time scale of COVID-19 transmission, the cornerstone of evidence-informed actions to reduce the burden of COVID-19 in Ontario is reducing risks of COVID-19 being introduced into households, thus reducing COVID-19 transmission and subsequent cases of clinical illness, hospitalization and death. Prior to widespread vaccine availability and uptake as was the case for the first half of 2021, protecting people from COVID infection relied almost entirely on the population's willingness to comply with relatively stringent NPIs as these were the only measures available to reduce risks of COVID being introduced into households and consequent risks of the health system being overwhelmed.

[22] See **Exhibit "T":** Lauren A. Paul et al., "Characteristics associated with household transmission of SARS-CoV-2 in Ontario, Canada" (October 26, 2020), medRxiv BMJ Yale, online <https://www.medrxiv.org/content/10.1101/2020.10.22.20217802v1.full.pdf+html> (accessed 26 June 2021).

29. COVID-19 infection occurring at a discrete location or event is referred to as outbreak, when the infection in question can be linked to a source case from the same location or event. Thus, the 'outbreak effect' can be thought of as the potential for transmission to attendees at such events. In public health practice, this outbreak effect would include all cases among attendees. Secondary cases arise from people with primary transmission returning to their households, or other prolonged confined spaces such as workplaces, and infecting people who did not attend the location/event. This can be termed the "network effect". Events with a modest outbreak effect, such as those occurring in a lower-risk setting or with fewer attendees, may nonetheless lead to a greater number of subsequent infections due to this network effect. For example, if a gathering of 100 people resulted in only 5 new primary transmissions, it might appear at first glance to have only negligibly contributed to the spread of COVID-19, (the outbreak effect). However, if each of those 5 people returns to a household where 4 more secondary transmission arise from each primary transmission, the event's overall impact is much higher (the network effect). Some portion of these 25 people may move on to other households or workplaces and contribute to tertiary transmissions, further increasing the network effect. Prior to vaccination, such as in early 2021, shortening transmission chains rested on measures to limit contacts among people and limits on the size and occurrence of gatherings was essentially the only available means to do so.

30. An example of these effects was provided by the US CDC's November 2020 publication of the results of an investigation into COVID-19 arising from the August 2020 Sturgis motorcycle rally held in South Dakota, a state with no limits on gatherings (attached as **Exhibit "U"**).[23] While border crossing restrictions meant that few Canadians could attend, the CDC report assessed these

[23] See **Exhibit "U"**: Melanie J. Firestone et al., "COVID-19 Outbreak Associated with a 10-Day Motorcycle Rally in a Neighboring State — Minnesota, August–September 2020", (November 27, 2020), MMWR 69(47) 1771-1776, online < https://www.cdc.gov/mmwr/volumes/69/wr/mm6947e1.htm>.

outbreak and network effects by establishing molecular linkage among cases in people living in Minnesota. Fifty-one persons who developed COVID-19 and attended the event were identified (outbreak effect) which led to a further 35 identified cases in households, social circles and workplaces of the 51 identified cases (network effect). Cases were relatively widespread with one-third of the counties in Minnesota having at least one of these 86 cases. In addition, the authors reported that 10 of the 51 cases stated they had close contacts while infectious but declined to provide details, highlighting the real limitations of contact tracing as a means of protecting people from COVID-19 infection.

31. At a population level, the overall risk of transmission is further increased when community prevalence of the virus is higher, since any encounter carries a higher chance of involving a person infected with COVID-19. In addition, gatherings that draw individuals from different households together increase risks of transmission to more households, increasing the expected burden of COVID-19. High rates of household transmission, with entire families being hospitalized during the most recent period of heightened incidence, highlight the importance of implementing public health measures that reduce the chances of COVID-19 entering a household.

D. WHY ARE MEASURES TO LIMIT COVID-19 NEEDED IN ONTARIO?

32. Seeking to protect persons from mortality and morbidity from COVID-19 and to reduce the likelihood the acute care system would be overwhelmed by persons requiring hospital care for COVID-19 infection, the government of Ontario implemented different bundles of temporary public health measures, generally referred to as non-pharmacologic interventions ("NPIs") since March 2020. NPIs seek to reduce close contact among persons from different households, and thus reduce COVID-19 transmission risk. NPIs implemented temporarily in Ontario are broadly similar to those implemented in most if not all OECD jurisdictions and include limits on occupancy of

indoor spaces, mobility limits, limits on and prohibitions of gatherings and events, and school closures.

33. These policy interventions are complemented by individual-focused**,** evidence-based mitigation measures such as requirements for face covering and physical distancing. Together these measures, both individual and policy level, can reduce, but not eliminate, the risk of COVID-19 transmission. Ontario's *Roadmap to Reopening* was released in May 2021[24] and indicated the government's intention of linking the end of NPIs to increasing levels of vaccination among Ontarians. Vaccination rates were not high enough during the spring 2021 wave, however, to significantly reduce the burden of COVID-19 on the population. As of the week ending April 3, 2021, only 14.5% of the population had received a single dose of a COVID-19.[25] This figure had risen to 63.1% by the week ending June 12, 2021,[26] reflecting a rapid roll-out of vaccination over the period leading up to the revocation of the Stay-At-Home Order on June 2, 2021,[27] and all public health units in the province being moved out of the Shutdown Zone and into the less restrictive Step 1 category on June 11, 2021.[28]

E. WHY DO LIMITS ON OUTDOOR GATHERINGS AND MOBILITY CONTRIBUTE TO REDUCING COVID-19 TRANSMISSION AND HARMS FROM COVID-19?

34. From an epidemiologic perspective, all gatherings as a class pose transmission risks that rise with increasing numbers of attendees, reflecting the declining probability that every person

[24] See **Exhibit "V":** Government of Ontario, "Roadmap to Reopen", (May 20, 2021), online < https://news.ontario.ca/en/backgrounder/1000159/roadmap-to-reopen>.
[25] See **Exhibit "W":** Public Health Ontario, "Ontario COVID-19 Data Tool: Single Dose Vaccinations", (April 3, 2021), online < https://www.publichealthontario.ca/en/data-and-analysis/infectious-disease/covid-19-data-surveillance/covid-19-data-tool?tab=vaccine>.
[26] See **Exhibit "X":** Public Health Ontario, "Ontario COVID-19 Data Tool: Single Dose Vaccinations", (June 12, 2021), online < https://www.publichealthontario.ca/en/data-and-analysis/infectious-disease/covid-19-data-surveillance/covid-19-data-tool?tab=vaccine>.
[27] See **Exhibit "Y":** O. Reg. 265/21: STAY-AT-HOME ORDER under the *Emergency Management and Civil Protection Act, R.S.O. 1990*, c. E.9, online <https://www.ontario.ca/laws/regulation/r21265>.
[28] See **Exhibit "Z":** O. Reg. 441/21: STAGES OF REOPENING under the *Reopening Ontario (A Flexible Response to COVID-19) Act, 2020*, S.O. 2020, c. 17, online <https://www.ontario.ca/laws/regulation/r21441>.

present will be COVID-free as the number of persons increases. While outdoor settings pose less risk of transmission than indoor settings,[29] even a low probability of transmission can generate a large number of new infections if a gathering includes enough people and therefore generates a high number of person-to-person interactions, more so if attendees do not distance or wear masks. These primary infections would in turn be expected to result in secondary infections once the gathering's attendees return to their households.

35. The study of outdoor transmission rates is further complicated by the fact that not all outdoor settings are equal. One study found that lower outdoor wind speed is associated with higher transmission rates.[30] This is also an indication that outdoor transmission does occur, because if there were no outdoor transmission at all, then weather conditions should have no impact on transmission rates, all other things being equal.

36. The probability of transmission at any gathering also increases when the rate of COVID-19 infection is high in the general population, as in Ontario in spring 2021, since that increases the odds that any given participant in a gathering has COVID-19. For public health practice, this arithmetical reality supports limits on activities that may pose low relative risks of COVID-19 transmission at the height of waves of infection, because the absolute risk (i.e. total number of infected persons in the population which will determine needs for health services) will nonetheless increase.

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[29] See **Exhibit "AA":** T. C. Bulfone et al., "Outdoor Transmission of SARS-CoV-2 and Other Respiratory Viruses: A Systematic Review", (February 24, 2021) J Infect Dis 223(4): 550-561, online <https://pubmed.ncbi.nlm.nih.gov/33249484/>.

[30] See **Exhibit "BB":** Sean A. P. Clouston et al., "A wind speed threshold for increased outdoor transmission of coronavirus: an ecological study", (November 27, 2021) BMC Infectious Diseases 21(1194), online < https://bmcinfectdis.biomedcentral.com/articles/10.1186/s12879-021-06796-z>.

37. The risk of transmission at an outdoor gathering would also increase if participants do not maintain sufficient distance from each other, do not use effective face coverings and participate in a gathering for a longer period of time. It is not feasible for public health authorities to ensure that every outdoor gathering across Ontario observes these practices. Informal gatherings, including political protests, may be unlikely to have an identified person in charge who has the power to enforce such measures, unlike in more structured environments such as a workplace, business or formal religious gathering. Political protests including shouting and/or singing, both of which increase transmission risks, would also be similarly unlikely to include an individual participant or participants able to stop fellow participants from shouting and singing.

38. Even if the thought experiment in which all participants at all outdoor gatherings observed distancing, wore face coverings 100% of the time and refrained from singing and shouting were plausible, transmission risks would still arise from ancillary activities innately associated with gatherings. As an example, attendees from different households may socialize together before or after the gathering, when there is less pressure to observe distancing measures. In addition, attendees may travel together to the gathering by public transit or carpooling. If the gathering includes people from widespread geographic areas, this could both increase exposure during travel as people travelled further and thus for longer durations and would also increase the risk of transmission from parts of the province with higher rates to other areas with lower rates.

39. To be effective, NPIs include broad, general limits on personal mobility. While a person does not literally increase the risk of COVID-19 transmission simply through the act of leaving their home, they are more likely to be exposed to higher-risk environments by having done so. Many commentators, including people with medical expertise, seem to conceive of mobility limits as if they are a suite of chemotherapy drugs, each able to be studied individually in a laboratory

setting and then in a human population and then in combination with other drugs. That granularity and the luxury of time to study each specific mobility limitation while a novel virus evolves dynamically across the global population is not only impossible but indulging in such studies of NPIs would arguably be public health malpractice. Where direct, granular public health rules targeting high-risk activities are insufficient to prevent increasing COVID-19 transmission, as in the spring 2021 wave, broad limits intended to reduce mobility generally are more likely to be effective. Broad, temporary restrictions also reflect the heightened urgency associated with the increased risk of transmission and the increased burden on the health care system that occurred during the peak of the first three waves of COVID-19 in Ontario.

40. The temporary limits in Ontario, more stringent than in many jurisdictions to the south, translate into thousands fewer people dead:

	ONTARIO	SWEDEN	BRAZIL	FLORIDA	TEXAS
POPULATION	14,000,000	10,159,183	213,956,756	21,600,000	29,500,000
COVID-19 DEATHS AS OF LATE JUNE/EARLY JULY, 2021	9,101[31]	14,643[32]	524,417[33]	37,772[34]	51724[35]
CRUDE DEATH RATE[36]	0.65/1000	1.44/1000	2.45/1000	1.75/1000	1.75/1000
PROJECTED ADDITIONAL DEATHS IN ONTARIO[37]	NA (zero)	+11,060 (+122%)	+25,200 (+277%)	+15,400 (+169%)	+15,400 (+169%)

VII. DO YOU AGREE OR DISAGREE WITH THE AFFIDAVITS OF DR. WARREN, AND DR. KETTNER?

i) Dr. Warren's affidavit

41. I have reviewed the affidavit of Dr. Warren.

42. I agree with Dr. Warren that outdoor transmission of COVID-19 is less likely than indoor transmission of COVID-19, all other variables being equal. I do not agree, however, that public health measures to respond to a new coronavirus can be based on assuming that it will share the identical transmission characteristics as tuberculosis and influenza. It is now clear, for example, that transmissibility varies even among the different variants of SARS-CoV-2. In early 2021,

[31] See **Exhibit "G"**, *supra* note 5.
[32] See Exhibit **"CC":** World Health Organization, "WHO Coronavirus (COVID-19) Dashboard: Sweden", (July 4, 2021), online < https://covid19.who.int/region/euro/country/se> (Accessed 26 June 2021).
[33] See Exhibit **"DD":** World Health Organization, "WHO Coronavirus (COVID-19) Dashboard: Brazil", (June 29, 2021), online < https://covid19.who.int/region/amro/country/br> (Accessed 30 June 2021).
[34] See **Exhibit "EE**": New York Times, "Tracking Coronavirus in Florida: Latest Map and Case Count", (June 25, 2021), online <https://www.nytimes.com/interactive/2021/us/florida-covid-cases.html> (Accessed 26 June 2021).
[35] Calculated, as cumulative deaths through 30 June 2021 from Excel data available from State of Texas Department of Health at <https://dshs.texas.gov/coronavirus/AdditionalData.aspx>.
[36] Number of reported cases/population; age-adjustment would yield slightly more accurate figures but the change due to age adjustment is insufficient to explain the greater than 2-fold variation.
[37] Calculated as (death rate in jurisdiction – death rate in Ontario)*population of Ontario

concerns about the delta variant were both real and dynamically evolving as knowledge of this variant accrued and was incorporated into policy advice. Dr. Warren's approach is contrary to the precautionary principle, which suggests being more cautious when a new virus arises instead of risking thousands of lives through assuming that it will share the same traits as a previous virus, particularly one from which it is phylogenetically distinct (influenza).

43. In any event, the transmissibility of tuberculosis is quite different than SARS-CoV-2. Tuberculosis infection can produce active disease or latent disease. Latent disease will cause clinical symptoms months to years later or perhaps not at all. By contrast, clinical symptoms of SARS-COV-2 occur within a few days of exposure. This time, from infection to clinical symptoms is defined as the serial interval and estimated to range from approximately 6 months to 1.5 years for tuberculosis.[38] By contrast the serial interval for SARS-COV-2 is estimated to range from 4 to 7 days.[39] In part as a mathematical consequence of this dramatically shorter serial interval, the effective reproduction number for TB, estimated to range from 0.24 to approximately 4 is rather less than that of SARS-COV-2, estimated to be 5 for delta and as high as 9 for the more recent omicron variant. Since TB is not at issue in this matter and the applicants take no issue with Ontario's approach to TB control, its relevance as a basis for policy making for COVID-19 appears to be weak, given that it behaves quite differently.

44. Even if SARS-CoV-2 transmission was ultimately determined to be identical to influenza transmission, there would still be reason to approach the former differently than the latter. Data from Ontario's experience through early 2021 confirm that the consequences of acquiring

[38] See **Exhibit "FF":** Y. Ma et al., "Quantifying TB transmission: a systematic review of reproduction number and serial interval estimates for tuberculosis", (July 4, 2018) Epidemiology & Infection 146(12) 1478–1494, online <hhttps://www.ncbi.nlm.nih.gov/pmc/articles/PMC6092233/>.
[39] See **Exhibit "GG":** M. Alene et al., "Serial interval and incubation period of COVID-19: a systematic review and meta-analysis", (March 11, 2021) BMC Infectious Diseases 21:257, online
< https://bmcinfectdis.biomedcentral.com/articles/10.1186/s12879-021-05950-x>.

influenza are generally less severe, with significantly lower mortality and hospitalization rates than for COVID-19. Accordingly, seasonal outbreaks of influenza do not result in the same sustained pressures on hospital and ICU capacity. It should also be pointed out that influenza has been thoroughly studied whereas COVID-19 is a new disease with even newer variants. The public health response to influenza has been finely tuned over decades. While obvious, it bears noting that there simply has not been the same lengthy period available for finely tuned public health measures to address COVID-19.

45. Dr. Warren's reliance on confirmed outbreaks from outdoor gatherings does not provide a complete picture of the population-level risks surrounding these events. First, an outbreak may never be accurately documented by public health authorities if participants do not participate in contact tracing, or if they have been exposed to multiple risks over the relevant time period (for example, travel together, which Dr. Warren acknowledges is an important source of infection). Second, as described earlier, public health practice and advice to governments require consideration of the risk of network effects of transmission, not only outbreak effects. This is a distinct practice and perspective from that of a physician without public health training or public health practice experience who focuses on individual health and therefore may not account for the large absolute number of infections, and associated burden, that can result from large numbers of people participating in activities with lower relative risks of transmission. Third, even if Dr. Warren is correct that outdoor gatherings themselves do not pose any risk, he does not account for associated activities such as socializing and travel, for the impossibility of contact tracing people who cannot be identified or who decline to participate, and for the difficulty of imposing preventative measures, such as limiting the duration and adhering to distancing and face covering in the less structured context of the gatherings at issue in this matter.

46. Dr. Warren acknowledges that "there is clear biological and epidemiological rationale for avoiding crowding" but is of the view that "there is an absence of high-quality evidence, such as randomized-controlled trials, that prove the effectiveness of avoiding crowding in particular groups or contexts" (page 174-175). This complaint fundamentally misunderstands the core limitation on public health practice in the face of a novel virus, which is that decisions with the highest possible stakes have to be made in the *absence* of high-quality evidence. In reality, waiting until randomized control trials were completed on the effectiveness of each NPI being considered in Ontario would have meant doing nothing while tens of thousands of avoidable deaths occurred. Randomized controlled trials of NPIs also raise ethical challenges that make them highly impractical to conduct during emergencies. As an example, the randomized controlled trial would require finding sufficient people to give their informed consent to participate in crowding despite the "clear biological and epidemiological rationale" suggesting that this would expose them to a deadly disease, weeks to months of follow-up, analytic gymnastics and molecular testing to distinguish crowding-associated infections from infections acquired through other exposures, and a level of resources for population health research which is unfathomable.

47. Even if such trials had already been produced within the first year of the COVID-19 under the exact conditions necessary to understand their effectiveness within Ontario, as Dr. Warren would require, they would have been in relation to prior variants and therefore arguably no longer "high-quality" with respect to the alpha and delta variants that emerged in 2021. The repeated emergence of variants with differing human health impacts has required decisions to be made with imperfect information throughout the pandemic.

iii) Dr. Kettner's affidavit

48. I have reviewed the affidavit of Dr. Kettner. Dr. Kettner focuses primarily on the outbreak effect associated with outdoor gatherings, whose limitations I have addressed above.

49. Dr. Kettner argues that contact tracing could have been used to estimate the rate of transmissions associated with outdoor gathering. Even with the NPIs Ontario implemented, the sheer number of cases rendered contact tracing near-impossible due to a lack of human resources to do the work. Even when human resources were available, the result was often less than theoretically effective due to delays in contacting cases, willful non-participation by some case persons and/or misrepresentation of their whereabouts and potential contacts, and the lack of 'total recall' of all possible exposure locations by all contacts. The biologic reality of presymptomatic transmission of COVID-19 creates additional limitations of the effectiveness of contact tracing of which Dr Kettner appears either unaware or if aware, has chosen to omit.

50. Dr. Kettner notes hospitalization rates declined in June 2021 (at page 233). This was a relevant input to the government's decision to remove temporary limits on outdoor gatherings in June, 2021. I am unable to determine if the expert is suggesting that the removal of limits on gatherings caused the decrease in hospitalizations. What is clear is that vaccination rates also significantly improved over this time period, and the transition to warmer weather likely also contributed to reduced transmission. If the expert's position is that allowing outdoor gatherings and more mobility within Ontario somehow contributed to decreased transmission, I would respectfully disagree.

51. Finally, Dr. Kettner relies on several publications that post-date the spring 2021 and the April 8, 2021 order at issue in this matter wave and therefore were not part of the public health evidence that could be considered at the time the limits on outdoor gatherings at issue in this matter

were implemented. These include the November, 2021 WHO guidance referred to at footnote 5 of the expert's affidavit, the CBC article referred to at footnote 6, (dated April 10, 2021), the Centers for Disease Control publication referred to at footnote 7 of his report, and the paper at footnote 8 (e-published 4 June 2021).

AFFIRMED by video conference by MATTHEW HODGE of the City of Toronto in the Province of Ontario before me on this 18th day of November, 2022 in accordance with O Reg 431/20, Administering Oath or Declarati

Commissioner for the Taking of Affidavits
LSO #61687J

MATTHEW HODGE

Court File No.: CV-22-006282-0000

RANDY HILLER	**-and -**	**HIS MAJESTY THE KING IN RIGHT OF THE PROVINCE OF ONTARIO**
Applicants		Respondent

ONTARIO
SUPERIOR COURT OF JUSTICE
Proceedings Commenced at Toronto

AFFIDAVIT OF MATTHEW HODGE

THE ATTORNEY GENERAL OF ONTARIO
Civil Law Division
Constitutional Law Branch
720 Bay Street, 4th Floor
Toronto, ON M7A 2S9
Fax: 416-326-4015

Padraic Ryan (LSO# 61687)
[redacted]
Ryan Cookson (LSO # 61448D)
[redacted]
Savitri Gordian (LSO #66891Q)
[redacted]
Counsel for the Respondent

This is **"Exhibit A"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

_____
A Commissioner, etc.

Job Specification

Position Title: Provincial Medical Officer-DASH
Job Code: MMD03 - Medical Manager
Job ID: 168233

Purpose of Position :

To provide effective medical leadership and strategic management of the Death Analytics for Safety and Health (DASH) Unit within the Office of the Chief Coroner (OCC) and Ontario Forensic Pathology Service (OFPS) to advance public health and community safety through the analysis, application and dissemination of death investigation data. Lead and oversee the effective extraction of data from investigative reports generated by the OCC/OFPS investigations to inform recommendations and policy reform to improve the health and safety of Ontarians.

Duties / Responsibilities :

Leadership
• Leads assessment and analytics activities at the OCC/OFPS geared at generating scientific and technical knowledge for evidence-informed mortality prevention, decision making, and planning.
• Leads the development and implementation of the DASH Unit strategic plan and associated project management and evaluation.
• Builds and maintains complex and highly politically sensitive relationships and partnerships with key internal and external stakeholders.
• Provides leadership and expertise into conducting research and analysis related to health and safety system trends, policy development and practices as well as related medical and technical implications.
• Identifies opportunities for the OCC/OFPS to contribute research-based knowledge and information to improve the health and safety of Ontarians.

Management
• Direct supervision of the DASH unit staff, including recruitment, training, performance management, and managing potential problems and conflicts.
• When requested, translate data and analytics to deliver or support policy review and reform, educational initiatives, and directives to improve the caliber of coroner investigations.
• Reviews current data to enable and support decision-making processes for the OCC/OFPS and its stakeholders.

Medical and Death Investigation
• Ensure accurate analysis and interpretation of death investigation data by providing direction on matters pertaining to medical sciences and death investigation.
• Act as the DASH Unit's senior medical resource, including interpretation and application of complex medical concepts and terminology.
• Oversee the conduct of comprehensive medical analysis, synthesis, and reporting of information with respect to death investigation data.
• Identify public health and safety issues and provide strategies and/or strategic partnerships to address them.
• Plan and deliver educational lectures and programs for coroners, pathologists, other medical professionals, including supervision of post graduate trainees from the health field, police, Crown attorneys, emergency response personnel, medical students, and other groups.
• Exchange knowledge and represent the OCC/OFPS at local, provincial, national, and international forums, as appropriate.
• Represent the OCC/OFPS on various ministry committees and advisory boards when requested.

Application of the Public Health Sciences & Principals
• Oversees the preparation of scientific and technical data produced from investigations conducted by the OCC/OFPS for the purpose of analysis and/or publication both internally and externally.
• Liaises and coordinates with stakeholders across multiple sectors – including government, public health, health agencies, academic institutions, and enforcement and investigative agencies – to ensure death investigation data analyses supports death prevention and policy development.
• Provides expertise to support the programs and services, research, and surveillance activities of the OCC/OFPS, geared at generating scientific and technical knowledge for evidence-informed mortality prevention, decision making, and planning.
• Provides subject-matter expertise and resource support to OCC/OFPS colleagues, ministries, and agencies.

Staffing and Licensing :

• A physician who is licensed and in good standing with the College of Physicians and Surgeons of Ontario

Knowledge :

• Clinical public health and/or policy typically acquired through certification or degree in Public Health or Community Health in order to apply clinical public health principles to data analysis.
• Knowledge of working with government and of legislative policy development processes of various levels, including specific knowledge of the Coroners Act, Anatomy Act, Vital Statistics Act, Long Term Care Homes Act, Mental Health Act, Occupational Health & Safety Act, Health Protection and Promotion Act and Regulated Health Professionals Act.
• Knowledge pertaining to developing and leading medical teams to apply public health sciences to analyze and disseminate death investigation data from medical findings.
• Knowledge of and ability to apply classification and coding procedures of various types of death for use in statistical analyses.
• General and forensic investigation techniques and related understanding of pathology and toxicology.
• Public health sciences and data analysis skills – including epidemiology, qualitative and quantitative research methods, and critical appraisal – to analyze, interpret and disseminate death investigation data to inform and evaluate health and safety initiatives.
• Knowledge and experience in the development of evidence-informed best practice guidelines and the knowledge translation required for their implementation.
• Public health and safety systems, including the healthcare system to understand how to integrate/share death investigation data and DASH research findings into the appropriate public health, safety, and prevention partners.
• Human resources management and administration to manage staff, resolve conflicts and establish goals and priorities.
• Leadership, strategic thinking, problem solving, innovation, and change management skills to develop effective strategies, attain goals, build consensus, and manage conflict.
• Oral and written communication skills to prepare and present a range of technical information appropriate to the audience.
• Political acuity to relay sensitive information and effectively inform, encourage engagement, and negotiate with a variety of internal and external stakeholders.
• Cultural competency and cultural safety skills required to work effectively with a wide variety of participants.
• Needs assessment, priority setting, program planning and evaluation skills to determine which DASH projects will yield the most public safety impact, timeframes for delivery and management of stakeholder expectations.
• Experience with budgeting, human resource planning and strategic planning.
• Applying an equity lens to prioritize projects and meet the needs of special populations.

Judgement :

• Work is performed independently within the direction and guidelines established by the Chief Coroner and Chief Forensic Pathologist.
• The position requires significant judgement in the application of medical and death investigation knowledge to data analysis.
• Judgement is exercised in: directing and assisting with data interpretation, reviewing investigation and laboratory information, and reviewing and approving recommendations; communication with the media, and internal and external stakeholders; determining which data and analyses to release, balancing family preferences, privacy and response to public safety issues.

Accountability - Programs :

• Accountable for the provision of leadership and medical expertise in the development, implementation, and maintenance of DASH Unit products, policies, and processes.
• Accountable for the quality of DASH Unit products, policies, and procedures, including identifying need for change.

Accountability – Personnel :

• Directly supervises the DASH Unit staff and is accountable for a full spectrum of management responsibilities, including mentorship, talent management, setting goals and performance standards and succession planning.
• Develops, builds, and leads through positive and values-based leadership, inclusive and engaged teams, and partnerships.
• Frames program vision and strategy for projects, programs, and operations.
• Determines human resource and program needs.
• Exercises managerial accountability and authority in the areas of program design, recruitment, and retention.

Accountability - Finance and Materials :

• Approves DASH Unit expenses, including staff travel and training. Position has delegated spending authority to a set per item and total limit. Responsible use of resources is required. Recommends spending beyond policy limits when required by providing a business case to the Chief Coroner.
• Responsible for advising senior management on specialized equipment acquisitions.

Accountability - Impact of Errors :

• The impact of decisions is such that errors could result in injustice, loss of public confidence, loss of community agency cooperation, possible legal action, damage to the credibility of the Office of the Chief Coroner and damage to public relations.

Contact - Internal :

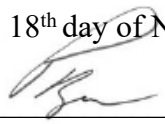
• Advises the Chief Coroner, Chief Forensic Pathologist, and other members of the Medical/Senior Management team at the OCC/OFPS on DASH Unit findings.
• Supports Investigating Coroners with research and evidence briefs.
• Maintains contact with content experts throughout the OCC/OFPS to discuss their analytic needs and advise on methods to organize, access and disseminate the data, including but not limited to death review committees, the Child and Death Youth Review Analysis (CYDRA) team and Inquest Unit.
• Liaise with Open Data Ontario on best practices for sharing DASH Unit data for the Open Data catalogue.

• Other ministries and agencies to help inform death preventative and community safety strategies (e.g. correctional services, Ministry of Health, Ministry of Labour Skills and Training).

Contact - External :

• Collaborates with a wide range of external partners, including but not limited to local, provincial, and national public health agencies; advocacy groups; research organizations; healthcare organizations; Children's Aid Societies; police services; and universities to design, conduct, and summarize research using death investigation data, including evidence – informed best practices in mortality prevention.
• Communicates analytic findings to the media, public, interest groups, and other stakeholders through reports, publications, and presentations.
• Maintains collaborative efforts with content experts throughout the public health and research fields to ensure continuity of information flow and currency with best practices.

This is **"Exhibit B"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

MATTHEW HODGE, MDCM, PhD, CCFP(EM), FRCPC

[redacted]

Informatics and metrics-savvy physician leader committed to quality improvement, developing people, value-for-money and reliable operational excellence supported by data and information systems. Results-focused physician executive with leadership experience in public health, health care delivery, and international health organizations; public health & preventive medicine specialist and practicing ER physician.

PROFESSIONAL EXPERIENCE & ACCOMPLISHMENTS

EMERGENCY DEPARTMENT PHYSICIAN, Toronto, ON **June 2011 - ongoing**

Providing clinical services in hospitals ranging from Rainy River to major academic centres in Toronto, currently at SRH, General & Birchmount sites and locum small hospital work in Grey-Bruce and NE Ontario.

CONSULTANT PHYSICIAN **June 2011 - ongoing**

Recent engagements include defining an analytic strategy to position a public health organization to focus its program efforts in early child development, redesigning public health inspection services, and ED operations consulting with Canadian startup Metricaid. Previous engagements have included LEAN-driven Emergency Department improvement projects, review and recommendations for restructuring and reorienting surveillance activities in a public health organization, and assessment of efficiency and provider mix in primary care. COVID work has included engagements with PHAC, PHO & Peel Region Public Health.

MEDICAL MANAGER, RMFCU. APFRB, MOHLTC, Toronto, ON **January 2016 – April 2017**

Providing clinical expertise to Risk Management & Fraud Control Unit (RMFCU) within the Corporate Services Division of the MOHLTC. Developed a strategic framework focused on deterrence, recovery and value to prioritize efforts and established analytic platform for post-payment review of expenditures.

CANCER CARE ONTARIO, Toronto, ON **March 2010 – June 2011**

Chief Medical Information Officer, & Director, Informatics

Led 140 informatics staff supporting cancer service management and Access-to-Care (Ontario-wide wait times for surgery, diagnostic imaging and Emergency Department care); represented CCO at provincial bodies including ER-ALC expert panel. Managed budget of CDN$16M.

Developed 'one informatics' plan to i) unify disparate informatics resources across the organization, ii) rationalize processes using LEAN and iii) engage and support hospitals and other health care delivery organizations directly in their performance improvement efforts; aligned enterprise architecture development, $2M electronic data warehouse project and business intelligence strategy around shared vision of the patient journey; led division with highest staff satisfaction scores.

UNITED NATIONS POPULATION FUND (UNFPA), New York, NY **January 2008 – February 2010**

Chief, Evaluation Branch, Division of Oversight Services

Led review and revision of evaluation program; subsequently promoted to Chief, Evaluation. Conducted or supervised 8 evaluations of country programmes with internal auditors; resulting tools established a shared audit & evaluation risk-based framework for evaluating relevance and strategic alignment of the Fund's country programmes, comprising $300M in annual expenditures. Reduced time from fieldwork to final report from over 360 days to 30 days. Led and participated in cross-functional audit/evaluation teams in the field in Africa and Asia. Contributed to the Fund's development of an evaluation policy.

CITY OF HAMILTON PUBLIC HEALTH SERVICES, Hamilton, ON **February 2005 – October 2007**

Associate Medical Officer of Health

Led epidemiology & evaluation within municipal public health department including responsibility for surveillance and emergency planning. Transformed $800K Public Health Research Education and Development (PHRED) program from unaccountable fund to competitive grants program; developed and implemented program evaluation cycle with self-assessment, epidemiologic best-evidence and peer review; led investigation, media and provincial liaison during legionella outbreak (2006) and provided ongoing medical expertise to communicable disease and environmental health investigations; represented Canada's

pubic health practitioners on Integration Working Group for Canada Health Infoway-funded communicable disease surveillance system (Panorama), 2006 - 2008

MCMASTER UNIVERSITY, Hamilton, ON **July 2005 - ongoing**

Associate Professor, Clinical Epidemiology & Biostatistics
Developed management education for Public Health & Preventive Medicine residents, course director 2012, 2013, 2014, 2016.

UNIVERSITY HEALTH NETWORK, Toronto, ON **January 2001 – April 2012**

Staff Physician, Emergency Department
Member, Practice Plan & Finance Committees

UNITED NATIONS CHILDREN'S EMERGENCY FUND (UNICEF) October 2003 – June 2004

Consultant, Evaluation Office
Completed thematic evaluations of midterm progress on Strategic Plan goals in immunization and HIV/AIDS; policy development for HIV/AIDS care and support and technical support to UNICEF-funded projects to prevent mother-to-child transmission of HIV infection in 11 countries.

MINISTRY OF HEALTH & LONG-TERM CARE, Toronto, ON **September 2002 – March 2003**

Senior Medical Consultant, Public Health Branch

Negotiated terms of MOHLTC pilot funding for colorectal cancer screening to be implemented by Cancer Care Ontario; SARS response.

UNITED NATIONS CHILDREN'S EMERGENCY FUND (UNICEF) September 2001 – September 2002

Senior Health Advisor, HIV/AIDS

WORLD HEALTH ORGANIZATION (WHO), Geneva, SUI **January 1999 – July 2001**

Medical Officer

EDUCATION AND PROFESSIONAL CERTIFICATIONS

MS, **Masters of Health Care Management, Harvard University**, 2011 (Mid-career physician management and leadership training program offered by Harvard School of Public Health)
MSIT, **Master of Science (Inf. Technology), Carnegie Mellon University,** 2008
MSc, **Development Finance, University of London**, 1999
MDCM, **McGill University**, 1996
PhD, **McGill University,** 1995 (MD-PhD Program, Thesis Title: Methods for Geographic Analyses of Health Services Use)
BA, **Economics, Yale University**, 1987
College of Physicians & Surgeons of Ontario (CPSO): Medical License #70425
Fellow, Royal College of Physicians and Surgeons of Canada, 2000
Public Health & Preventive Medicine
Diplomate, American Board of Preventive Medicine, 2007
Clinical Informatics Certification, American Board of Preventive Medicine, 2013
Certificate of Special Competence in Emergency Medicine, (CCFP(EM)), 2012

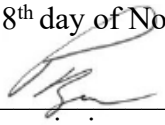
COMMUNITY CONTRIBUTIONS

Advisor, MARS Discovery District: providing advice to start-ups in the Health practice, 2014-ongoing
Public Health Physicians of Canada, formerly National Specialty Society for Community Medicine
President, 2009 – 2011; Treasurer, 2008 - 2009
Event Physician, Athletics Canada National Cross Country Championships, 2007 – 2010

PUBLICATIONS

Available upon request

This is **"Exhibit C"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Public Health Physicians of Canada
PHPC MSPC
Médecins de santé publique du Canada

CANADA'S MEDICAL EXPERTS FOR HEALTHY

Canada’s Public Health Physicians are specialty-trained medical professionals focused on promoting, protecting and improving our communities’ health and well-being.

While other physicians concentrate on diagnosing and treating individual patients, Public Health Physicians see entire communities as their patients. Their expertise and focus help ensure that all Canadians can live healthier, safer lives.

Governments, communities and organizations rely on Public Health Physicians’ unique training and expertise to inform fair public health policies, evaluate data, develop programs to prevent illness and injuries, and respond in times of emergencies such as outbreaks and natural disasters. When a Medical Officer of Health speaks to decision-makers, in public or to the media, it is a Public Health Physician speaking.

Public Health Physicians Identify Causes and Deliver Solutions to Prevent Illness and Improve Health

Public Health Physicians use data, evidence, public engagement, research, education and more, all toward the ultimate goal of building healthier communities for all Canadians. Communities where fewer people get sick, get hurt, live with chronic diseases or are forced to depend on an already overburdened health and social support system for their care and wellbeing.

Public Health Physicians focus on identifying, responding, and addressing the contributors that negatively affect our populations' health, such as people living in poverty, with addictions, in isolation, in marginalized and remote communities. While their work is frequently not high profile, it has often had an enormous impact, adding years to life and life to years for many Canadians.

Public Health Physicians Protect the Health of Populations

Public Health Physicians are primarily concerned with the social and environmental factors that impact health within specific communities, calling upon their unique

population health training and expertise. They identify and work to prevent the root causes of poor health, disease, injuries and premature death instead of calling on costly medical treatment and hospital care as the go-to response. Their tireless work behind the scenes can reduce other healthcare professionals' workload and lower the need for hospital stays and emergency room visits.

Certified Experts in Public Health and Preventive Medicine

After completing medical school, those pursuing a career as a Public Health and Preventive Medicine Physician must complete an additional five years of residency that includes clinic and hospital training, courses in public health sciences and clinical experience in public health settings. Once certified, these medical specialists work in public health departments at all government levels, hospitals, universities, family practice settings, industry and non-governmental organizations. They use their medical training differently from many physicians, as most Public Health Physicians work principally behind the scenes, having limited contact with individual patients in clinics and hospitals.

Public Health Emergencies Need the Voices of Public Health

Public Health Physicians bring unique and valuable perspectives, specialized training, and relevant expertise during public health emergencies. Expertise in population health is very different from expertise in one-to-one health. That's why political leaders and decision-makers turn to Public Health Physicians for guidance during large-scale disasters and outbreaks. Ensuring that Public Health Physicians' perspectives, knowledge, expertise, and voices are present in the media and other public forums reduces confusion and speculation and ultimately leads to a better-informed public during large-scale public emergencies.

Public Health Is an Area Where Resources and Investments Pay Off

Supporting Public Health Physicians and others working in public health is key to improving Canadians' health and well-being. A stronger, more vibrant public health infrastructure and healthier communities will be realized when Public Health Physicians' expertise is consistently part of discussions and decisions that assess and adopt public health policies and community health programs.

This page is part of PHPC's public awareness campaign to clarify the role and impact of public health physicians in Canada.

Download shareable campaign components:

Social media content Facebook Twitter LinkedIn

Download the info-graphic

DID YOU KNOW?

DID YOU KNOW?

Public Health Physicians Address Substance Abuse, Harm Reduction and Stigma.

Public Health Physicians are working to address a serious issue that is impacting the health, wellbeing and life expectancy of Canadians, particularly younger Canadians.

DID YOU KNOW? 

Public Health Physicians Have Made Canada a Healthier Country.

Public Health Physicians were central in planning, implementing, and evaluating non-smoking by-laws and promoting smoking prevention.

DID YOU KNOW? 

Public Health Physicians Help Address Inequities in Society.

Public Health Physicians are helping to shine a light on and striving to eliminate Tuberculosis, which is a social disease with a medical aspect and demonstrates the inequities in our societies.

DID YOU KNOW? 

Public Health Physicians Balance the Health of Populations and Public Health Measures.

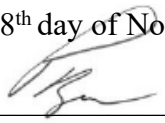
During the COVID-19 pandemic and other outbreaks, Public Health Physicians have been often behind the scenes but central to managing outbreaks, identifying priorities, tracking infection rates, supporting large-scale public testing and vaccinations.

DID YOU KNOW? 

Investing in Public Health Has Always Been an Investment with Healthy Returns.

Investing in public health has long-term benefits and returns on investments far more comprehensive than investments in healthcare. Public health helped to contain smallpox, cholera, typhoid and yellow fever and introduced water testing, rodent elimination, seatbelts, vaccinations and much more. Public health has added decades to life expectancy and saved millions of lives.

This is **"Exhibit D"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Court file No CV-22-006282-0000

ONTARIO
SUPERIOR COURT OF JUSTICE

B E T W E E N:

RANDY HILLIER

Applicant

-and-

HIS MAJESTY THE KING IN RIGHT OF THE PROVINCE OF ONTARIO

Respondent

ACKNOWLEDGMENT OF EXPERT'S DUTY

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1. My name is Dr. Matthew Hodge. I live in the City of Toronto in the Province of Ontario.

2. I have been engaged by the Attorney General of Ontario to provide evidence in relation to the above-noted court proceeding.

3. I acknowledge that it is my duty to provide evidence in relation to this proceeding as follows:

   (a) to provide opinion evidence that is fair, objective and non-partisan;

   (b) to provide opinion evidence that is related only to matters that are within my area of expertise; and

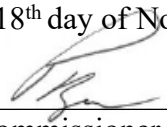
   (c) to provide such additional assistance as the court may reasonably require, to determine a matter in issue.

4. I acknowledge that the duty referred to above prevails over any obligation which I may owe to any party by whom or on whose behalf I am engaged.

Date: 18 NOV 2022

Dr. Matthew Hodge

This is **"Exhibit E"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Ontario Health Plan for an Influenza Pandemic

Chapter 1: Introduction

March, 2013

Ontario

Ministry of Health and Long-Term Care
Emergency Management Branch
1075 Bay Street, Suite 810
Toronto, Ontario
Canada M5S 2B1
416-212-8022 (local); 1-866-212-2272 (long distance)
emergencymanagement.moh@ontario.ca

Ontario Health Plan for an Influenza Pandemic

Chapter 1: Introduction

Audience

- health sector employers, health care providers and other health workers, emergency planners, health administrators and other provincial health system partners

Chapter objectives

- to introduce and orient readers to the 2013 Ontario Health Plan for an Influenza Pandemic (OHPIP)

Introduction

The Ministry of Health and Long-Term Care (MOHLTC) leads the development of the OHPIP to support the provincial health system to prepare for and respond to an influenza pandemic.

Since the release of the first iteration of the plan in 2004, the OHPIP has been regularly updated to reflect new knowledge, information and best practices. This process is supported by the OHPIP Steering Committee – which consists of representatives from health associations, unions, regulatory bodies and government organizations – and a variety of workgroups (See Appendix A – OHPIP Steering Committee and workgroup members).

The OHPIP supported the provincial health system's response to the 2009 H1N1 influenza pandemic (pH1N1). Although a number of simulated scenarios have been held over the years to exercise components of the OHPIP, pH1N1 was the first opportunity to use the plan to guide the response to a pandemic.

The 2013 version of the OHPIP was updated to incorporate the priority lessons learned and best practices from pH1N1. More information about Ontario's evaluation of the response to pH1N1 can be found in Pandemic (H1N1) 2009: A Review of Ontario's Response and The H1N1 Pandemic – How Ontario Fared: A Report by Ontario's Chief Medical Officer of Health.

Previous versions of the OHPIP have used World Health Organization (WHO) and Public Health Agency of Canada (PHAC) response plans as a conceptual foundation. These pandemic response plans are in the process of being revised based on the lessons learned and best practices from pH1N1. Some concepts that were previously incorporated in the OHPIP aren't in the 2013 iteration as they haven't yet been updated by the WHO and PHAC. For example, the WHO's six-phase description of a pandemic featured in previous versions of the OHPIP and Canadian Pandemic Influenza Plan for the Health Sector (CPIP). An evaluation by an external review committee on the functioning of the International Health Regulations (2005) in relation to pH1N1 recommended that the WHO simplify the pandemic phase structure. As the WHO has not released an updated plan since the evaluation was released, the phase structure is not included in this version of the OHPIP.

This is the final iteration of the OHPIP. The Ontario Influenza Response Plan *(*OIRP) will eventually replace it. Through this new plan, the provincial health system's focus will shift from preparing for an influenza pandemic to creating and building effective seasonal influenza responses and escalating those measures during a pandemic. The OIRP will link to updated pandemic response plans from the WHO and PHAC, and it will also address the next steps documented in this version of the OHPIP and outstanding lessons learned and best practices from pH1N1. The OIRP will outline influenza responses for the entire health system, including government, primary health care, community care, hospitals and public health.

Roles and responsibilities

All health system partners have a role to play during the response to an influenza pandemic, from the WHO at the international level to health sector employers and health workers at the community level.

The MOHLTC leads the Government of Ontario's response to an influenza pandemic through health system coordination and direction.[1] Within the MOHLTC's emergency response structure, there are many individuals and groups who provide operational and/ or strategic direction to guide the response. For example, the Chief Medical Officer of Health (CMOH) has legislated responsibilities under the Health Protection and Promotion Act (HPPA) and is the MOHLTC's Executive Lead during the response to an influenza pandemic. This means that the CMOH provides strategic leadership for the MOHLTC's response.

In the OHPIP, references to the MOHLTC include the Minister, CMOH and other individuals/ groups in the MOHLTC (e.g., Deputy Minister, Ministry Action Group). Please see the Ministry Emergency Response Plan for more detail on the MOHLTC's emergency response structure and decision-making process.

Table 1 outlines general roles and responsibilities of health system partners during an influenza pandemic. Each OHPIP chapter includes more detailed roles and responsibilities relevant to the chapter topic.

[1] As per the Emergency Management and Civil Protection Act, the MOHLTC assumes the role of primary ministry for emergencies, declared and undeclared, when the primary Government of Ontario response falls under the ministry's emergency responsibilities of "human health, disease and epidemics" or "health services during an emergency" as assigned by Order in Council (OIC) 1157/2009. The MOHLTC responds to the impacts on the health of Ontarians and on the health system.

TABLE 1. GENERAL INFLUENZA PANDEMIC RESPONSE ROLES AND RESPONSIBILITIES[2]

Party	Roles and responsibilities
WHO	Coordinate international response activities under the International Health Regulations Perform international surveillance and provide an early assessment of pandemic severity in order to help countries determine the level of intervention needed in the response Declare an influenza pandemic Select the pandemic vaccine strain and determine the time to begin production of the pandemic vaccine
PHAC	Coordinate national pandemic influenza response activities, including nation-wide surveillance, international liaison and coordination of the vaccine response, as outlined in the CPIP

[2] The information in this table is intended to provide general information about roles and responsibilities of different parties during an influenza pandemic. It is not a comprehensive listing of roles or obligations of a party. Roles, responsibilities and obligations of a party vary in specific circumstances.

Party	Roles and responsibilities
MOHLTC (through the Ministry Emergency Operations Centre (MEOC))	Liaise with PHAC and other provinces and territories Collaborate with Public Health Ontario (PHO) to use surveillance information to determine severity Develop recommendations[3] and provincial response strategies[4] for the provincial health system, as well as others affected by public health measures Communicate with provincial health system partners through situation reports, Important Health Notices (IHNs), the Health Care Provider Hotline, the Health Stakeholder Teleconference, the MOHLTC website and other methods Develop and issue directives[5], orders and requests as per the HPPA, Long-Term Care Homes Act and other relevant provincial legislation[6] Communicate with the public through media briefings, the MOHLTC website and other methods Solicit and respond to feedback and input from provincial health system partners Deploy supplies & equipment from the MOHLTC stockpile to health workers and health sector employers Deploy antivirals from the MOHLTC stockpile to community-based pharmacies and other dispensing sites

[3] This term refers to best practices as well as guidance on the risk posed by the pandemic. Recommendations related to occupational health and safety (OHS) may be considered by health sector employers to be reasonable precautions in the application of the Occupational Health and Safety Act (OHSA).

[4] Provincial response strategies include the surveillance strategy, public health measures strategy, outpatient care & treatment strategy, antiviral distribution strategy, immunization strategy and supplies & equipment strategy

[5] Directives are sent from the CMOH to health care providers or other health entities as per the HPPA.

[6] The OHSA continues to apply during an influenza pandemic and prevails when there is a conflict between that act and any other legislation.

Party	Roles and responsibilities
Public Health Ontario (PHO) (through the MEOC)	Support the MOHLTC to use surveillance information to determine severity Lead and coordinate the provincial surveillance strategy Coordinate and provide provincial influenza laboratory testing Provide scientific and technical advice to the MOHLTC (e.g., advice on infection prevention and control measures) Generate knowledge translation tools and offer training opportunities to supplement the MOHLTC's recommendations, directives and response strategies
Ministry of Labour (MOL)	Provide OHS advice to the MOHLTC (through the MEOC) Enforce the OHSA and its regulations
Emergency Management Ontario	Coordinate the provincial response to an influenza pandemic, with an emphasis on coordinating responses to non-health system impacts and consequences as outlined in the Provincial Coordination Plan for an Influenza Pandemic
Local Health Integration Networks (LHINs)[7]	Liaise between transfer payment (TP) organizations and the MOHLTC Participate in the coordination of local care & treatment
Public health units (PHUs)[8]	Follow MOHLTC recommendations, directives, orders and requests Develop and issue orders[9] Lead local implementation of the surveillance strategy Lead local implementation of immunization Participate in the coordination of local care & treatment Lead local implementation of public health measures Continue to provide other public health services

[7] Other LHIN roles during an influenza pandemic are currently under development.

[8] Throughout the OHPIP, PHU includes boards of health, medical officers of health (MOHs) and other PHU health workers (e.g., public health inspectors, epidemiologists, public health nurses, etc.). See the HPPA and Ontario Public Health Standards for more information on the roles and responsibilities of various PHU parties.

[9] This refers to orders made by MOHs and public health inspectors as per the HPPA.

Party	Roles and responsibilities
Health liaison organizations (provincial associations, unions and regulatory bodies)	Liaise between members and the MOHLTC (see Chapter 2: Health Sector Communications) Share best practices among sector/ membership
Health workers and health sector employers[10]	Follow MOHLTC recommendations, directives, orders and requests Follow PHU orders Continue to provide safe and effective care Participate in the coordination of local care & treatment Participate in research and surveillance activities Practice and role model appropriate behaviour to protect clients/ patients/ residents (C/P/Rs) and prevent further spread of influenza (e.g., get immunized; practise respiratory etiquette and hand hygiene; stay home when sick)
Other employers	Implement public health measures Follow MOHLTC orders and requests Follow PHU orders Encourage immunization among employees Be immunized as soon as possible
Public	Follow public health measures such as staying home when symptomatic, performing hand hygiene and keeping commonly touched surfaces clean Follow MOHLTC and PHU orders Be immunized as soon as possible

Ontario's approach to an influenza pandemic

The 2013 OHPIP is a response document. As opposed to providing detailed planning guidance for provincial health system partners, it outlines anticipated response activities

[10] See Chapter 5: Occupational Health & Safety and Infection Prevention & Control and Chapter 9: Primary Health Care.

based on the severity of the pandemic virus. The actual response activities will be confirmed by the MOHLTC at the time of a pandemic based on the epidemiology of the virus (see Chapter 3: Surveillance), impacts on the provincial health system and behavioural responses of the public. Before these things are known, the MOHLTC considers the precautionary principle in making decisions. During the planning phase, provincial health system partners are encouraged to review the response activities outlined in the OHPIP and take steps to ensure they are able to perform their role during an influenza pandemic. Health system partners are also encouraged to have continuity of operations plans in place that enable them to respond to any type of business disruption, including an influenza pandemic.

The MOHLTC recognizes that planning to respond to an influenza pandemic is not enough.

To ensure an effective pandemic response, health workers and health sector employers need to appropriately respond to seasonal influenza each year – including consistently applying appropriate OHS & infection prevention & control (IPAC) measures; effectively promoting and administering influenza immunization programs for C/P/Rs, health workers and members of the public; implementing timely epidemiological and laboratory surveillance; engaging and tailoring interventions to the needs of vulnerable populations; and promoting appropriate public health measures

Preparedness tip

Health organizations should develop a continuity of operations plan to support their ability to respond to emergencies, such as an influenza pandemic. PHUs can use the Ontario Public Health Standards' Public Health Emergency Preparedness Protocol to guide their planning.

Ontario's influenza pandemic response objectives

The objectives of the MOHLTC's response to an influenza pandemic are consistent with those in the CPIP:

- first, to minimize serious illness and overall deaths through appropriate management of Ontario's health system
- second, to minimize societal disruption in Ontario as a result of an influenza pandemic

Guiding principles

The actions of the MOHLTC during a pandemic response are based on the following guiding principles. Many of these principles are useful in guiding the decision making of

other parties, including health sector employers, health workers, emergency planners and other public health leaders.

Evidence

The MOHLTC uses scientific and technical evidence to inform decision-making, including evidence on the risk posed by the pandemic. The MOHLTC partners closely with PHO to obtain, understand and communicate the evidence.

Legislation

The MOHLTC responds based on provincial legislative requirements and responsibilities.

Precautionary principle

The MOHLTC does not await scientific certainty before taking action to protect health. For example, the MOHLTC considers the precautionary principle when developing recommendations and directives related to OHS & IPAC measures, especially during the early stages of an influenza pandemic when scientific evidence on the severity of the novel virus is limited.[11]

See Chapter 5: Occupational Health & Safety and Infection Prevention & Control for more information on the application of the precautionary principle to OHS.

Ontario Public Service values

The MOHLTC uses the Ontario Public Service values to inform decision making during an influenza pandemic.

Work is underway federally to develop an ethical framework for the CPIP. Future versions of the OIRP will include an ethical framework that aligns with that in the CPIP.

Health equity

The MOHLTC considers the needs of vulnerable populations[12] when developing response and recovery measures.

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[11] As outlined in the HPPA, the CMOH must consider the precautionary principle when issuing a directive to a health care provider or health care entity related to health worker health and safety in the use of any protective clothing, equipment or device.

[12] The OHPIP defines vulnerable populations as a group of people who, because of the determinants of health, are more likely to be exposed to influenza, more likely to

To accomplish this, the MOHLTC may use the Health Equity Impact Assessment (HEIA), a decision support tool developed by the ministry to identify how a health program, service or policy impacts population groups in different ways. Work is underway at the MOHLTC to adapt the HEIA for a health emergency management context to ensure that provincial and local interventions do not exacerbate health disparities during an emergency.

Communication principles

The MOHLTC bases its communications with the provincial health system and the public on the following principles[13]:

- timeliness
- transparency
- accessibility
- credibility

Assumptions

The 2013 OHPIP is based on the following assumptions:

Origin and Timing

- The next pandemic could emerge anywhere in the world – including in Ontario.
- The next pandemic could emerge at any time of year.
- Ontario has little lead time between when a pandemic virus is first identified and when it arrives in the province.

Transmission

- The pandemic virus behaves like seasonal influenza viruses in significant ways, including the incubation period, period of communicability and methods of transmission.
- The pandemic strain is primarily community spread; that is, it is transmitted from person-to-person in the community as well as in institutional settings.

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experience a serious impact because of exposure, less likely to benefit from response and recovery measures and/ or who may be negatively affected by response and recovery measures.

[13] See Chapter 2: Health Sector Communications for more information on the application of these principles to the MOHLTC's two-way communications with the health system.

Pandemic Epidemiology

- An influenza pandemic consists of two or more waves – or intense periods – of viral transmission.
- The novel influenza virus displaces other circulating seasonal strains during the pandemic.

Clinical Features

- As with seasonal influenza, the severity of the pandemic cannot be predicted, may be partially determined by the effectiveness of interventions such as treatment with antivirals and is not easily determinable at the start of an outbreak. (See Severity of an influenza pandemic for more information on the scenarios used to guide the development of the 2013 OHPIP).
- As with seasonal influenza, the clinical severity of the illness experienced by Ontarians who are infected by the pandemic virus varies considerably: some individuals who are infected do not display any clinical symptoms, while others become quite ill and may require hospitalization and may even die.
- The groups at increased risk for severe disease and complications during an influenza pandemic are similar to those for seasonal influenza; however, there may be additional high-risk groups because of specific features of the pandemic virus.
- Vulnerable populations that typically experience a disproportionate burden of negative health outcomes, or are more vulnerable to these outcomes, because of the effects of the social determinants of health are more severely affected by the pandemic than other members of the community. This includes Ontarians with low incomes, who face language barriers, and who are homeless.

Interventions

- Vaccine is available in time to have an impact on the overall pandemic; however, it is not available for the first wave.
- The MOHLTC maintains an antiviral stockpile to provide treatment for individuals that meet its clinical recommendations.
- The efficacy and dose requirements of antivirals are not known until the pandemic begins and may differ from that of seasonal influenza; therefore, recommendations may change.

Severity of an influenza pandemic

Given that the severity of a pandemic cannot be known in advance, the anticipated response activities outlined in the 2013 OHPIP are based on a number of severity scenarios adapted from draft work undertaken by the Centers for Disease Control and Prevention. In this model, severity is measured along two dimensions – transmissibility of the virus and clinical severity of illness. There are four severity scenarios – ranging from a mild scenario that is similar to seasonal influenza (low transmissibility and low

clinical severity) to the most severe scenario with high transmission and high clinical severity rates.

As well, the OHPIP severity model includes an initial stage before severity is known when the limited availability of surveillance data does not allow for confident identification of severity. The severity may not be clearly known until after an influenza pandemic is over. The MOHLTC uses surveillance data to estimate severity (see Chapter 3: Surveillance).

This model has been used to provide information on the types of responses that may be used during an influenza pandemic. As more information about the severity of an influenza pandemic is available, the MOHLTC will establish and communicate the provincial response strategies such as the outpatient care & treatment strategy, immunization strategy, public health measures strategy, antiviral distribution strategy and surveillance strategy.

Figure 1 outlines the four severity scenarios used in the OHPIP. Table 2 outlines how various influenza pandemics and seasonal epidemics are categorized in this model and the major health system impacts.

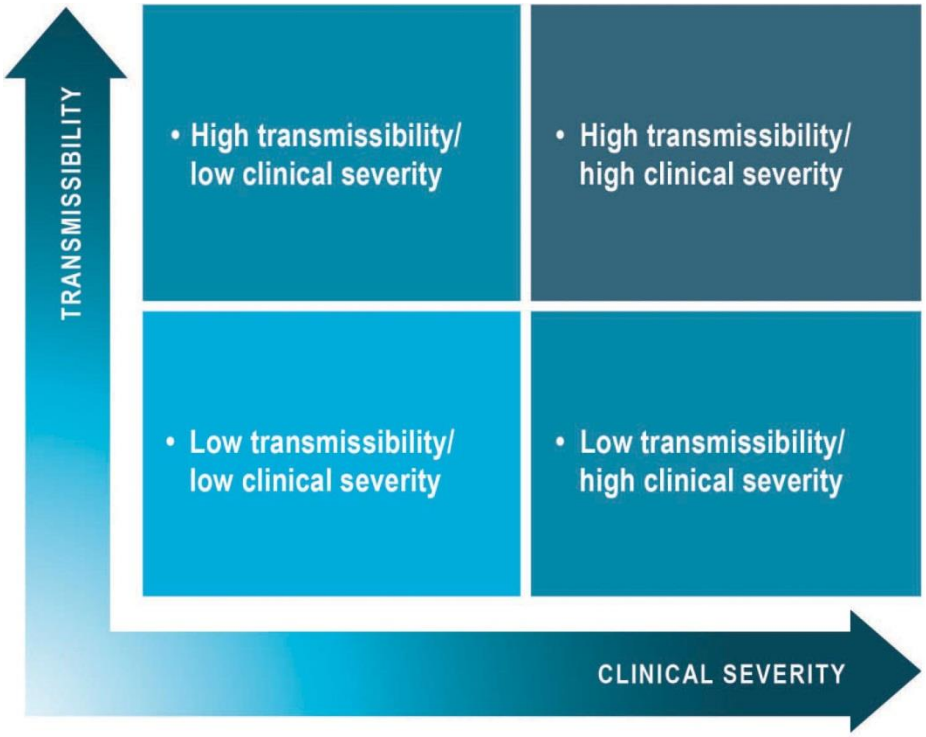

FIGURE 1. FOUR SEVERITY SCENARIOS USED IN THE OHPIP

TABLE 2. EXAMPLES AND IMPACT OF SEVERITY SCENARIOS

Overall severity	Characteristics	Examples	Impact on health system
Before severity is known	Limited surveillance data available	Either in the pre-pandemic phase or early in the pandemic, before there is enough information available to determine the severity of the pandemic	Unknown
Low transmissibility & low clinical severity	Cumulative attack rate[14]: < 21% R_0 (basic reproduction number)[15]: <1.6 Case Fatality Rate (CFR)[16]: <0.25%	Typical seasonal influenza epidemics 2009 influenza pandemic 1968 influenza pandemic	Comparable to seasonal influenza
High transmissibility & low clinical severity	Cumulative attack rate: ≥21% $R_0 \geq 1.6$ CFR: <0.25%	1927-28 seasonal influenza epidemic	Significant workplace absenteeism High burden on outpatient and acute services
Low transmissibility & high clinical severity	Cumulative attack rate: < 21% R_0: <1.6 CFR: ≥0.25%	1957 influenza pandemic	High burden on critical health care services

[14] The cumulative attack rate is the percentage of people who (are expected to) become symptomatic at some point during the influenza pandemic.

[15] The basic reproductive number is the number of secondary cases one case should produce in a completely susceptible population.

[16] The case fatality rate is the ratio of deaths within a designated population of cases over the course of a pandemic.

Overall severity	Characteristics	Examples	Impact on health system
High transmissibility & high clinical severity	Cumulative attack Rate: ≥21% R_0≥1.6 CFR: ≥0.25%	1918 influenza pandemic	Significant need for public health measures High burden on critical health care services

In addition to the characteristics of the virus, other factors – including the effectiveness of interventions, the behavioural response of Ontarians, the capacity of Ontario's health system and the social determinants of health – determine the impact of the pandemic.

Another consideration is that novel influenza viruses may differentially affect specific populations. For example, while the severity of a pandemic may be comparable to seasonal influenza (low transmissibility and low clinical severity), transmissibility or clinical severity could be significantly higher in specific population groups (e.g., children and youth). Therefore, the MOHLTC may need to develop recommendations and response strategies during an influenza pandemic to address specific population needs.

Next steps

In the development of the OIRP, the MOHLTC will work with its partners to:

- continue to clarify the role of LHINs in influenza pandemic response
- align the OIRP with the CPIP, including
  - the measurement of pandemic severity
  - ethical framework
- further develop strategies to support vulnerable populations, including adapting the HEIA for a health emergency management context

Appendix A – OHPIP Steering Committee and workgroup members

The MOHLTC is grateful to the following organizations and their members for their contributions to the 2012-13 OHPIP Steering Committee, workgroups and consultations:

- Aboriginal Affairs and Northern Development Canada
- Association of Family Health Teams of Ontario
- Association of Iroquois and Allied Indians
- Association of Local Public Health Agencies
- Association of Municipalities of Ontario
- Association of Ontario Health Centres
- Chiefs of Ontario
- Critical Care Services Ontario
- Emergency Management Ontario, Ministry of Community Safety and Correctional Services
- Emergency Nurses Association of Ontario
- Federation of Health Regulatory Colleges of Ontario
- First Nations and Inuit Health Branch, Ontario Region
- Independent First Nations
- Local Health Integration Networks
- Ministry of Children and Youth Services
- Ministry of Community and Social Services
- Ministry of Labour
- Nishnawbe Aski Nation
- Nurse Practitioners Association of Ontario
- Ontario Association for Non-Profit Homes and Services for Seniors
- Ontario Association of Community Care Access Centres
- Ontario Association of Medical Laboratories
- Ontario College of Family Physicians
- Ontario Community Support Association
- Ontario Home Care Association

- Ontario Hospital Association
- Ontario Long-Term Care Association
- Ontario Medical Association
- Ontario Nurses' Association
- Ontario Pharmacists' Association
- Ontario Public Services Employees Union
- Public Health Agency of Canada, Ontario and Nunavut Region
- Public Health Ontario
- Public Services Health & Safety Association
- Registered Nurses' Association of Ontario
- Union of Ontario Indians (Anishinabek Nation)

Appendix B – Glossary

Additional precautions

Additional precautions (i.e., contact precautions, droplet precautions and airborne precautions) that are necessary in addition to routine practices for certain pathogens or clinical presentations. These precautions are based on the method of transmission (e.g., contact, droplet, airborne). (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in All Health Care Settings).

Adverse event

Adverse events are an unexpected and undesired incident directly associated with the care or services provided to the client/patient/resident (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Infection Prevention and Control Programs in Ontario).

Aerosol-generating medical procedure

Aerosol-generating medical procedures are any procedure carried out on a client, patient or resident that can induce the production of aerosols as a result of manipulation of a person's airway. Examples of aerosol-generating medical procedures include intubation and related procedures (e.g., manual ventilation, open endotracheal suctioning); cardiopulmonary resuscitation; bronchoscopy; sputum induction; nebulized therapy; surgery and autopsy; and bi-level positive airway pressure (i.e., BiPAP) (Source: Canadian Pandemic Influenza Plan for the Health Sector).

Affiliated clients/ patients

Also known as rostered clients/ patients. Affiliated clients/ patients are formally enrolled with a primary health care organization, such as a family health team, community health centre or Aboriginal health access centre. Clients/ patients that are affiliated with a primary health care organization typically do not seek primary health care services in other locations.

Airborne precautions

Airborne precautions are used in addition to routine practices for clients/ patients/ residents known or suspected of having an illness transmitted by the airborne route (i.e., by small droplet nuclei that remain suspended in the air and may be inhaled by others)

(Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Client/ patient/ resident

Any person receiving health care services within a health care setting (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Infection Prevention and Control Programs in Ontario).

Client/ patient/ resident environment

The immediate space around a client/ patient/ resident that may be touched by the client/ patient/ resident and may also be touched by the health care provider when providing care. The client/ patient/ resident environment includes equipment, medical devices, furniture (e.g., bed, chair, bedside table), telephone, privacy curtains, personal belongings (e.g., clothes, books) and the bathroom that the client/ patient/ resident uses. In a multi-bed room, the client/ patient/ resident environment is the area inside the individual's curtain. In an ambulatory setting, the client/ patient/ resident environment is the area that may come into contact with the client/ patient/ resident within their cubicle. In a nursery/ neonatal setting, the patient environment is the isolette or bassinet and equipment outside the isolette/bassinet that is used for the infant. Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Cohorting

The assignment of a geographic area such as a room or a care area to two or more clients/ patients/ residents who are either colonized or infected with the same microorganism, with staffing assignments restricted to the cohorted group of patients (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Contact tracing

The process of identifying relevant contacts of a person with an infectious disease and ensuring that they are aware of their exposure (Source: Provincial Infectious Disease Advisory Committee's Sexually Transmitted Infections Case Management and Contact Tracing Best Practice Recommendations).

Directives

Instructions that may be issued by the Chief Medical Officer of Health under the terms of the Health Protection and Promotion Act. A health care provider or health care entity that is served with a directive must comply with it.

Eye protection

A device that covers the eyes and is used by health care providers to protect the eyes when it is anticipated that a procedure or care activity is likely to generate splashes or sprays of blood, body fluids, secretions or excretions, or within two metres of a coughing client/patient/resident. Eye protection includes safety glasses, safety goggles, face shields and visors (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Fit-test

A qualitative or quantitative method to evaluate the fit of a specific make, model and size of respirator on an individual. Fit-testing is to be done periodically, at least every two years and whenever there is a change in respirator face piece or the user's physical condition that could affect the respirator fit (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Flu assessment centre

Temporary services during an influenza pandemic provided by primary health care organizations or emergency departments to provide influenza care & treatment services to community members who cannot rapidly access primary health care, with temporary financial and material support of the Ministry of Health and Long-Term Care.

Hand hygiene

A general term referring to any action of hand cleaning. Hand hygiene relates to the removal of visible soil and removal or killing of transient microorganisms from the hands. Hand hygiene may be accomplished using soap and running water or an alcohol-based hand rub. Hand hygiene also includes surgical hand antisepsis (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Health and safety representative

Workplaces with more than five workers and no joint health and safety committee must have a health and safety representative [section 8(1)]. Like joint health and safety committee members, the representative is committed to improving health and safety conditions in the workplace. (Source: Ministry of Labour's A Guide for Joint Health and Safety Committees and Representatives in the Workplace).

Health care-associated infection

A term relating to an infection that is acquired during the delivery of health care services (also known as '*nosocomial infection'*) (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Health care facility

A set of physical infrastructure elements supporting the delivery of health care services. A health care facility does not include a client's/ patient's home or physician offices where health care services may be provided (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Health care provider

Any person delivering health care services to a client/ patient/ resident. This includes, but is not limited to, the following: emergency service workers, physicians, dentists, nurses, respiratory therapists and other health professionals, personal support workers, clinical instructors, students and home health care workers. In some non-acute settings, volunteers might provide care and would be included as a health care provider. See also, *Staff* (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Health Care Provider Hotline

24/7 line for health care providers to contact the Ministry of Health and Long-Term Care's Emergency Management Branch (1-866-212-2272). This Hotline can be used by health system partners to reach the ministry during the response to an emergency. It is also operational during non-emergencies to enable health system partners to inform the ministry of a hazard or risk that has the potential to become an emergency.

Health care setting

Any location where health care services are provided, including settings where emergency care is provided, hospitals, complex continuing care, rehabilitation hospitals, long-term care homes, mental health facilities, outpatient clinics, community health centres and clinics, physician offices, dental offices, offices of allied health professionals and home health care (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Health care services

Direct client/ patient/ resident care, including diagnostic, treatment and care services.

Health Equity Impact Assessment

The Ministry of Health and Long-Term Care's Health Equity Impact Assessment is a decision support tool that walks users through the steps of identifying how a program, policy or similar initiative impacts population groups in different ways. The Health Equity Impact Assessment surfaces unintended potential impacts. The end goal is to maximize positive impacts and reduce negative impacts that could potentially widen health disparities between population groups — in short, more equitable delivery of the program, service or policy.

Health liaison organization

A provincial health association, union or regulatory body that liaises between its members and the Ministry of Health and Long-Term Care during an emergency. These organizations are a critical conduit for information collection, analysis and dissemination. Health liaison organizations typically participate in the Health Stakeholder Teleconference. See Chapter 2: Health Sector Communications for more information.

Health organization

An organization or agency that receive funding from the Ministry of Health and Long-Term Care to provide health services.

Health sector

Part of the economy dealing with health-related issues in society. (Source: WHO's Health System Performance Website)

Health sector employer

A person in a health setting who employs one of more workers or contracts for the services of one or more workers and includes a contractor or subcontractor who performs work or supplies services and a contractor or subcontractor who undertakes with an owner, constructor, contractor or subcontractor to perform work or supply services.(Source: Based on the Occupational Health and Safety Act)

Health services

Services delivered by the health system, including health promotion, disease prevention, diagnostic, treatment and care services.

Health setting

Organizations and agencies that receive funding through the Ministry of Health and Long-Term Care to provide health services.

Health system

The people, institutions and resources, arranged together in accordance with established policies, to improve the health of the population they serve, while responding to people's legitimate expectations and protecting them against the cost of ill-health through a variety of activities whose primary intent is to improve health. (Source: WHO's Health System Performance Website).

Health worker

A person who performs work or supplies services for monetary compensation in a health setting (Source: based on the Occupational Health and Safety Act)

High-risk group

Population with an increased likelihood of becoming ill and/ or suffering serious health outcomes as a consequence of pandemic influenza virus infection.

Infection

The entry and multiplication of an infectious agent in the tissues of the host. Asymptomatic or sub-clinical infection is an infectious process running a course similar to that of clinical disease but below the threshold of clinical symptoms. Symptomatic or clinical infection is on resulting in clinical signs and symptoms (disease) (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Infection prevention & control

Evidence-based practices and procedures that, when applied consistently in health care settings, can prevent or reduce the risk of transmission of microorganisms to health care providers, other clients/patients/residents and visitors (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Infection prevention & control professional(s)

Trained individuals responsible for a health care setting's infection prevention & control activities. In Ontario, an infection prevention & control professional must receive a minimum for 80 hours of instruction in a Community and Hospital Infection Control Association of Canada endorsed infection control program within six months of entering their role and must acquire and maintain Certification in Infection Control when eligible (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Infection prevention & control program

A health care facility or organization (e.g., hospital, long-term care, continuing complex care, home care) program responsible for meeting the recommended mandate to decrease infections in the client/ patient/ resident, health care providers and visitors. The program is coordinated by health care providers with expertise in infection prevention & control and epidemiology (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Infection Prevention and Control Programs in Ontario).

Influenza

A highly contagious, febrile, acute respiratory infection of the nose, throat, bronchial tubes and lungs caused by the influenza virus. It is responsible for severe and potentially fatal clinical illness of epidemic and pandemic proportions (Source: Canadian Pandemic Influenza Plan for the Health Sector).

Influenza-like illness

A cluster of symptoms resembling and that could be caused by influenza, without laboratory confirmation. Case definitions for influenza-like illness vary, and are provided during an influenza pandemic by the Ministry of Health and Long-Term Care,

Integrated Public Health Information System

The information technology system used by public health units to report case information on all reportable communicable diseases that are outlined in the Health Protection and Promotion Act. Public health units are responsible for collecting case information on reportable communicable diseases occurring within their boundaries and entering this information into this system.

Isolation

Separation, for the period of communicability, of infected persons or animals from others in such places and under such conditions as to prevent or limit the direct or

indirect transmission or the infectious agent from those infected to those who are susceptible or who may spread the agent to others. (Source: Canadian Pandemic Influenza Plan for the Health Sector)

Joint health and safety committee

Committee composed of people who represent the workers and the employer, as described under the Occupational Health and Safety Act. Together, they are committed to improving health and safety conditions in the workplace. Committees identify potential health and safety problems and bring them to the employer's attention. As well, members must be kept informed of health and safety developments in the workplace. (Source: Ministry of Labour's A Guide for Joint Health and Safety Committees and Representatives in the Workplace).

Key population groups for immunization

The key population groups for immunization are those groups that are eligible to receive the pandemic vaccine. Given that vaccine availability will increase over time, the key population groups will expand during the course of the pandemic immunization program (i.e., additional population groups will be added as more vaccine becomes available).

Local Health Integration Network transfer payment agency

Also known as Local Health Integration Network Health Service Providers. Organizations that Local Health Integration Networks are responsible for, including hospitals, divested psychiatric hospitals, community care access centres, community support service organizations, community mental health and addictions agencies, community health centres and long-term care homes.

Long-term care

A broad range of personal care, support and health services provided to people who have limitations that prevention them from full participation in the activities of daily living. The people who use long-term care services are usually the elderly, people with disabilities and people who have a chronic or prolonged illness (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Environmental Cleaning for Prevention and Control of Infections).

Mandatory public health measures

Extraordinary actions that are supported by the Health Protection and Promotion Act designed to address and counter specific public health threats.

Ministry Emergency Operations Centre

Site where the Ministry of Health and Long-Term Care coordinates its response to an emergency.

Ministry of Health and Long-Term Care

Throughout the Ontario Health Plan for an Influenza Pandemic, the Ministry of Health and Long-Term Care includes the Minister, Chief Medical Officer of Health and the rest of the Ministry of Health and Long-Term Care. For information on how emergency decisions are made in the MOHLTC, please see the Ministry Emergency Response Plan.

N95 respirator

A personal protective device that is worn on the face and covers the nose and mouth to reduce the wearer's risk of inhaling airborne particles. A National Institute for Occupational Safety and Health-certified N95 respirator filters particles one micron in size, has 95% filter efficiency and provides a tight facial seal with less than 10% leak (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in All Health Care Settings).

Outpatient settings

Pertaining to a health care organization that provides influenza care & treatment services for clients/ patients who are not hospitalized or admitted to a long-term care home. It includes primary health care organizations, hospital emergency departments, community-based pharmacies and home care settings.

Pandemic

An epidemic disease of widespread prevalence around the globe (Source: Canadian Pandemic Influenza Plan for the Health Sector).

Pandemic Precautions

Occupational health & safety and infection prevention & control precautions recommended in health care settings during an influenza pandemic (e.g., use of N95 respirators for health workers at risk of exposure to a client/ patient/ resident with influenza-like illness or that client/ patient/ resident's environment)

Personal protective equipment

Clothing or equipment worn by health workers for protection against hazards (Source: Based on Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in All Health Care Settings).

Point of care

The place where three elements occur together: the client/ patient/ resident, the health care provider, and care or treatment involving client/ patient/ resident contact (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Infection Prevention and Control Programs in Ontario).

Precautions

Interventions to reduce the risk of transmission of microorganisms (e.g., client/ patient/ resident-to-client/ patient/ resident, client/ patient/ resident-to-worker, contact with the environment, contact with contaminated equipment). (Source: PIDAC's Best Practices for Environmental Cleaning for Prevention and Control of Infections)

Precautionary principle

A principle used by the Ministry of Health and Long-Term Care and Chief Medical Officer of Health to guide decision-making during an emergency. According to this principle, reasonable steps to reduce risk should not await scientific certainty (Source: Spring of Fear, Justice Archie Campbell).

Primary health care

Primary care (the provision of integrated, accessible health care services by clinicians who are accountable for addressing a large majority of personal health care needs, developing a sustained partnership with clients/ patients and practicing in the context of family and community), disease prevention, health promotion, population health and community development within a holistic framework, with the aim of providing essential community-focused health care (Sources: World Health Organization, Institute of Medicine). Primary health care organizations include family health teams, community health centres, Aboriginal health access centres, departments of family medicine, nurse practitioner-led clinics and solo practitioners such as family physicians, general practitioners and pediatricians.

Provincial Infectious Disease Advisory Committee

A multidisciplinary scientific advisory body that provides to the Chief Medical Officer of Health evidence-based advice regarding multiple aspects of infectious disease identification, prevention and control (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Public Health Agency of Canada

A national agency that promotes improvement in the health status of Canadians through public health action and the development of national guidelines (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Environmental Cleaning for Prevention and Control of Infections).

Public health measures

Non-pharmaceutical interventions that help to slow the spread of disease in the community.

Public Health Ontario

Formerly known as the Ontario Agency for Health Protection and Promotion. An arm's-length government agency dedicated to protecting and promoting the health of all Ontarians and reducing inequities in health. Public Health Ontario was created by legislation in 2007 and began operations in July 2008 with a mandate to provide scientific and technical advice to those working to protect and promote the health of Ontarians. Its vision is to be an internationally recognized centre of expertise dedicated to protecting and promoting the health of all Ontarians through the application and advancement of science and knowledge (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Infection Prevention and Control in Perinatology).

Recommendations from the Ministry of Health and Long-Term Care

This term refers clinical, occupational health & safety and infection prevention & control guidance. Recommendations related to occupational health & safety may be considered reasonable precautions in the application of the Occupational Health and Safety Act.

Regional Infection Control Networks

Networks that coordinate and integrate resources related to the prevention, surveillance and control of infectious diseases across all health care sectors and for all health care providers, promoting a common approach to infection prevention & control and utilization of best-practices within the region (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Environmental Cleaning for Prevention and Control of Infections).

Respiratory etiquette

Personal practices that help prevent the spread of bacteria and viruses that cause acute respiratory infections (e.g., covering the mouth when coughing, care when disposing of tissues) (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Routine practices

The system of infection prevention & control practices recommended by the Public Health Agency of Canada to be used with all clients/ patients/ residents during all care activities to prevent and control transmission of microorganisms in all health care settings (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Seal-check

A procedure that the health care provider must perform each time an N95 respirator is worn to ensure it fits the wearer's face correctly to provide adequate respiratory protection (Source: Provincial Infectious Disease Advisory Committee's Routine Practices and Additional Precautions in all Health Care Settings).

Sentinel health care provider

A health care provider that participates in a sentinel surveillance system. In Ontario, sentinel health care providers participate in Public Health Agency of Canada's FluWatch Program or the national Sentinel Vaccine Effectiveness Study. Ideally, Ontario would have adequate numbers of sentinel health care providers, representative of the population of the province, so that the information gathered from FluWatch and the Sentinel Vaccine Effectiveness Study could be applied to the population as a whole.

Seroprevalance

The proportion of a population that is seropositive – i.e., has been exposed to the influenza virus.

Surgical mask

Also known as procedure mask. Surgical masks are used as physical barriers to protect users from hazards, such as splashes of large droplets of blood or body fluids. Surgical masks are used for several different purposes, including being placed on sick people to limit the spread of infectious respiratory secretions to others. (Source: Based on United States Department of Labor Occupational Safety and Health Administration Fact Sheet: Respiratory Infection Control).

Surveillance

The systematic ongoing collection, collation and analysis of data with timely dissemination of information to those who require it in order to take action (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Infection Prevention and Control Programs in Ontario).

Syndromic surveillance

The detection of individual and population health indicators of illness (i.e., signs and symptoms of infectious disease) that are discernible before confirmed laboratory diagnoses are made (Source: Provincial Infectious Disease Advisory Committee's Best Practices for Infection Prevention and Control Programs in Ontario).

Vaccine delivery agent

Health care providers who administer immunization outside of a public health unit.

Visitor

An individual who does not have an established relationship with a health organization. Visitors may be household contacts and friends that accompany clients/ patients to outpatient settings or visit clients/ patients/ residents in inpatient settings.

Voluntary public health measures

The behaviours and the environmental supports that create the conditions that support good public health practices.

Vulnerable population

A group of people who, because of the determinants of health, are more likely to be exposed to influenza, more likely to experience a serious impact because of exposure,

less likely to benefit from response and recovery measures and/ or who may be negatively affected by response and recovery measures.

Appendix C – Acronyms

AHAC	Aboriginal health access centre
BAL	bronchoalveolar lavage
CAEFISS	Canadian Adverse Events Following Immunization Surveillance System
CCIS	Critical Care Information System
CDC	Centers for Disease Control and Prevention
CFR	case fatality rate
CHC	community health centre
CMOH	Chief Medical Officer of Health
C/P/R	client/ patient/ resident
CPIP	Canadian Pandemic Influenza Plan for the Health Sector
EDSS	Emergency Department Syndromic Surveillance
EMCPA	Emergency Management and Civil Protection Act
ETT	endotracheal tube
FAC	flu assessment centre
F/P/T	federal - provincial - territorial
FF100	first few hundred
FHT	family health team
HCRF	Health Care and Residential Facilities regulation
HEIA	Health Equity Impact Assessment
HNS	Health Network System
HPPA	Health Protection and Promotion Act
HSR	health and safety representative
IHN	Important Health Notice
ILI	influenza-like illness
IMPACT	Immunization Monitoring Program ACTive
IPAC	infection prevention & control
iPHIS	Integrated Public Health Information System
IRS	internal responsibility system
JHSC	joint health and safety committee
LHIN	Local Health Integration Network

LTCHA	Long-Term Care Homes Act
MEOC	Ministry Emergency Operations Centre
MOH	medical officer of health
MOHLTC	Ministry of Health and Long-Term Care
MOL	Ministry of Labour
MRSA	methicillin-resistant *S. aureus*
NACI	National Advisory Committee on Immunization
NML	National Microbiology Laboratory
NP	nasopharyngeal
OHIP	Ontario Health Insurance Plan
OHPIP	Ontario Health Plan for an Influenza Pandemic
OHS	occupational health & safety
OHSA	Occupational Health and Safety Act
PEOC	Provincial Emergency Operations Centre
PHAC	Public Health Agency of Canada
PHO	Public Health Ontario
PHOL	Public Health Ontario Laboratories
PHU	public health unit
PICB	Performance Improvement and Compliance Branch
PIDAC	Provincial Infectious Disease Advisory Committee
PPE	personal protective equipment
R_0	basic reproduction number
RACE	recognize the hazard, assess the risk, control the risk and evaluate the controls
RICN	Regional Infection Control Network
RIDT	rapid influenza diagnostic testing
RP/AP	routine practices and additional precautions (i.e., PIDAC's Routine Practices and Additional Precautions in All Health Care Settings)
SARS	Severe Acute Respiratory Syndrome
TP	transfer payment
UIIP	Universal Influenza Immunization Program
VDA	vaccine delivery agent
WHO	World Health Organization

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Ontario

This is **"Exhibit F"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

A Commissioner, etc.

World Health Organization

< Go back to all Coronavirus disease 2019 Q&As

Coronavirus disease (COVID-19)

12 October 2020 | Q&A

Latest update 13 May 2021 - WHO is continuously monitoring and responding to this pandemic. This Q&A will be updated as more is known about COVID-19, how it spreads and how it is affecting people worldwide. For more information, regularly check the WHO coronavirus pages. https://www.who.int/covid-19

What is COVID-19?

What are the symptoms of COVID-19?

What happens to people who get COVID-19?

Among those who develop symptoms, most (about 80%) recover from the disease without needing hospital treatment. About 15% become seriously ill and require oxygen and 5% become critically ill and need intensive care.

Complications leading to death may include respiratory failure, acute respiratory distress syndrome (ARDS), sepsis and septic shock, thromboembolism, and/or multiorgan failure, including injury of the heart, liver or kidneys.

In rare situations, children can develop a severe inflammatory syndrome a few weeks after infection.

Who is most at risk of severe illness from COVID-19?

Are there long-term effects of COVID-19?

How can we protect others and ourselves if we don't know who is infected?

When should I get a test for COVID-19?

What test should I get to see if I have COVID-19?

What about rapid tests?

I want to find out if I had COVID-19 in the past, what test could I take?

What is the difference between isolation and quarantine?

What should I do if I have been exposed to someone who has COVID-19?

How long does it take to develop symptoms?

Is there a vaccine for COVID-19?

What should I do if I have COVID-19 symptoms?

Are there treatments for COVID-19?

Are antibiotics effective in preventing or treating COVID-19?

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WHO TEAM Emergencies Preparedness

Related

COVID-19 hub

Advice for the public

All COVID-19 Q&As

WHO Information Network on Epidemics (EPI-WIN)

Science in 5 series: WHO experts explain the science related to COVID-19

This is **"Exhibit G"**
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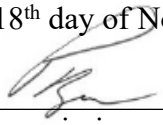

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Public Health Ontario | Santé publique Ontario

Ontario COVID-19 Data Tool

The Ontario COVID-19 Data Tool provides epidemiological information on COVID-19 activity in Ontario to-date. Explore the most recent COVID-19 data including: daily case counts, hospitalizations and deaths (Case trends), total or recent cases counts by age and sex, map by public health unit, source of COVID-19 infection (acquisition), outbreaks and laboratory testing.

Additions to the Ontario COVID-19 Data Tool as of May 28th, 2021:

- Vaccine uptake data on the Summary, Map and Vaccines sections
- COVID-19 reproduction number and doubling time

The COVID-19 Data Tool is updated Monday to Fridays at 11:30 a.m. except on statutory holidays. For weekend case counts see the **Daily Epidemiological Summary.**

For questions about the data, please contact **EPIR@oahpp.ca**.

Summary | Case trends | Age and sex | Map | Acquisition | Reproduction | Outbreaks | Lab tests | Vaccines | Technical notes | Glossary

Summary +

Date

24 Jun 2021

Confirmed COVID-19 cases in Ontario

As of June 24, 2021

Daily cases, rates, hospitalizations and deaths by public health unit can be found in **Case trends**.

Change in cases

256

Recent cases

5,469

reported in last 14 days
1.0% of cases

Total cases

543,571

3,656.9 per 100,000

Total hospitalized

27,643

186.0 per 100,000
5.1% of cases

Total deaths

9,101

61.2 per 100,000
1.7% of cases

COVID-19 cases in Ontario with a variant of concern detected

As of June 24, 2021

Find daily case counts of COVID-19 variants of concern by public health unit in **Case trends**.

Total case counts for B.1.1.7 include all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on a positive N501Y and negative E484K mutation.

Total cases

B.1.1.7	**143,035**
B.1.351	**1,161**
P.1	**4,270**

Laboratory tests for COVID-19 in Ontario

As of June 24, 2021

See daily historical data in **Lab tests**.

New tests

26,561

178.7 tests per 100,000

Daily % positive

1.3

Total tests

15,805,892

106,333.7 tests per 100,000

COVID-19 vaccine uptake in Ontario

As of June 23, 2021 Vaccine data are updated weekly on Thursdays.

See the **Vaccine** and **Map** tabs for more vaccination data.

At least one dose

9,753,684

65.6% of population

Fully vaccinated

3,348,673

22.5% of population

Change in cases reflects new cases reported since the previous day.

Recent cases include cases reported within the past 14 days with a three day lag from the time of data extraction.

Rate is per 100,000 population.

Hospitalizations include all cases reported as ever being hospitalized during their infection.

Percent positive refers to the percentage of tests performed that were positive for COVID-19 and does not translate to the number of specimens or persons testing positive.

New tests refer to the number of tests performed and do not reflect the number of specimens or persons tested.

COVID-19 variants of concern (VOC) cases are confirmed COVID-19 cases where a designated VOC was identified by genomic analysis of their SARS-CoV-2 positive specimen. Lineage B.1.1.7 includes cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation

- **PANGO lineage B.1.1.7** first detected in England.
- **PANGO lineage B.1.351** first detected in South Africa.
- **PANGO lineage P.1** first detected in Brazil.

Interpret the VOC and mutation case counts with caution. Daily counts may change due to the varying time required to complete VOC testing and/or genomic analysis following the initial positive test for SARS-CoV-2 and may result in totals differing from past publicly reported case counts. Additionally, changes to the VOC testing algorithm may occur over time. Refer to the Technical Notes for more information.

Vaccine series: the number of vaccine doses within a schedule that has been approved by Health Canada. COVID-19 vaccine

products available in Ontario have either a one-dose (i.e. Janssen) or two-dose (i.e. Moderna, Pfizer-BioNTech, AstraZeneca or COVISHIELD) schedule. Note: Janssen vaccines have not yet been distributed in Ontario.

At least one dose: refers to individuals that have received at least one dose of a COVID-19 vaccine. Reflects individuals that have received the first dose of a two-dose series, as well as those that have completed a COVID-19 vaccine series.

At least one dose coverage: the proportion of the total population of Ontario, or a public health unit, that has received at least one dose of a COVID-19 vaccine. Reflects individuals that have received the first dose of a two-dose series, as well as those that have completed a COVID-19 vaccine series

Fully vaccinated: refers to individuals that have received both doses of a two-dose COVID-19 vaccine series (i.e. dose two of two) or one dose of a one-dose COVID-19 vaccine series (i.e. dose one of one). Reflects individuals that have completed a COVID-19 vaccine series.

Fully vaccinated coverage: the proportion of the total population of Ontario, or a public health unit, that has received both doses of a two-dose COVID-19 vaccine series (i.e. dose two of two) or one dose of a one-dose COVID-19 vaccine series (i.e. dose one of one). Reflects individuals that have completed a COVID-19 vaccine series.

« Previous Next »

Related Information

Coronavirus Disease 2019 (COVID-19)

External Resources

COVID-19 case data: All Ontario - Government of Ontario

COVID-19 cases in schools and child care centres - Ministry of Education

COVID-19 Hospitalizations - Government of Ontario

COVID-19 Vaccines Status - Government of Ontario

Updated 30 June 2021

This is **"Exhibit H"**
to the Affidavit of Matthew Hodge,
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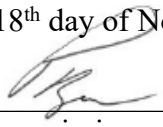

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Government of Canada | Gouvernement du Canada

COVID-19 daily epidemiology update

Updated: June 29, 2021, 7 pm EST

Summary of COVID-19 cases across Canada and over time. Contains detailed data about the spread of the virus over time and in different regions of the country. Includes breakdowns by age and sex or gender. Provides an overview of hospitalizations and deaths, testing, variants of concern and exposures.

Key updates as of June 29, 2021, 7 pm EST

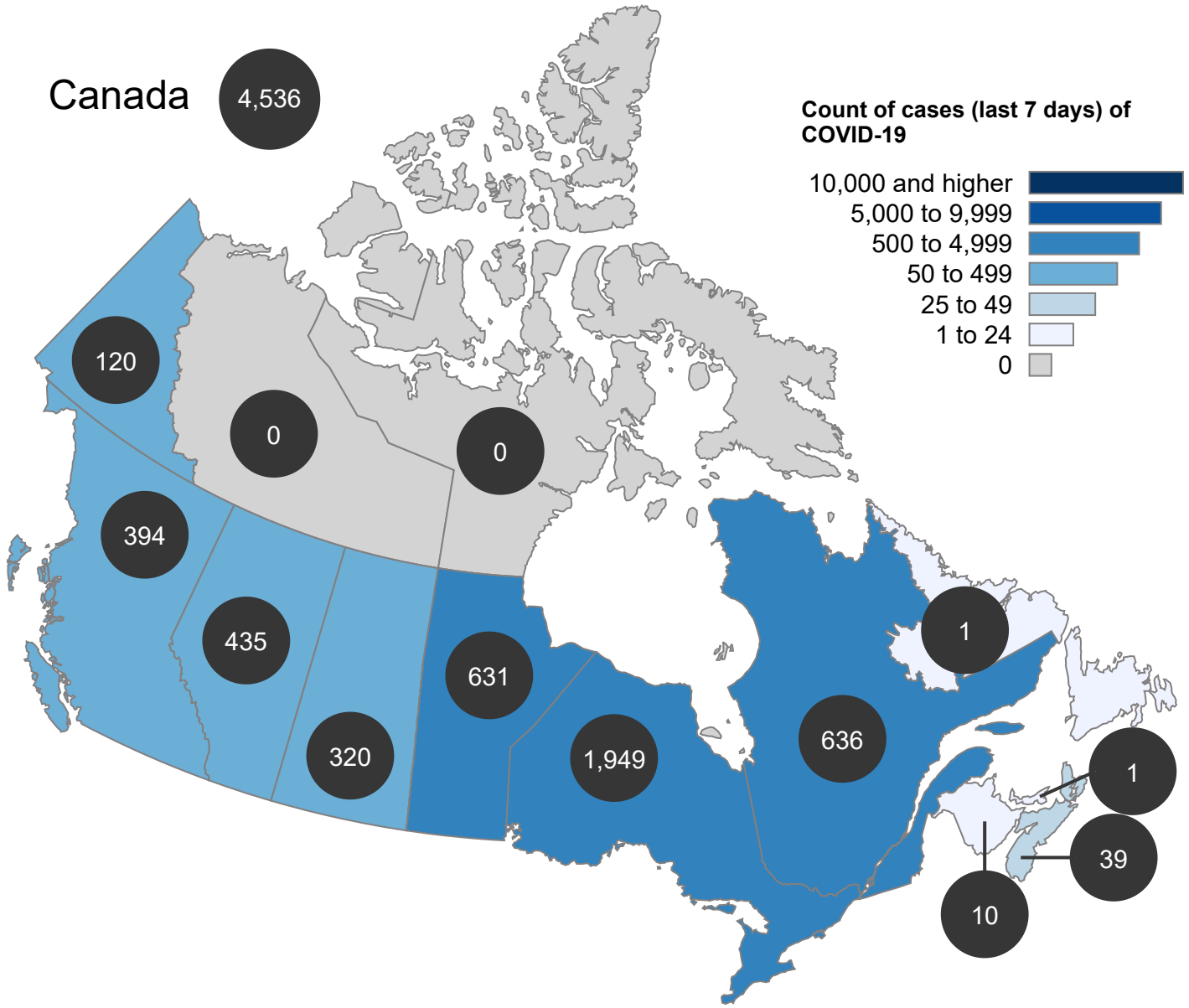
Cases today	Total cases	Active cases	Total resolved	Deaths today	Total deaths
602	1,414,736	7,447	1,381,016	35	26,273

Total tests performed	Daily percent positive (last 7 days)	Daily tests per 100,000 population (last 7 days)
36,705,571	1.2%	156

- We update these sections daily at 7:00 PM EST: Key updates, Current situation and National overview. Laboratory data represents specimens received by labs up to June 27, 2021 to allow time to process results.
- We update these sections every Friday: Epidemic curve, Demographics, How people were exposed, and Severe illness and outcomes.
- Most cases (65.0%) and deaths (77.5%) were reported by Ontario and Quebec.
- Of the 13 jurisdictions reporting updates, no new cases were reported in 3 provinces or territories in the past 24 hours.
- Of the 13 jurisdictions reporting updates, no new deaths were reported in 9 provinces or territories in the past 24 hours.

Current situation

Figure 1a. Count of cases (last 7 days) of COVID-19, by province/territory as of June 29, 2021



The count of cases (last 7 days) of COVID-19 in **Canada** was **4,536** as of June 29, 2021.

This information is based on data our provincial and territorial partners published on cases, deaths, and testing daily, and are current as of the day they are published. Today's numbers are current as of June 29, 2021. For the most up to date data for any province, territory or city, please visit their website. The number of cases or deaths reported on previous days may differ slightly from those on the provincial and territorial websites as these websites may update historic case and death counts as new information becomes available.

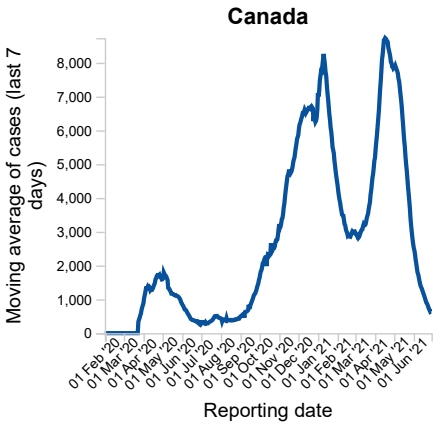
Areas in Canada with cases of COVID-19 as of June 29, 2021

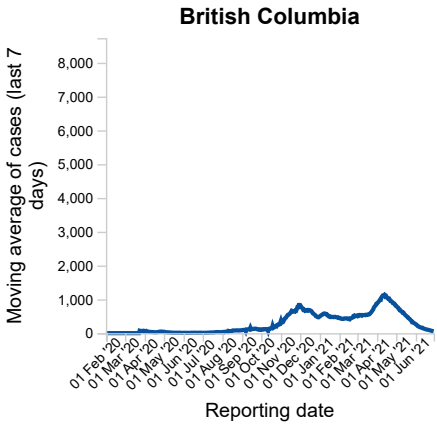
	Total cases		Cases last 7 days		Active cases		Resolved	Deaths		Deaths last 7 days		Total tests performed	Moving average tests performed last 7 days		Moving average positivity last 7 days
Location	Count	Rate*	Count	Rate*	Count	Rate*	Count	Count	Rate*	Count	Rate*	Count	Count	Rate*	Percent
Canada	**1,414,736**	**3,722**	**4,536**	**12**	**7,447**	**20**	**1,381,016**	**26,273**	**69**	**119**	**0**	**36,705,571**	**59,346**	**156**	**1.2%**
British Columbia	147,578	2,867	394	8	893	17	144,931	1,754	34	11	0	2,883,199	5,135	100	1.4%
Alberta	231,911	5,245	435	10	1,132	26	228,480	2,299	52	9	0	4,670,457	5,614	127	1.3%
Saskatchewan	48,823	4,142	320	27	464	39	47,791	568	48	4	0	910,196	1,579	134	3.2%
Manitoba	56,097	4,067	631	46	1,408	102	53,550	1,139	83	10	1	867,383	1,828	133	6.3%
Ontario	544,713	3,697	1,949	13	2,409	16	533,150	9,154	62	72	0	15,747,264	22,492	153	1.3%
Quebec	374,731	4,370	636	7	878	10	362,646	11,207	131	12	0	9,791,320	17,537	205	0.5%
Newfoundland and Labrador	1,385	265	1	0	9	2	1,369	7	1	0	0	300,841	702	135	0.1%
New Brunswick	2,329	298	10	1	26	3	2,258	45	6	0	0	373,609	594	76	0.2%
Nova Scotia	5,832	596	39	4	51	5	5,689	92	9	0	0	935,353	3,519	359	0.2%
Prince Edward Island	207	130	1	1	1	1	206	0	0	0	0	174,182	258	162	0.0%
Yukon	332	790	120	285	176	419	152	4	10	1	2	9,129	N/A	N/A	N/A
Northwest Territories	128	283	0	0	0	0	128	0	0	0	0	24,745	29	65	0.5%
Nunavut	657	1,670	0	0	0	0	653	4	10	0	0	17,817	58	147	0.0%

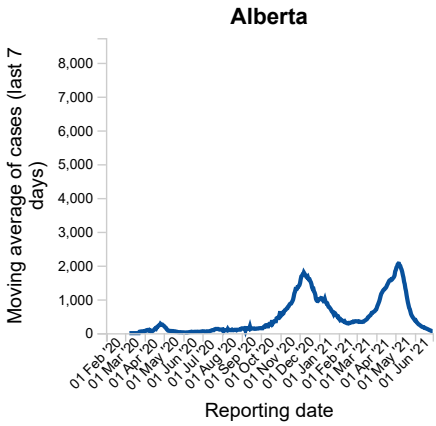
* Rate per 100,000 population

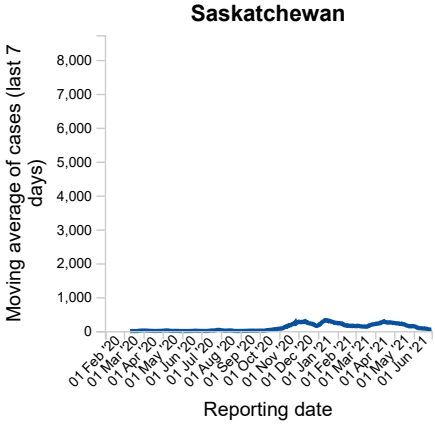
Figure 1b. Moving average of cases (last 7 days) of COVID-19 in Canada as of June 29, 2021, 7 pm EST

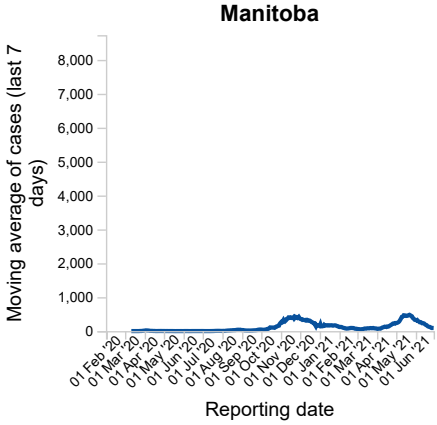
The figures below show cases over time. The range of dates (January 31st, 2020 - present date) is the same for each figure. This allows you to compare the provinces and territories on the same timescale.

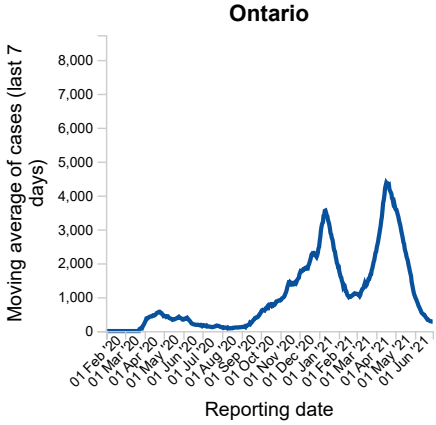


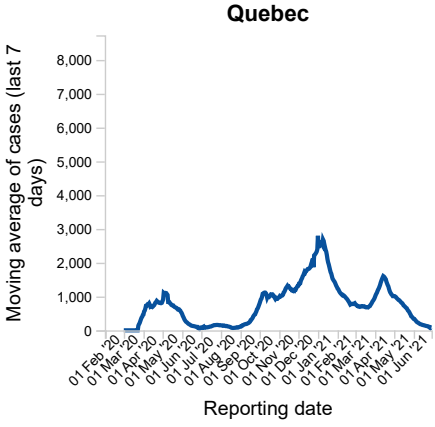


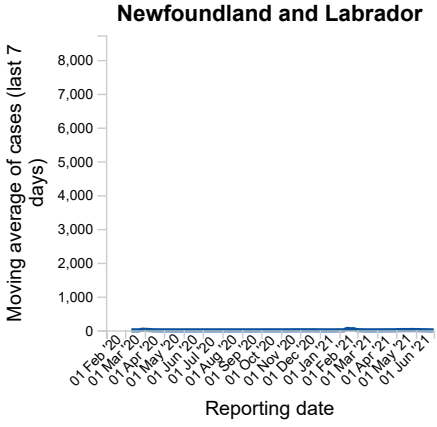


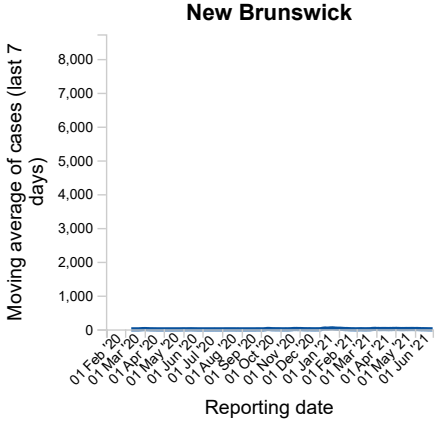


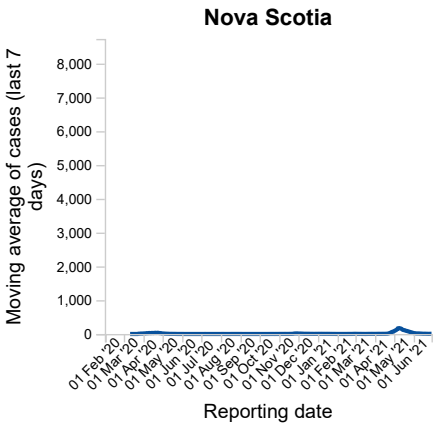


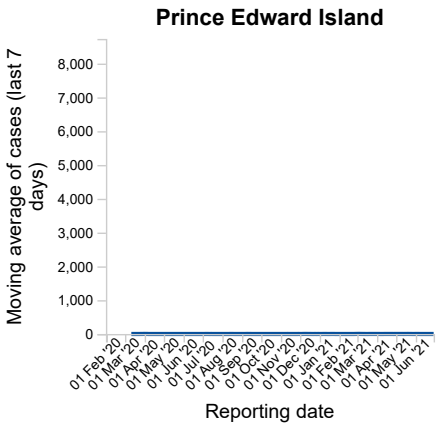


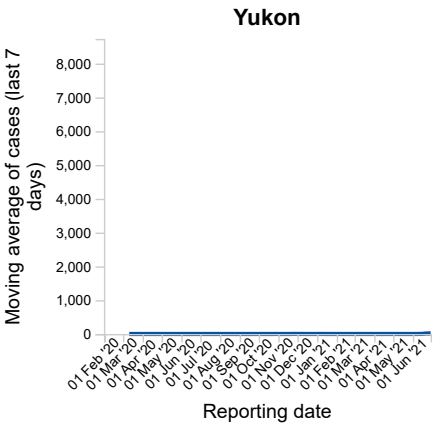


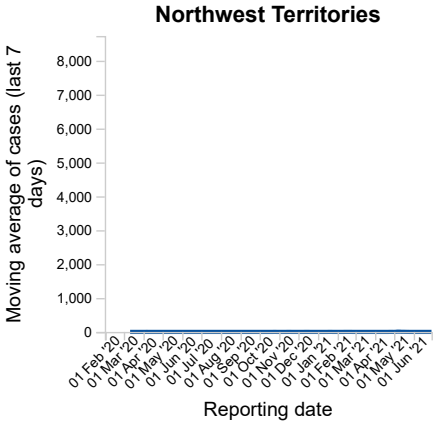


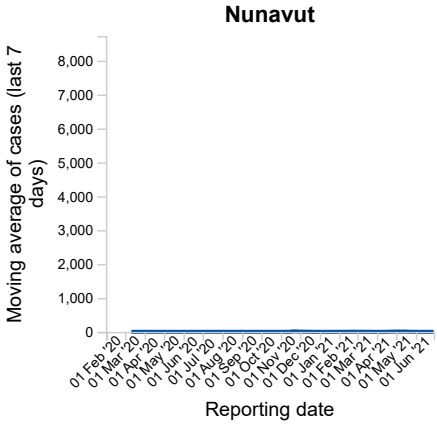












This information is based on data our provincial and territorial partners published on cases, deaths, and testing daily, and are current as of the day they are published. Today's numbers are current as of June 29, 2021. For the most up to date data for any province, territory or city, please visit their website. The number of cases or deaths reported on previous days may differ slightly from those on the provincial and territorial websites as these websites may update historic case and death counts as new information becomes available.

Downloadable data (in .csv format).

Note: Out of the total number of people tested, 76 were repatriated travellers, of which 13 were cases.

National overview

There have been over **36,705,571** COVID-19 tests performed in Canada or **965,803 tests per 1 million people**. Of these, **4.0%** were positive. For information about testing trends, please see the Detailed weekly epidemiological report (PDF).

Table 1. Daily* change in the number of cases, deaths and tests performed, by province or territory, as of June 29, 2021, 7 pm EST

Location	New cases	New deaths	Tests performed
Canada	**602**	**35**	**61,585**
British Columbia	29	0	3,664
Alberta	61	4	22,232
Saskatchewan	52	2	1,425
Manitoba	61	0	1,575
Ontario	299	25	13,071
Quebec	71	4	15,365
Newfoundland and Labrador	0	0	561
New Brunswick	3	0	401
Nova Scotia	1	0	3,077
Prince Edward Island	1	0	138
Yukon	24	0	N/A
Northwest Territories	0	0	13
Nunavut	0	0	63

* The new cases, deaths and tests reflect the difference between a province or territory's current report and their last report. Some provinces and territories do not update daily.

N/A means that no daily update was provided by the province or territory.

Variants of concern (VOC) in Canada

All viruses, including COVID-19, change or mutate over time. Not all mutations are of concern. However, some changes result in variants of concern (VOC). A VOC (Variants of concern) has changes that are significant to public health.

For example, they might:

- spread more easily
- cause more severe illness
- require different treatments, or
- not respond the same to current vaccines

The Public Health Agency of Canada (PHAC) updates VOC (Variants of concern) information from Sunday to Thursday at 7:00 PM EDT, using publicly reported information from the provinces and territories.

Table 2. Cumulative number of cases involving variants of concern (VOC) publicly reported, as of June 29, 2021

Location	B.1.1.7 variant	B.1.351 variant	P.1 variant
Canada	**221,763**	**2,149**	**17,974**
British Columbia	12,054	151	9,709
Alberta	45,508	159	2,752
Saskatchewan	6,634	10	322
Manitoba	6,630	72	205
Ontario	143,381	1,315	4,439
Quebec	6,989	420	511
Newfoundland and Labrador	187	6	1
New Brunswick	180	4	1
Nova Scotia	73	12	1
Prince Edward Island	26	0	0
Yukon	3	0	31
Northwest Territories	77	0	2
Nunavut	21	0	0

Note:

- The table reports publicly available information from the provinces and territories. In case of discrepancies, the provincial or territorial data should be considered current and correct.

- PHAC is in the process of replacing this table with a graphical view that is more representative of the mix of variants present in Canada in the coming weeks. This new graphical view will include all variants of concern including B.1.617 and variants of interest.

There are many variants being tracked internationally and across Canada. Most of these are similar to the original variants that emerged in 2020. VOCs (Variants of concern) now represent a majority of COVID-19 cases in Canada.

Four VOCs (Variants of concern) have been detected in most provinces and territories:

- B.1.1.7
- B.1.351
- P.1
- B.1.617

The **B.1.1.7 variant** continues to account for most VOCs (Variants of concern) classified to date in Canada.

The **B.1.617 variant** has only been recently identified and thus is less understood. Its 3 sub-lineages may have different properties. Early data from the U.K. indicate that the B.1.617.2 sub-lineage may be more transmissible overall, either similar to or perhaps more transmissible than the B.1.1.7 variant. However, laboratory data suggest that currently authorized vaccines are also effective against this sub-lineage. The B.1.617.1 and B.1.617.3 sub-lineages are less well-known, but may be less affected by vaccines. There are many variants being tracked internationally and across Canada, most of which are similar to the original variants that emerged in 2020.

The impact of the B.1.617 variant and its sub-lineages is still being assessed in Canada, where the variant has been identified in all 10 provinces and 1 territory. Genomic surveillance has also identified all 3 sub-lineages (B.1.617.1, B.1.617.2 and B.1.617.3).

Of these 3:

- B.1.617.1 accounted for most of the identified cases in March and April 2021
- B.1.617.2 accounted for most of the identified cases detected at the border
- B.1.617.3 accounts for a very small proportion (1%) of identified cases

Canada is collecting evidence to determine if each of these sub-lineages meets the definition for a variant of concern or a variant of interest.

New variants will continue to appear. It is crucial to remain vigilant and take all available measures to limit spread.

Detailed case information

The tables and figures below reflect detailed case information provided to the Public Health Agency of Canada (PHAC) by health authorities in the provinces and territories. This data is updated every week. It may change as we get more information about cases.

Updated: June 25, 2021, 7 pm EST

Epidemic curve

As of June 25, 2021, 7 pm EST, PHAC has received detailed case report data on 1,410,946 cases. Both exposure and symptom onset date were available for 1,254,652 (88.9%) cases [1].

The shaded area on the far right of Figure 2 represents lag time. This is the period of time (1 to 2 weeks) before the latest cases are reported to PHAC. This delay is a result of the time required to seek health care, get tested and receive results. It also takes time for public health authorities to gather information on cases. We update this information as it becomes available.

Figure 2. COVID-19 cases (n=1,411,021 [1]) in Canada by date of illness onset [2] as of June 25, 2021, 7 pm EST (total cases)

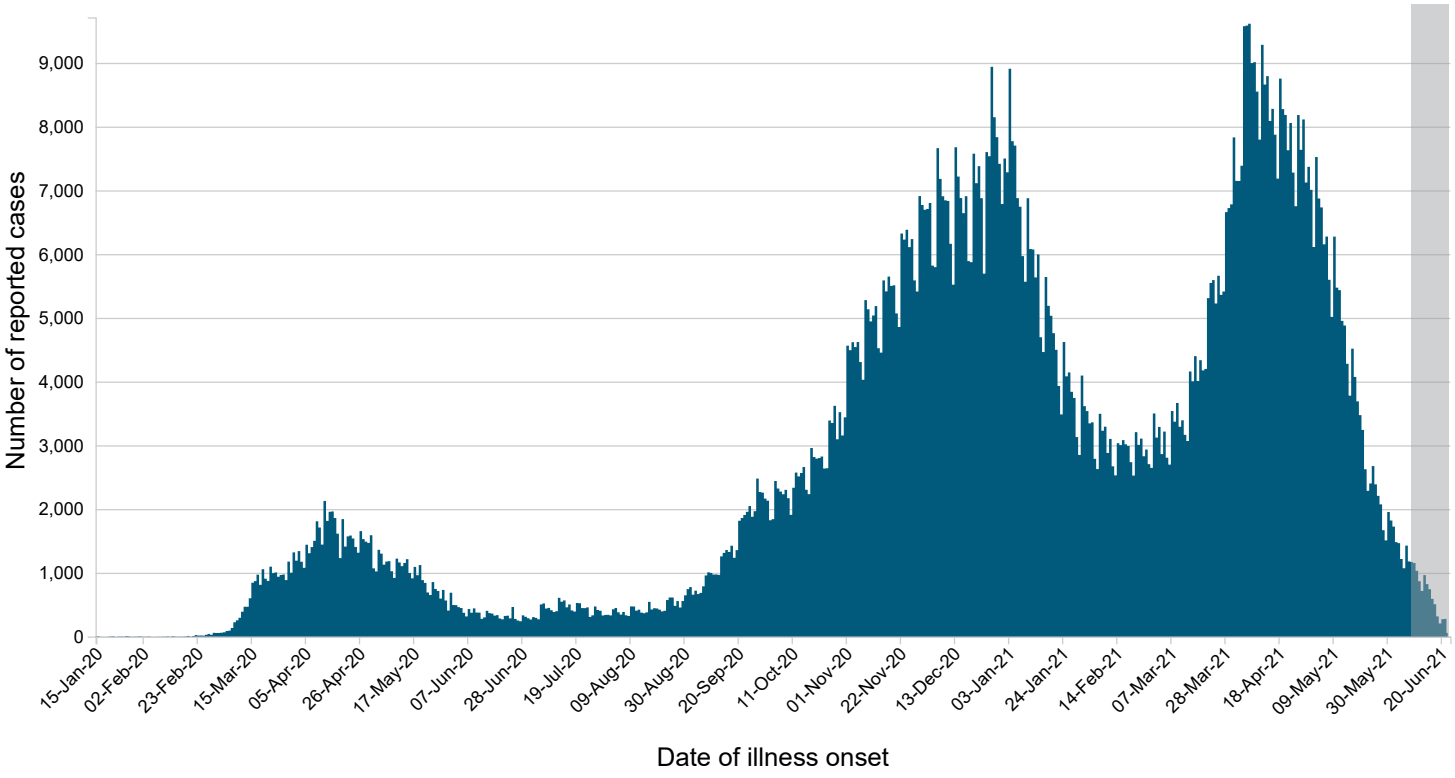


Figure 2. COVID-19 cases (n=1,254,652 [1]) in Canada by date of illness onset [2] as of June 25, 2021, 7 pm EST (by exposure)

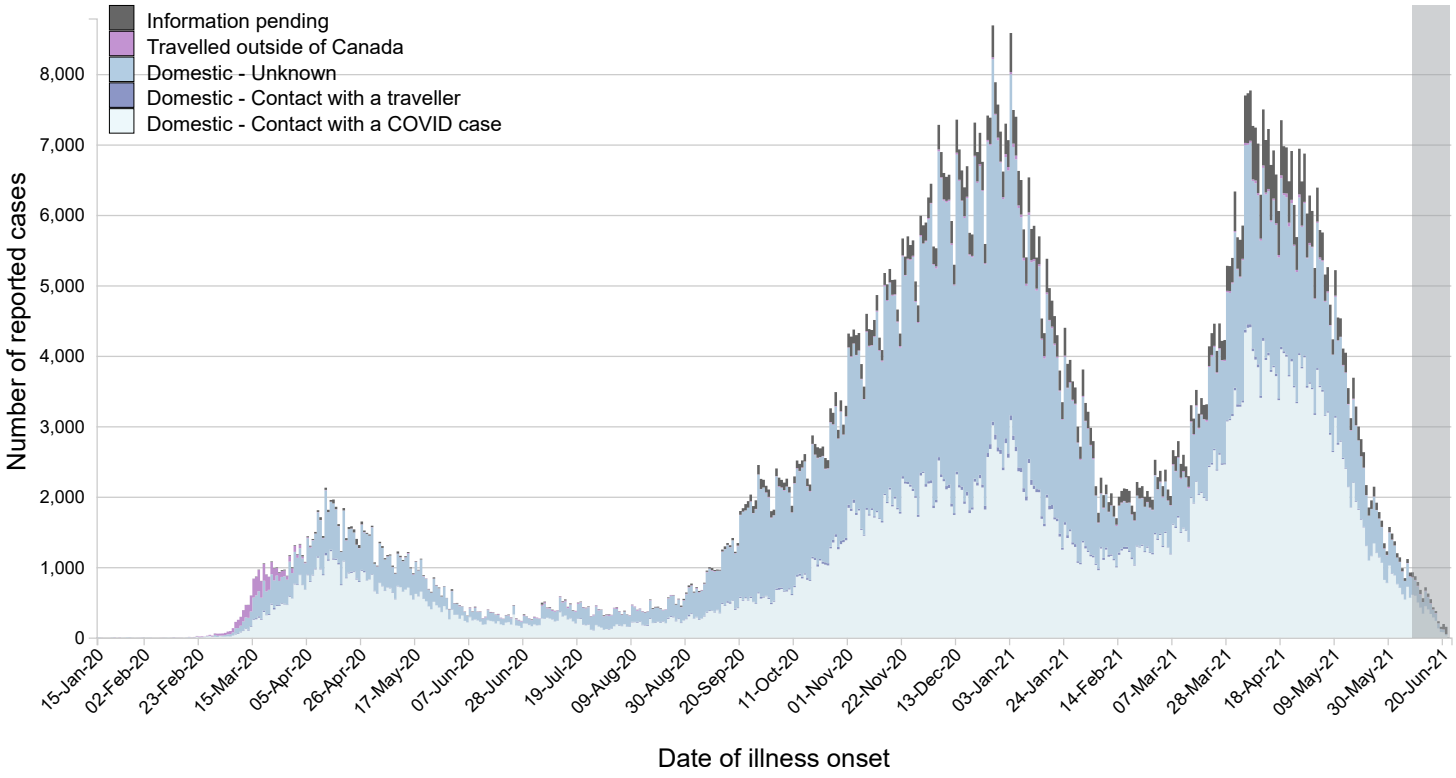


Figure 2. COVID-19 cases (n=1,410,571 [1]) in Canada by date of illness onset [2] as of June 25, 2021, 7 pm EST (by age - 10 year groups)

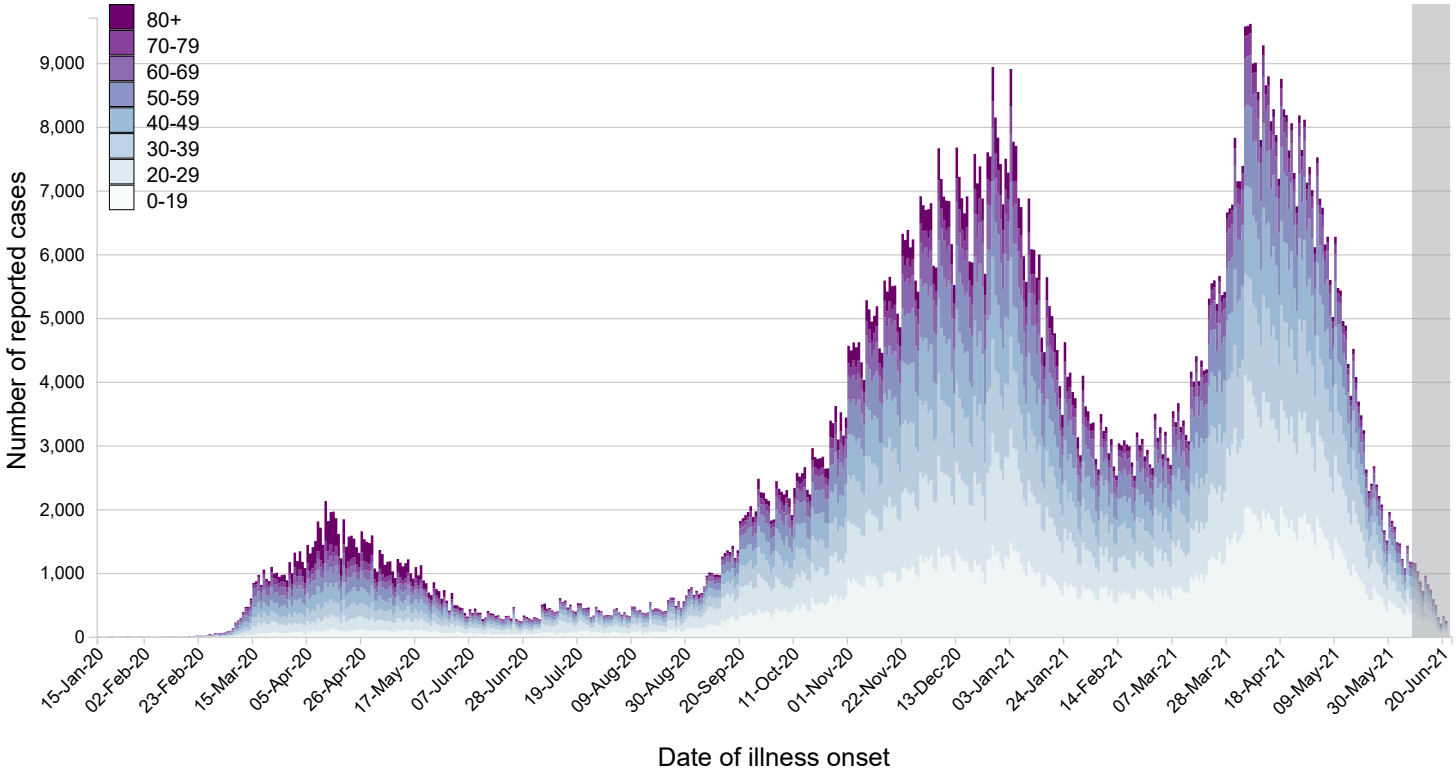
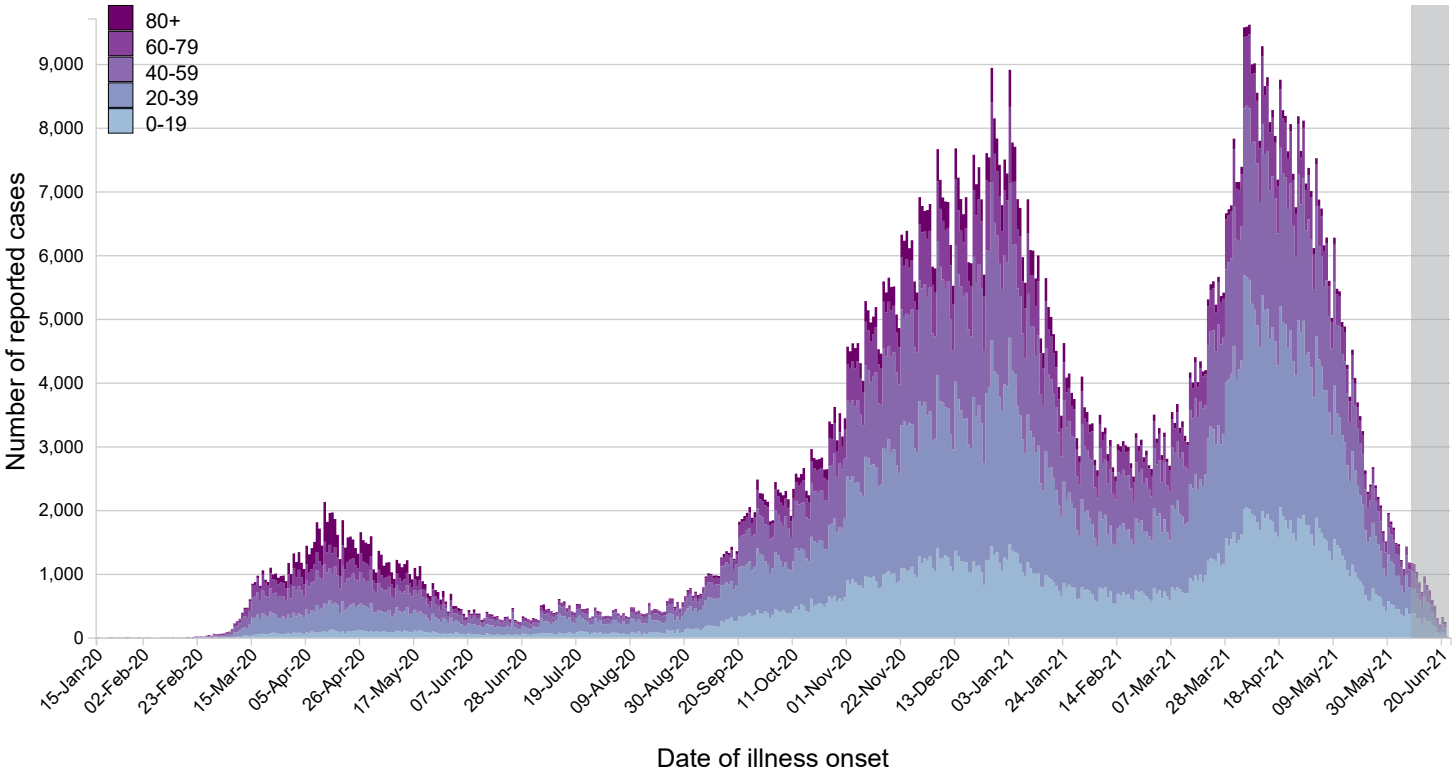


Figure 2. COVID-19 cases (n=1,410,571 [1]) in Canada by date of illness onset [2] as of June 25, 2021, 7 pm EST (by age - 20 year groups)



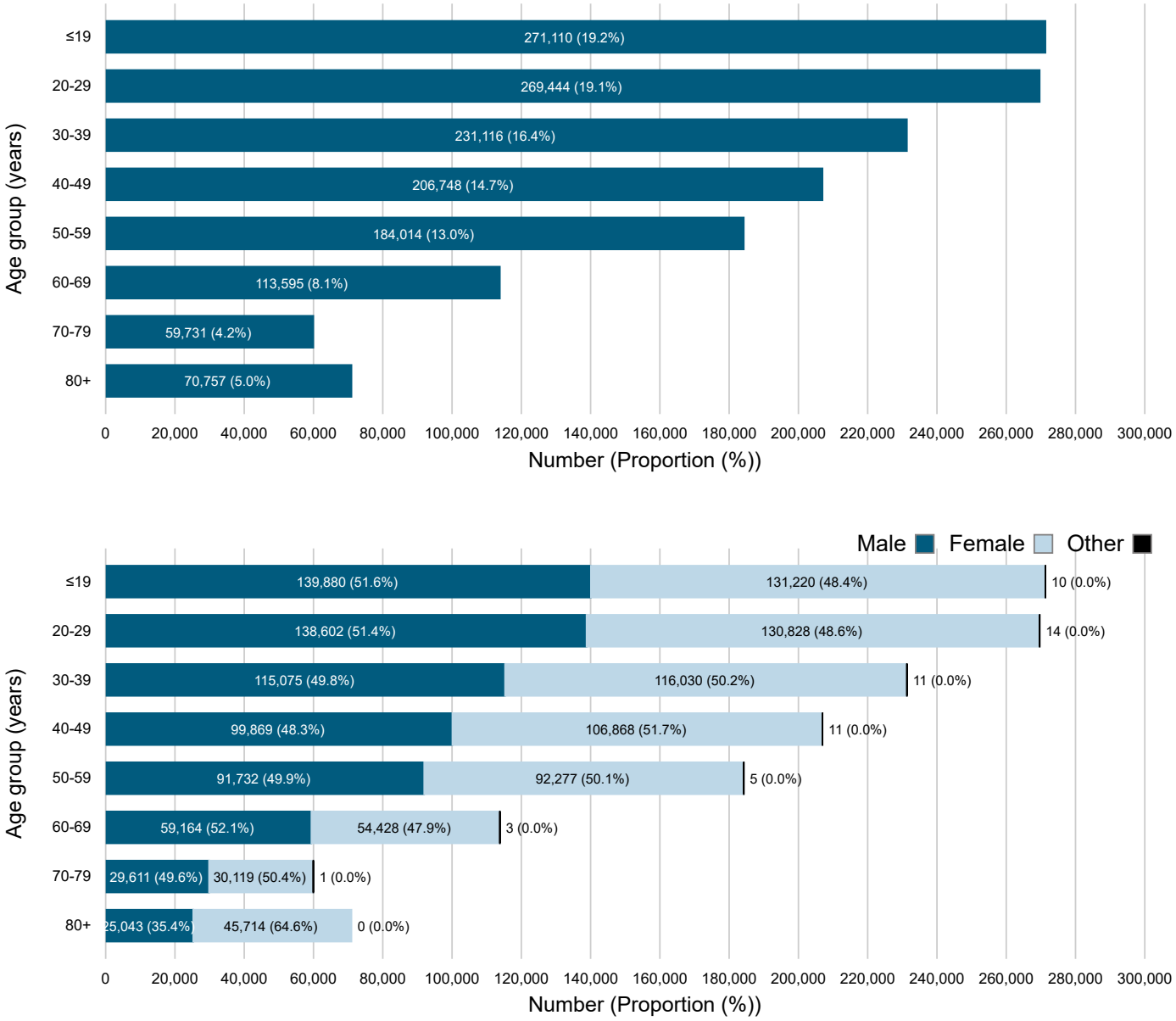
This figure may underestimate the total number of cases among returning travelers. Exposure history is not available for all cases and jurisdictions have not all consistently reported exposure history to PHAC throughout the pandemic.

Demographics

We have detailed case report data from 1,410,946 cases. We know the age of patients in 100.00% of cases, and both age and gender in 99.69% of cases.

Of the cases reported in Canada so far, 50.3% were female and 35.6% were between 20 and 39 years old (Figure 3).

Figure 3. Age distribution of COVID-19 cases (n=1,410,946 [1]) in Canada as of June 25, 2021, 7 pm EST [4]



Age by gender [4] distribution of COVID-19 cases (n=1,410,946 [1]) in Canada, June 25, 2021, 7 pm EST

Age group (years)	Number of cases with case reports (percentage)	Number of male cases (percentage)	Number of female cases (percentage)	Number of other cases (percentage)
≤19	271,110 (19.2%)	139,880 (20.0%)	131,220 (18.5%)	10 (18.2%)
20-29	269,444 (19.1%)	138,602 (19.8%)	130,828 (18.5%)	14 (25.5%)
30-39	231,116 (16.4%)	115,075 (16.5%)	116,030 (16.4%)	11 (20.0%)
40-49	206,748 (14.7%)	99,869 (14.3%)	106,868 (15.1%)	11 (20.0%)
50-59	184,014 (13.0%)	91,732 (13.1%)	92,277 (13.0%)	5 (9.1%)
60-69	113,595 (8.1%)	59,164 (8.5%)	54,428 (7.7%)	3 (5.5%)
70-79	59,731 (4.2%)	29,611 (4.2%)	30,119 (4.3%)	1 (1.8%)
80+	70,757 (5.0%)	25,043 (3.6%)	45,714 (6.5%)	0 (0.0%)
Total	1,406,515 (100%)	698,976 (100%)	707,484 (100%)	55 (100%)

How people were exposed [3]

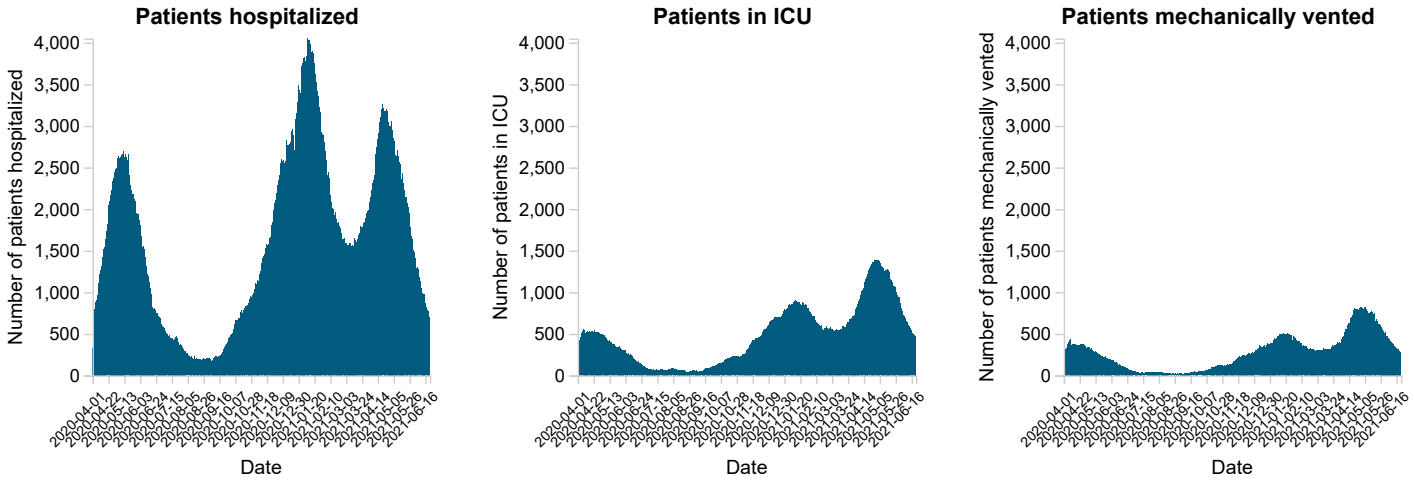
In Canada, detailed case report data were provided for 1,410,946 cases. We have exposure history for 1,254,652 (88.9%) cases. The probable exposure setting of these cases [1] are:

- any exposure that occurred in Canada: **1,167,909 (93.1%)**, including
  - from contact with a known COVID case: **583,505 (46.5%)**
  - from contact with a traveller: **8,451 (0.7%)**
  - from an unknown source: **575,953 (45.9%)**
- currently unknown (information pending): **77,135 (6.1%)**
- travelled outside of Canada: **9,608 (0.8%)**

Severe illness and outcomes

Hospital use

Figure 4. Daily number of hospital beds and ICU beds occupied by COVID-19 patients as of June 21, 2021



Between June 14, 2021 and June 21, 2021:

- the number of **hospital beds** occupied by COVID-19 patients **decreased** from **981** to **696** beds.
- the number of **ICU beds** occupied by COVID-19 patients **decreased** from **563** to **471** beds.
- the number of **COVID-19 patients who were mechanically vented decreased** from **337** to **282**.

Hospitalizations and deaths to date

We have detailed case report data on 1,410,946 cases, and hospitalization status for 988,451 (70.1%) of them:

- **74,044** cases **(7.5%)** were hospitalized, of whom:
  - **13,789 (18.6%)** were admitted to the ICU
  - **1,919 (2.6%)** needed mechanical ventilation

The provinces and territories provided detailed case report forms for **26,172** deaths related to COVID-19.

Figure 5a. Age and gender [4] distribution of COVID-19 cases hospitalized in Canada as of June 25, 2021, 7 pm EST (n=73,902 [1])

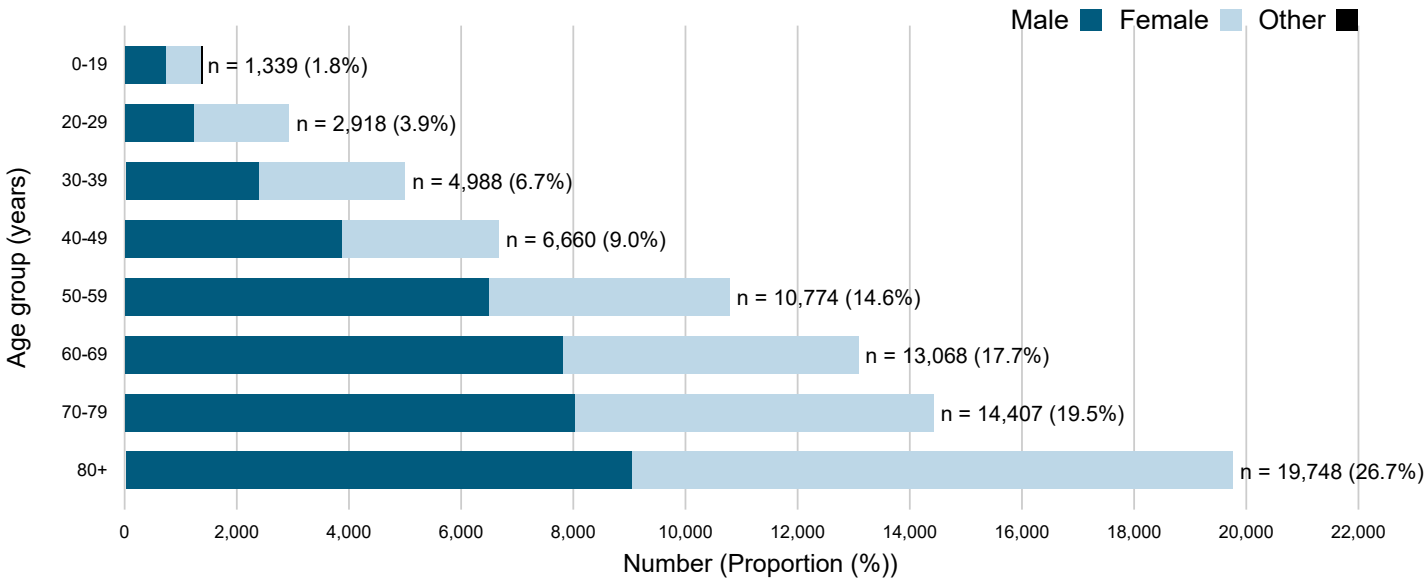


Figure 5b. Age and gender [4] distribution of COVID-19 cases admitted to ICU in Canada as of June 25, 2021, 7 pm EST (n=13,754 [1])

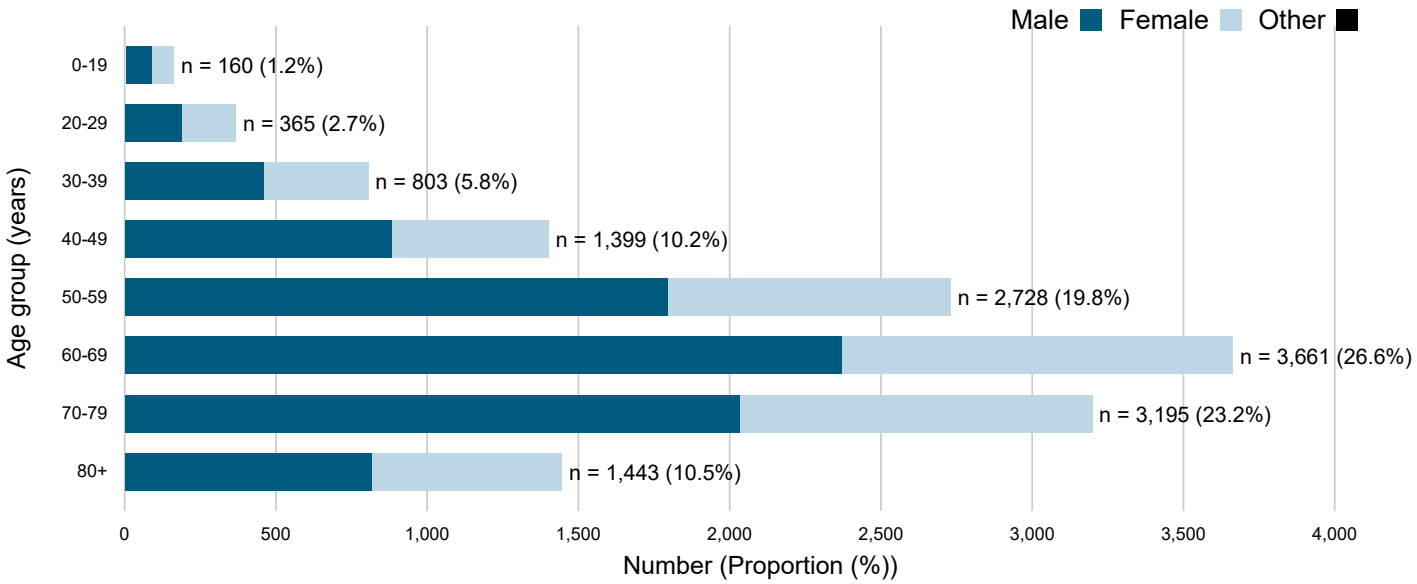
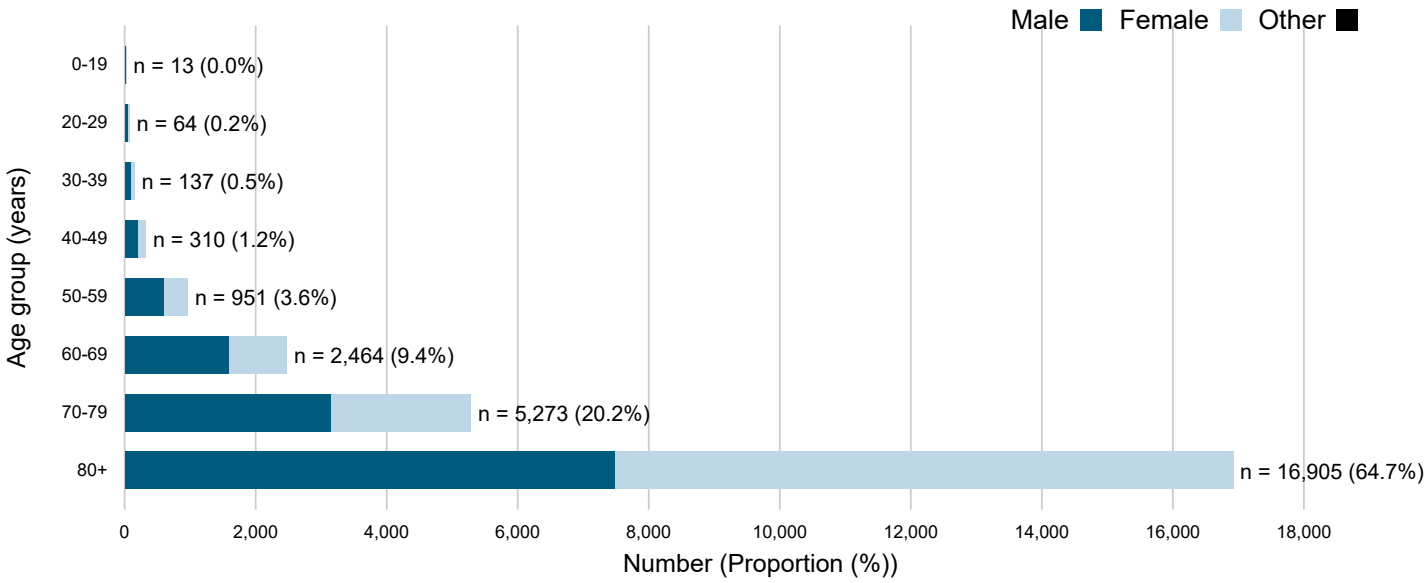


Figure 5c. Age and gender [4] distribution of COVID-19 cases deceased in Canada as of June 25, 2021, 7 pm EST (n=26,117 [1])



Data note: Figure 5 includes COVID-19 cases hospitalized, admitted to ICU, and deceased for which age and gender information were available. Therefore, some COVID-19 hospitalizations, ICU admissions, and deaths may not be included in Figure 5.

Age and gender [4] distribution of COVID-19 cases hospitalized in Canada as of June 25, 2021, 7 pm EST (n=73,902 [1])

Age group (years)	Number of cases with case reports (percentage)	Number of male cases (percentage)	Number of female cases (percentage)	Number of other cases (percentage)
0-19	1,339 (1.8%)	714 (1.0%)	624 (0.8%)	1 (0.0%)
20-29	2,918 (3.9%)	1,231 (1.7%)	1,687 (2.3%)	0 (0.0%)
30-39	4,988 (6.7%)	2,389 (3.2%)	2,599 (3.5%)	0 (0.0%)
40-49	6,660 (9.0%)	3,870 (5.2%)	2,790 (3.8%)	0 (0.0%)
50-59	10,774 (14.6%)	6,486 (8.8%)	4,288 (5.8%)	0 (0.0%)
60-69	13,068 (17.7%)	7,802 (10.6%)	5,266 (7.1%)	0 (0.0%)
70-79	14,407 (19.5%)	8,010 (10.8%)	6,397 (8.7%)	0 (0.0%)
80+	19,748 (26.7%)	9,040 (12.2%)	10,708 (14.5%)	0 (0.0%)

Age and gender [4] distribution of COVID-19 cases admitted to ICU in Canada as of June 25, 2021, 7 pm EST (n=13,754 [1])

Age group (years)	Number of cases with case reports (percentage)	Number of male cases (percentage)	Number of female cases (percentage)	Number of other cases (percentage)
0-19	160 (1.2%)	89 (0.6%)	71 (0.5%)	0 (0.0%)
20-29	365 (2.7%)	189 (1.4%)	176 (1.3%)	0 (0.0%)
30-39	803 (5.8%)	459 (3.3%)	344 (2.5%)	0 (0.0%)
40-49	1,399 (10.2%)	881 (6.4%)	518 (3.8%)	0 (0.0%)
50-59	2,728 (19.8%)	1,795 (13.1%)	933 (6.8%)	0 (0.0%)
60-69	3,661 (26.6%)	2,371 (17.2%)	1,290 (9.4%)	0 (0.0%)
70-79	3,195 (23.2%)	2,031 (14.8%)	1,164 (8.5%)	0 (0.0%)
80+	1,443 (10.5%)	817 (5.9%)	626 (4.6%)	0 (0.0%)

Age and gender [4] distribution of COVID-19 cases deceased in Canada as of June 25, 2021, 7 pm EST (n=26,117 [1])

Age group (years)	Number of cases with case reports (percentage)	Number of male cases (percentage)	Number of female cases (percentage)	Number of other cases (percentage)
0-19	13 (0.0%)	6 (0.0%)	7 (0.0%)	0 (0.0%)
20-29	64 (0.2%)	39 (0.1%)	25 (0.1%)	0 (0.0%)
30-39	137 (0.5%)	87 (0.3%)	50 (0.2%)	0 (0.0%)
40-49	310 (1.2%)	200 (0.8%)	110 (0.4%)	0 (0.0%)
50-59	951 (3.6%)	588 (2.3%)	363 (1.4%)	0 (0.0%)
60-69	2,464 (9.4%)	1,580 (6.0%)	884 (3.4%)	0 (0.0%)
70-79	5,273 (20.2%)	3,148 (12.1%)	2,125 (8.1%)	0 (0.0%)
80+	16,905 (64.7%)	7,470 (28.6%)	9,435 (36.1%)	0 (0)

Provincial, territorial and international reporting

For more information, please refer to provincial or territorial COVID-19 webpages:

- British Columbia
- Alberta
- Saskatchewan
- Manitoba
- Ontario
- Quebec
- Newfoundland and Labrador
- New Brunswick
- Nova Scotia
- Prince Edward Island
- Yukon
- Northwest Territories
- Nunavut
- World Health Organization
- Centers for Disease Control and Prevention
- European Centre for Disease Control and Prevention

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1 This figure is based on cases for which a case report form was received by the Public Health Agency of Canada from provincial or territorial partners.

2 The shaded area represents a period of time (lag time) where it is expected that cases have occurred but have not yet been reported nationally. The earliest of the following dates were used as an estimate: Onset date, Specimen Collection Date, Laboratory Testing Date, Date Reported to Province or Territory, or Date Reported to PHAC.

3 Exposure information may not be available for all cases. Some jurisdictions haven't consistently reported to PHAC how people were exposed throughout the pandemic. As a result, this may underestimate the total number of cases by different exposures, especially among returning travelers.

4 Where available, gender data was used; when gender data was unavailable, sex data was used. Reliable data on gender diverse respondents are unavailable due to small counts.

Date modified:
2021-06-29

This is **"Exhibit I"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

A Commissioner, etc.

COVID-19 Weekly Epidemiological Update

Data as received by WHO from national authorities, as of 18 April 2021, 10 am CET

In this edition:

- Global overview
- Special focus: Update on WHO COVID-19 global rapid risk assessment
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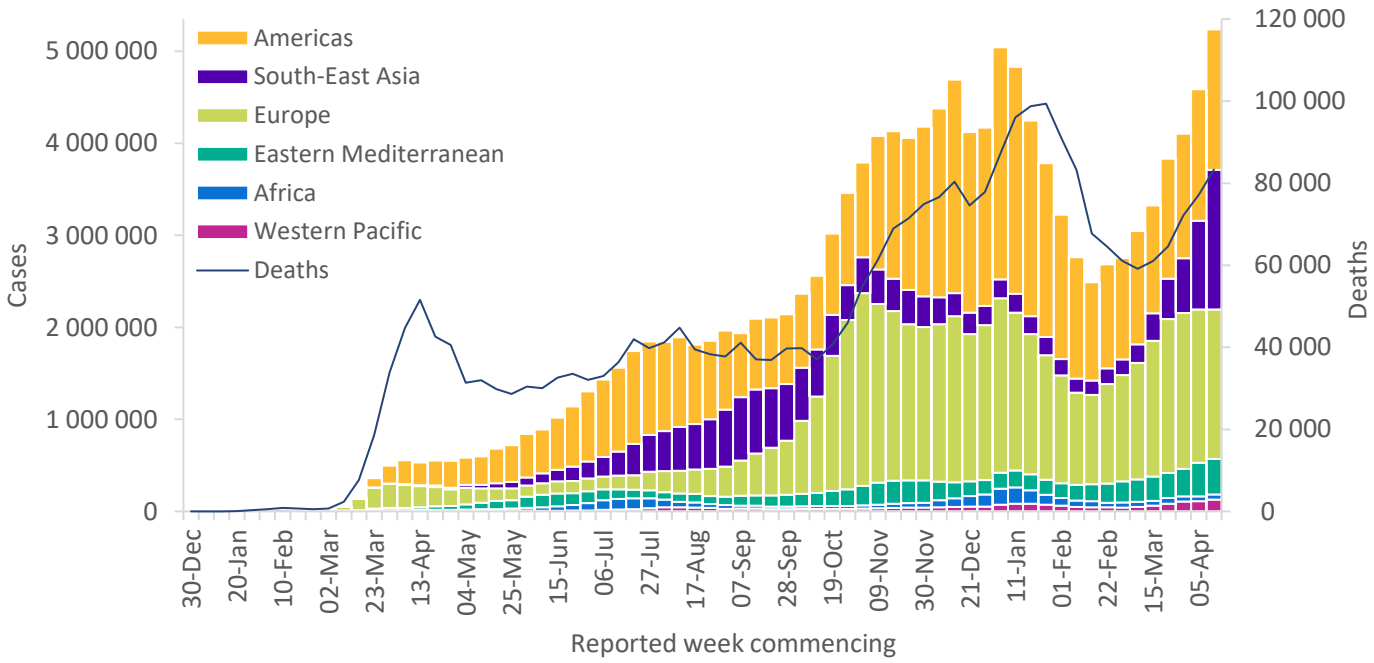
Global overview

Globally, new COVID-19 cases increased for the eighth consecutive week, with more than 5.2 million new cases reported in the last week – surpassing the previous peak in early January 2021 (Figure 1). The number of new deaths increased for the fifth consecutive week, an 8% increase as compared to the previous with over 83 000 new deaths reported. Last week the reported cumulative COVID-19 death toll surpassed 3 million lives; the pace of deaths is accelerating, it took nine months to reach 1 million deaths, another four to surpass 2 million, and just three to reach 3 million deaths.

Figure 1. COVID-19 cases reported weekly by WHO Region, and global deaths, as of 18 April 2021**



**See *Annex: Data, table and figure notes*

While all regions except the European Region reported an increase in incident cases in the last week, the largest increase continues to be reported by the South-East Asia Region, largely driven by India, followed by the Western Pacific Region (Table 1). All regions except the European and Western Pacific regions reported an increase in the number of weekly deaths, with the largest increase in the South-East Asia Region due to an

increase in deaths in India, followed by the Eastern Mediterranean Region, largely due to an increase in new deaths in the Islamic Republic of Iran.

The countries reporting the highest number of new cases represent three of the six WHO regions: India (1 429 304 new cases; 64% increase), the United States of America (477 778 new cases; 2% increase), Brazil (459 281 new cases; 1% decrease), Turkey (414 312 new cases; 17% increase), and France (233 275 new cases; 12% decrease).

Table 1. Newly reported and cumulative COVID-19 cases and deaths, by WHO Region, as of 18 April 2021**

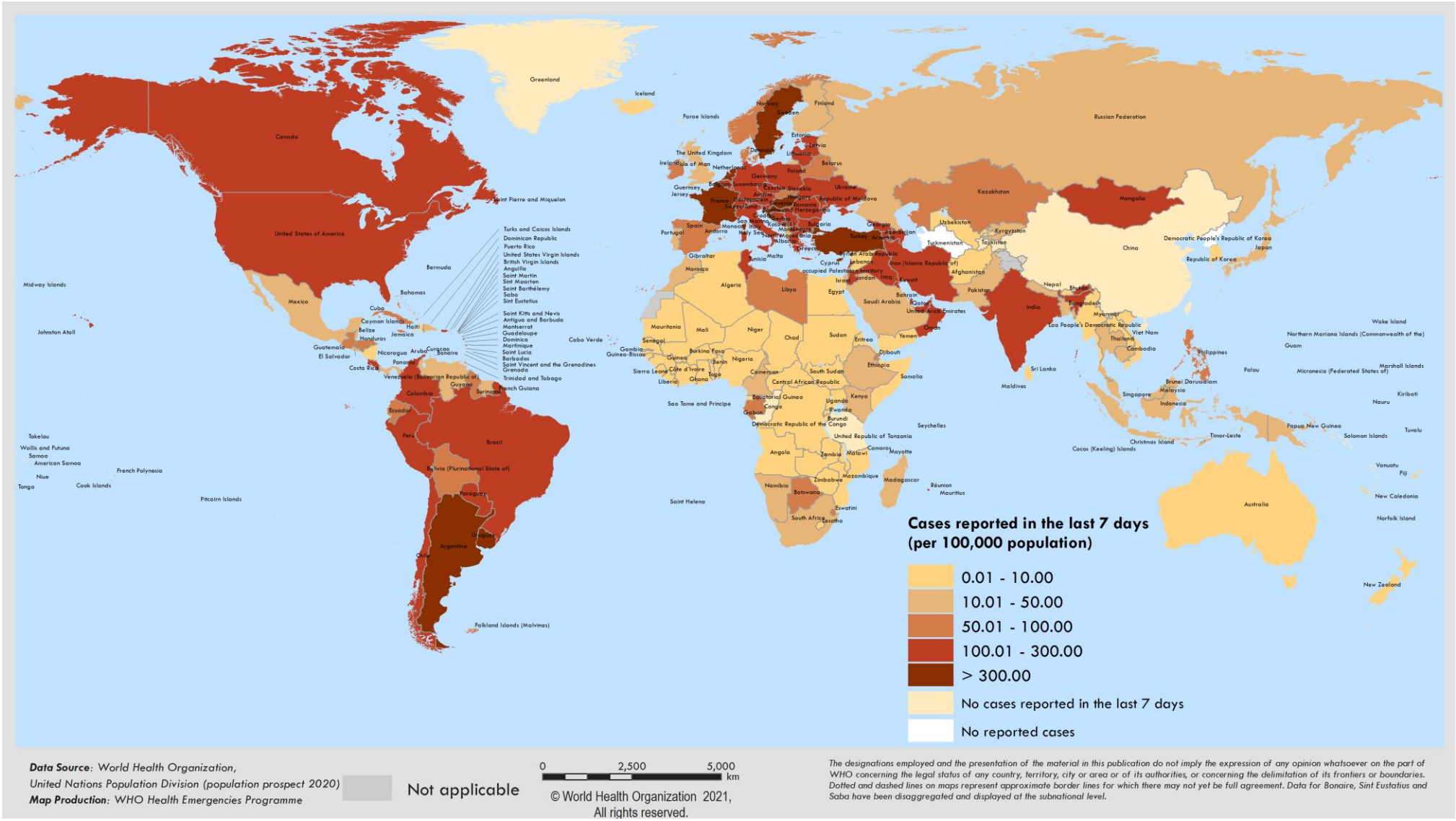
WHO Region	New cases in last 7 days (%)	Change in new cases in last 7 days *	Cumulative cases (%)	New deaths in last 7 days (%)	Change in new deaths in last 7 days *	Cumulative deaths (%)
Americas	1 525 505 (29%)	7%	59 551 000 (42%)	39 482 (47%)	8%	1 444 736 (48%)
Europe	1 624 060 (31%)	-3%	49 208 464 (35%)	26 302 (32%)	-3%	1 035 294 (34%)
South-East Asia	1 518 708 (29%)	57%	17 696 534 (13%)	9 447 (11%)	49%	237 832 (8%)
Eastern Mediterranean	386 176 (7%)	6%	8 444 694 (6%)	5 460 (7%)	23%	170 580 (6%)
Africa	54 297 (1%)	7%	3 225 261 (2%)	1 170 (1%)	14%	80 715 (3%)
Western Pacific	128 176 (2%)	15%	2 205 688 (2%)	1 444 (2%)	-8%	34 918 (1%)
Global	**5 236 922 (100%)**	**14%**	**140 332 386 (100%)**	**83 305 (100%)**	**8%**	**3 004 088 (100%)**

**Percent change in the number of newly confirmed cases/deaths in past seven days, compared to seven days prior*
**See *Annex: Data, table and figure notes*

For the latest data and other updates on COVID-19, please see:

- WHO COVID-19 Dashboard
- WHO COVID-19 Weekly Operational Update

Figure 2. COVID-19 cases per 100 000 population reported by countries, territories and areas, 12-18 April 2021**



**See *Annex: Data, table and figure notes*

Special Focus: Update on WHO COVID-19 global rapid risk assessment, 13 April 2021

As the COVID-19 pandemic, response and our understanding of the SARS-CoV-2 virus continue to evolve, WHO's most recent assessment is that the global public health risk remains very high. Under the Emergency Response Framework, WHO undertakes risk assessments and situation analyses on a regular basis to inform our response to emerging issues. In addition, WHO periodically formally reviews the current risk status of risks through an in-depth hazard, exposure and context assessment; as well as a review of the vulnerabilities and capacities to respond and to investigate the current risk to human health, risks of ongoing spread globally, and risk of insufficient control capacities. Such assessments are used as an internal-WHO decision- making tool, but they also additionally to support independent deliberations, including (but not limited to) meetings of the IHR Emergency Committee. Ten COVID-19 rapid risk assessments have been undertaken to date, and additional assessments have been completed for specific events surrounding the emergence of SARS-CoV-2 variants of concern (VOCs). Here, we provide a synopsis of the most recent in-depth global rapid risk assessment.

The COVID-19 pandemic shows no signs of easing, with global case and death incidence increasing at a concerning rate since mid-February 2021; a third of the global cumulative COVID-19 cases and deaths has been reported in the last three months alone, with weekly cases reaching similar levels as the previous peak in January 2021. Marked geographical variation in the pandemic trajectory continues to be observed at regional and country levels, with sharp rises observed in the South-East Asia, Eastern Mediterranean and Western Pacific regions in recent weeks. The global infection fatality ratio (IFR) was estimated between 0.1% to 1.0%, an increase from January largely driven by an increase in the Region of the Americas. Globally mortality rates continue to be higher for those over 40 years as well as for males as compared to females.

The resurgences in the last four months have likely been driven in part by both the emergence of SARS-CoV-2 VOCs and inconsistent use/early easing of public health and social measures (PHSM). As surveillance and sequencing activities to detect SARS-CoV-2 variant cases are strengthened, the number of countries reporting the three variants designated as global VOCs has increased. All three VOCs are associated with increased transmission. Additionally, some have been associated with increased disease severity (VOC 202012/01 and 501Y.V2), increased risk of immune escape (501Y.V2 and P.1), and/or significant reductions in neutralization (501Y.V2 and P.1) by convalescent or post-vaccine sera compared to wild-type/non-VOC variants, suggesting increased risk of vaccine failure or reinfection. In addition to the VOCs, six variants have thus far been designated as SARS-CoV-2 variants of interest (VOIs), and a further 19 variants are currently under investigation, highlighting that especially as global incidence remains high, there is continued risk of emergence of more variants with phenotypic implications and global importance in the coming months.

The high burden of COVID-19 globally has continued to challenge surveillance systems, leading to a large gap in the completeness of demographic information shared for reported cases. In line with the WHO surveillance guidelines, efforts are being made to strengthen surveillance and reporting, however, many challenges persist especially for low-income countries. The ongoing pandemic also continues to challenge public health and healthcare capacities in most countries, as often the same human resources are spread across clinical management and outbreak response activities including vaccine rollout. The recent increase in cases reported in most regions has added to the healthcare workload and aggravated shortages of resources and the capacity to care for both those with COVID-19 and patients with other illnesses; over 90% of countries have reported some level of service disruptions and almost 40% have reported disruptions to essential primary health care services.

Infection prevention and control (IPC) and PHSM have proven to be critical in mitigating and limiting transmission and deaths due to COVID-19. The use of PHSM must be continuously monitored and adjusted, especially in the context of VOCs, to account for the intensity of transmission as well as the capacity of the health system at both national and sub-national levels. While reports confirm that most people continue to support PHSM as part of national COVID-19 response strategies, pandemic fatigue is occurring, undermining the impact of PHSM on transmission. In some countries, a lack of trust in government responses and increasing

frustration and uncertainty about the duration of the pandemic, coupled with the economic impacts of the response to COVID-19, have led to protests against PHSM.

The cornerstone of treatment for COVID-19 remains early detection and clinical assessment along with the use of oxygen and systemic corticosteroid therapy for those with severe or critical COVID-19. Markets for personal protective equipment (PPE), PCR tests, and medical oxygen equipment have begun to adjust to the higher demand, and the Biomedical Consortium (part of the UN Supply Chain) continues to support the scale-up of oxygen supply in under-resourced settings, where supply chains remain vulnerable to manufacturing and transport shutdowns/restrictions. The supply chain network, however, continues to face constraints in the availability of containers and ships, adding challenges in maintaining the cold-chain requirements of COVID-19 vaccines from production to administration.

As of 12 April 2021, four vaccines have received Emergency Use Listing by WHO. A total of 781 million doses of COVID-19 vaccines have been administered in 196 economies. However, 24 economies (including 12 from the African Region and seven from the Western Pacific Region) have not yet started vaccination. The current uneven and inequitable access and distribution of COVID-19 vaccines is exacerbating global inequalities, which coupled with the emergence of VOCs, risks prolonging the pandemic.

With a COVAX target of 20-30% population coverage with a single vaccine dose by the end of the year, and considering that the proportion of the population with immunity acquired through infection is likely less than 25%, much of the global population is still susceptible to infection. Additionally, the degree and duration of immunity conferred by natural infection, COVID-19 vaccination or the combination of both are still being investigated, and some studies suggest that those who receive vaccines may still transmit SARS-CoV2 infection to susceptible contacts. While global vaccine acceptance generally remains high, country variations have been observed due to a multitude of reasons, including exposure to misinformation as well as the attitudes of local healthcare professionals, who can play an important role in building or undermining vaccine confidence.

While our understanding of the SARS-CoV-2 virus and the complex immune response triggered by it continues to grow, much still remains unknown including the effectiveness of vaccination in reducing transmission; the duration of immunity; the role of children in transmission; and the frequency and nature of post-COVID-19 condition (“long COVID”). The emergence of VOCs introduces further unknowns such as the potential for immune escape and as to how these changes in the virus affect the global epidemiology.

Additional resources

- Further information about WHO risk assessment process

Special Focus: Pandemic influenza surveillance – drawing a parallel with the COVID-19 pandemic

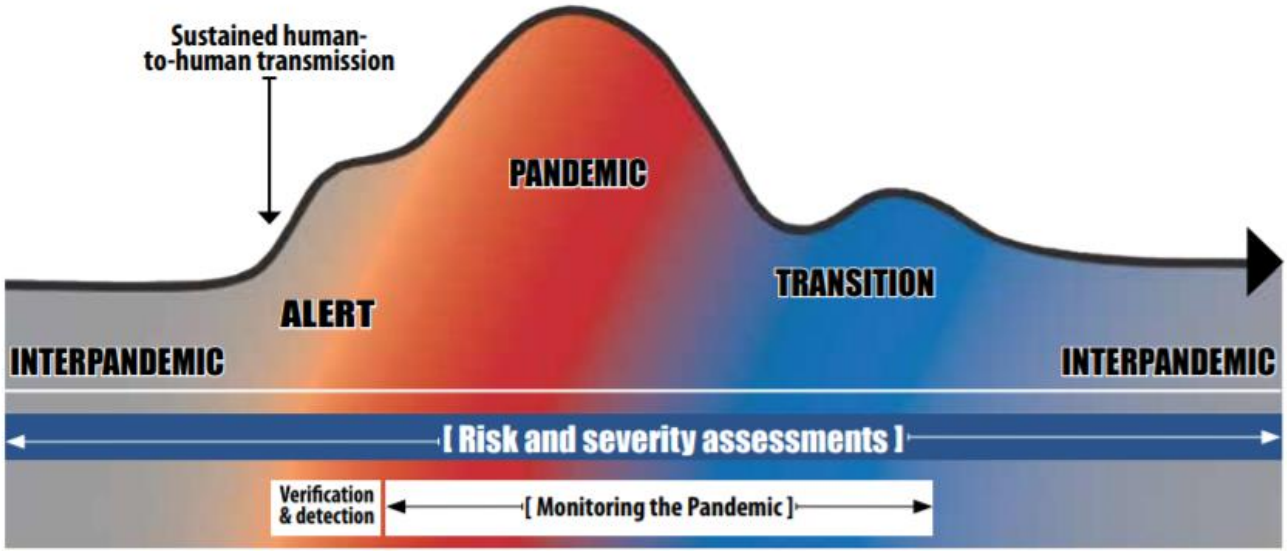
Surveillance approaches for the COVID-19 pandemic have combined the use and adaptation of existing systems as well as the establishment of new systems to meet the surveillance objectives. The Global Influenza Surveillance and Response System (GISRS) is an example of this, and has been leveraged to support the critical need to monitor trends in concurrent community circulation of both SARS-CoV-2 and seasonal influenza (see 9 March 2021 Special Focus for background information). Here, we look at parallels between surveillance approaches to influenza and the COVID-19 pandemic.

Critically, under both influenza and COVID-19 pandemic scenarios, surveillance relies upon multiple systems to:

- Verify and detect emergence and transmission,
- Monitor the geographic spread and related morbidity and mortality, and
- Assess the severity and inform development and update of vaccines and other control measures.

The WHO guidance on public health surveillance during an influenza pandemic highlight the different surveillance objectives and components needed at different phases before, during and after a pandemic (Figure 3).

Figure 3: The continuum of pandemic influenza phases (Source: WHO, 2017)



Alert Phase

In the alert phase, surveillance objectives are focused on the detection of all cases and the verification of human-to-human transmission, with an aim to interrupt virus transmission and its geographic spread and understand the virus. Event-based surveillance, active case finding and routine influenza and other respiratory virus surveillance systems (e.g., GISRS), are useful in this phase.

Event-based surveillance (EBS) is undertaken routinely by public health authorities globally to support the rapid detection and early response to signals of outbreaks of influenza and other respiratory viruses with the potential to spread from animals to humans or cause human-to-human transmission. EBS can be used for example to detect signals of clusters/outbreaks of severe respiratory disease, infections among healthcare workers, unexpected changes in routine surveillance data trends, unusually high sales of pharmaceuticals used for respiratory disease treatment, illnesses in humans linked to animal outbreaks, etc. EBS is used routinely to support COVID-19 surveillance – supporting epidemic intelligence activities for the detection and investigation of unusual epidemiological trends or changes, which combined with surveillance from other formal and informal sources, support ongoing COVID-19 situation awareness, risk assessment and an evidence-based response.

Active case finding through contact tracing and cluster/outbreak investigation are recommended for interrupting SARS-CoV-2 transmission and are similarly recommended for finding new suspected cases, documenting potential human-to-human transmission, and providing targeted interventions to decrease the risk of illness and interrupt further transmission of pandemic influenza viruses.

Pandemic Phase

Once it is clear community transmission is occurring, monitoring the situation remains critical to inform risk assessments and adjust public health interventions. During this phase, it is important to understand the virus evolution and its geographic spread, severity of disease and groups at high risk for severe disease. Surveillance activities would focus on obtaining high quality data and favour specificity over sensitivity (i.e., would not necessarily attempt to identify all cases). Wherever possible, the use and strengthening of existing surveillance systems should be favoured. Often different systems capture information for mild illness, severe illness requiring hospitalization, and mortality, which collectively provide a foundation for surveillance during the pandemic phase.

A healthcare-based surveillance approach serves as the primary approach for year-round influenza surveillance and is considered an essential surveillance approach for COVID-19 as well. During periods of heightened surveillance, other community-based case investigation and surveillance activities serve to provide additional epidemiological information.

- *Sentinel surveillance*: Existing influenza surveillance systems that use a sentinel approach emphasize collecting quality data for epidemiological and virological surveillance from a limited number of surveillance sites. Sentinel healthcare facilities are chosen based on representativeness, feasibility, and sustainability**.** The use of strict case definitions and testing all or a subset of cases is for surveillance purposes and not for case management or outbreak investigation. During a pandemic, ongoing sentinel surveillance aids in tracking trends; geographical spread; impact of response measures; transmission and virus characteristics, including the evolution and emergence of variants; and vaccine effectiveness. A sentinel approach to monitoring COVID-19 is recommended as a complementary approach to comprehensive surveillance at present and many countries use existing sentinel influenza surveillance systems to monitor trends in COVID-19 activity and virus characteristics.
- *Non-sentinel surveillance:* Influenza virological surveillance also relies on non-sentinel surveillance, where specimens may be collected from non-sentinel sites and where the results are more often used for clinical management and diagnostics. Compared to sentinel surveillance, information coming from non-sentinel surveillance is often not as detailed, and the cases selected for testing may not meet standard case definitions.
- *Universal surveillance*: Many countries perform universal surveillance for influenza and other respiratory pathogens, often relying on electronic health record data to collect information on all patients seeking care for an influenza-like illnesses (ILI) or severe acute respiratory illness (SARI), or individuals with a suspected or confirmed laboratory diagnosis of a notifiable respiratory pathogen (including influenza or COVID-19), to either supplement or replace sentinel surveillance. Currently COVID-19 surveillance aims to capture data from any and all COVID-19 cases, no matter where they are diagnosed.
- *Mortality surveillance:* Many countries monitor influenza-related mortality through surveillance of influenza-related deaths (using death certificates) or through statistical analysis of excess mortality attributed to influenza. The regular counting of COVID-19 deaths on a daily or weekly basis is currently recommended as part of COVID-19 surveillance mortality monitoring, including through death certificates. While not commonly done during influenza epidemics, more frequent collection and reporting of influenza-related deaths may be warranted during the pandemic phase.

- *Other sources:*
    - It is estimated that around half of individuals infected with influenza do not seek healthcare for their illness.[1] Participatory surveillance for ILI involves the ongoing collection of self-reporting of symptoms from a voluntary cohort of participants who may not seek healthcare for their illness and complements data from healthcare-based surveillance systems. Some countries are also adapting current participatory surveillance systems or developing new ones for monitoring COVID-19.
    - Special studies and modelling can generate information on transmission dynamics, risk and severity during a pandemic. Work done since the 2009 influenza pandemic as part of pandemic influenza preparedness activities have informed the COVID 19 response.
    - Sero-epidemiological and transmission study protocols developed for use in a future influenza pandemic were immediately updated for use in the COVID-19 pandemic.

Reporting of data to WHO

Current public health guidance recommends SARS-CoV-2 infections to be nationally notifiable, with case-based reporting on a voluntary basis, and detailed aggregated data reporting requested on a weekly basis to WHO.

During further influenza pandemics, similar reporting requirements may be recommended initially. As the pandemic continues, countries would shift towards monitoring the situation, and the consistent and timely reporting of routine aggregated influenza data to regional and global WHO platforms may shift to weekly reporting of routine influenza surveillance data. It remains critical to draw lessons and sustain the momentum of the COVID-19 response to further strengthen and standardize both local and global surveillance systems to enable a robust approach to future pandemics caused by influenza and other pathogens.

Additional resources

- Global epidemiological surveillance standards for influenza
- Manual for the laboratory diagnosis and virological surveillance of influenza
- WHO Guidance for Surveillance during an Influenza Pandemic
- Protocol to investigate non-seasonal influenza and other emerging acute respiratory diseases

[1] Ma W, et al. (2018) The healthcare seeking rate of individuals with influenza like illness: a meta-analysis, Infectious Diseases, 50:10, 728-735, https://doi.org/10.1080/23744235.2018.1472805

Special Focus: Update on SARS-CoV-2 Variants

WHO, in collaboration with national authorities, institutions and researchers, routinely assesses if variants of SARS-CoV-2 result in changes in transmissibility, clinical presentation and severity, or if they impact public health and social measures (PHSM). Systems have been established to detect "signals" of potential variants of concern (VOCs) or variants of interest (VOIs) and assess these based on the risk posed to global public health (see also working definitions). National authorities may choose to designate other variants of local interest/concern. Detailed information on currently circulating VOCs and VOIs is available in previously published editions of the Weekly Epidemiological Update. Here we provide a brief update on the geographical distribution of the three VOCs as of 20 April 2021, as well as an update on detected VOIs (Table 2).

As surveillance activities to detect SARS-CoV-2 variants are strengthened at local and national levels, including by strategic genomic sequencing, the number of countries/areas/territories (hereafter countries) reporting VOCs and VOIs has continued to increase. Since our last update on 13 April, VOC 202012/01 has been detected in five additional countries, variant 501Y.V2 in five additional countries, and variant P.1 has been reported in two additional countries. As of 20 April, a total 137 countries have reported VOC 202012/01 (Figure 4), 85 countries variant 501Y.V2 (Figure 5), and 52 countries variant P.1 (Figure 6) – see also Annex 2. The information presented here should be interpreted with due consideration of surveillance limitations, including differences in sequencing capacities and prioritization of samples for sequencing between countries.

Table 2: SARS-CoV-2 variants of concern (VOC) and variants of interest (VOI), as of 20 April 2021*

	Nextstrain clade	Pango lineage	GISAID clade	Alternate names	First detected in	Earliest samples	Characteristic mutations
VOC	20I/501Y.V1	B.1.1.7	GR	**VOC 202012/01**[†]	United Kingdom	Sep 2020	H69/V70 del, Y144 del, N501Y, A570D, P681H, S106/G107/F108 del
	20H/**501Y.V2**[†]	B.1.351	GH	VOC 202012/02	South Africa	Aug 2020	L242/A243/L244 del, K417N, E484K, N501Y, S106/G107/F108 del
	20J/501Y.V3	B.1.1.28.1, alias **P.1**[†]	GR	VOC 202101/02	Brazil and Japan	Dec 2020	K417T, E484K, N501Y, S106/G107/F108 del
VOI	20C	B.1.525	G/484K.V3	-	United Kingdom and Nigeria	Dec 2020	H69-V70 del, Y144 del, Q52R, E484K, Q677H, D614G, and F888L
	20C/S.452R	B.1.427/ B.1.429	GH/452R.V1	CAL.20C/L452R	United States of America	Jun 2020	L452R, W152C, S13I, D614G
	20B/S.484K	B.1.1.28.2, alias P.2	GR	-	Brazil	Apr 2020	L18F, T20N, P26S, F157L, E484K, D614G, S929I, V1176F
	Not yet assigned	B.1.1.28.3, alias P.3	Not yet assigned	PHL-B.1.1.28	Philippines and Japan	Feb 2021	141-143 del, E484K, N501Y, P681H
	20C	B.1.526 with E484K or S477N	GH	-	United States of America	Nov 2020	L5F, T95I, D253G, D614G, A701V, E484K or S477N
	20C	B.1.616	GH	-	France	Jan 2021	G142 del, D66H, Y144V, D215G, V483A, D614G, H655Y, G669S, Q949R, N1187D

[†]*While work is ongoing to establish standardized nomenclature for key variants, these are the names by which WHO will refer to them in this publication.*

Figure 4. Countries, territories and areas reporting SARS-CoV-2 VOC 202012/01, as of 20 April 2021

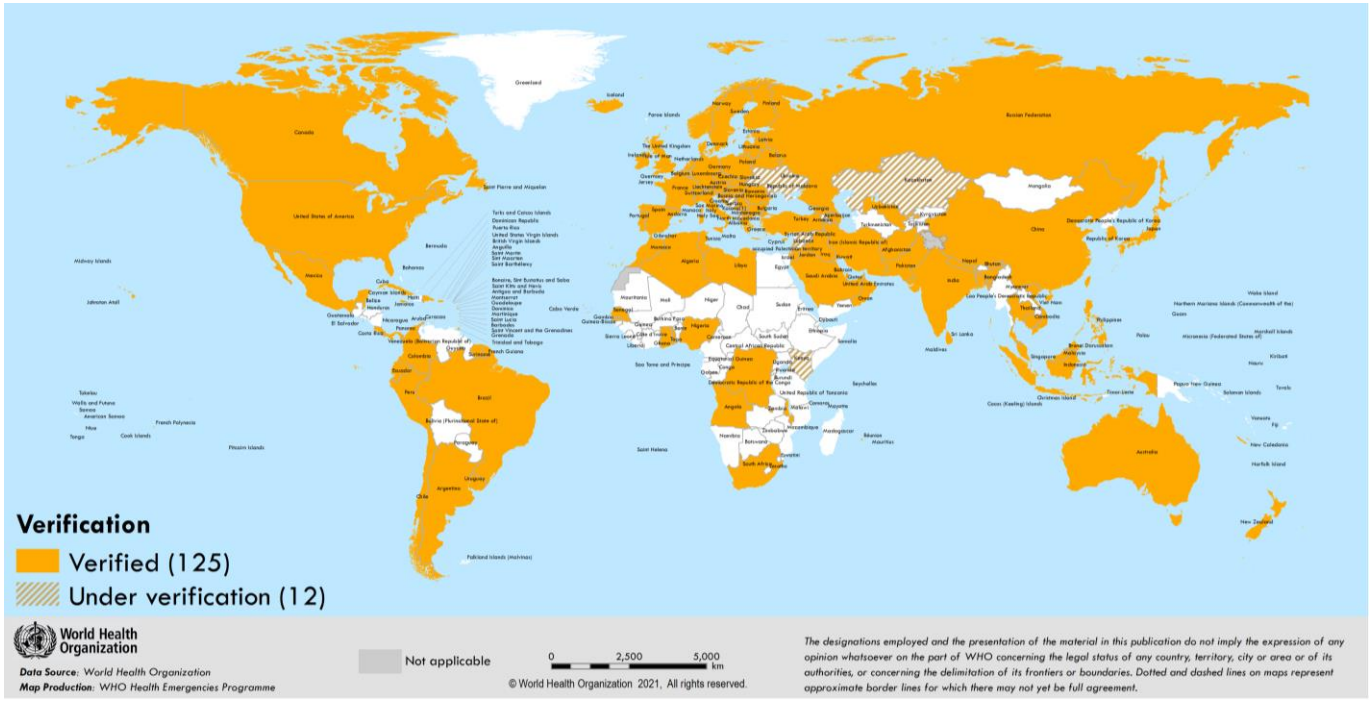


Figure 5. Countries, territories and areas reporting SARS-CoV-2 variant 501Y.V2, as of 20 April 2021

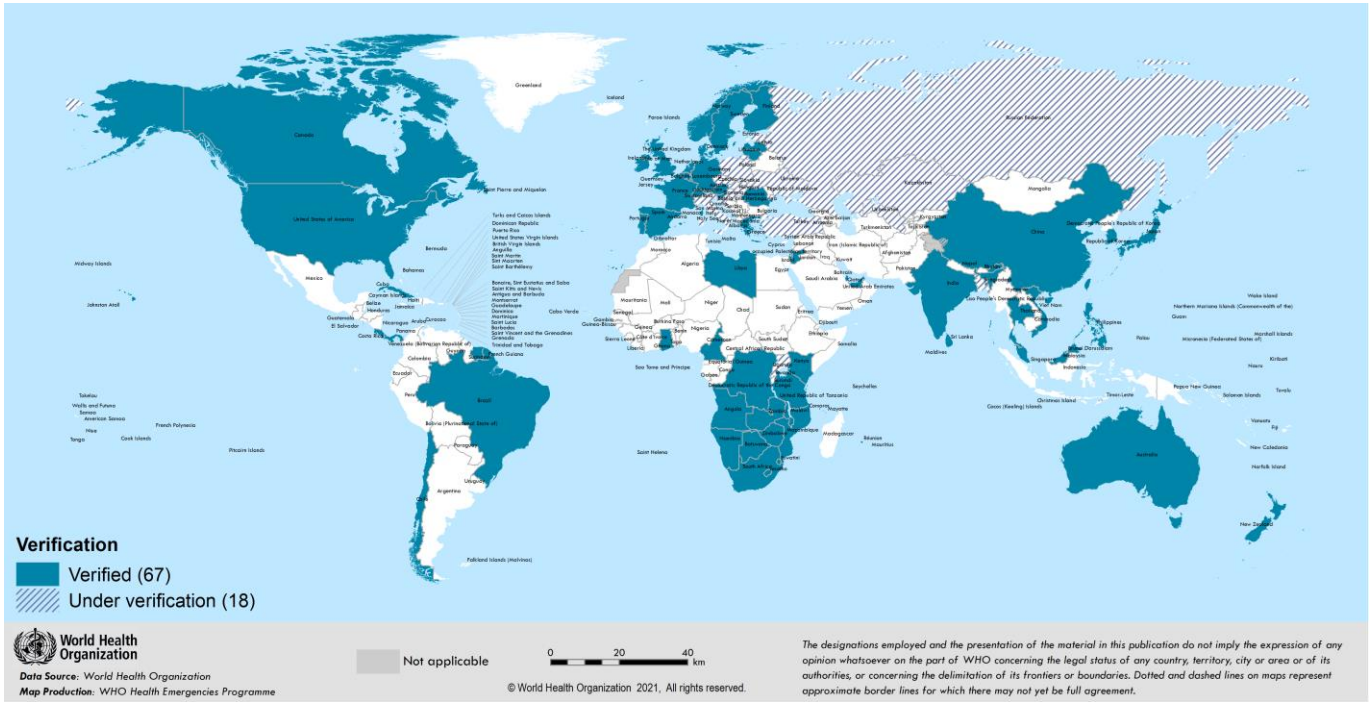
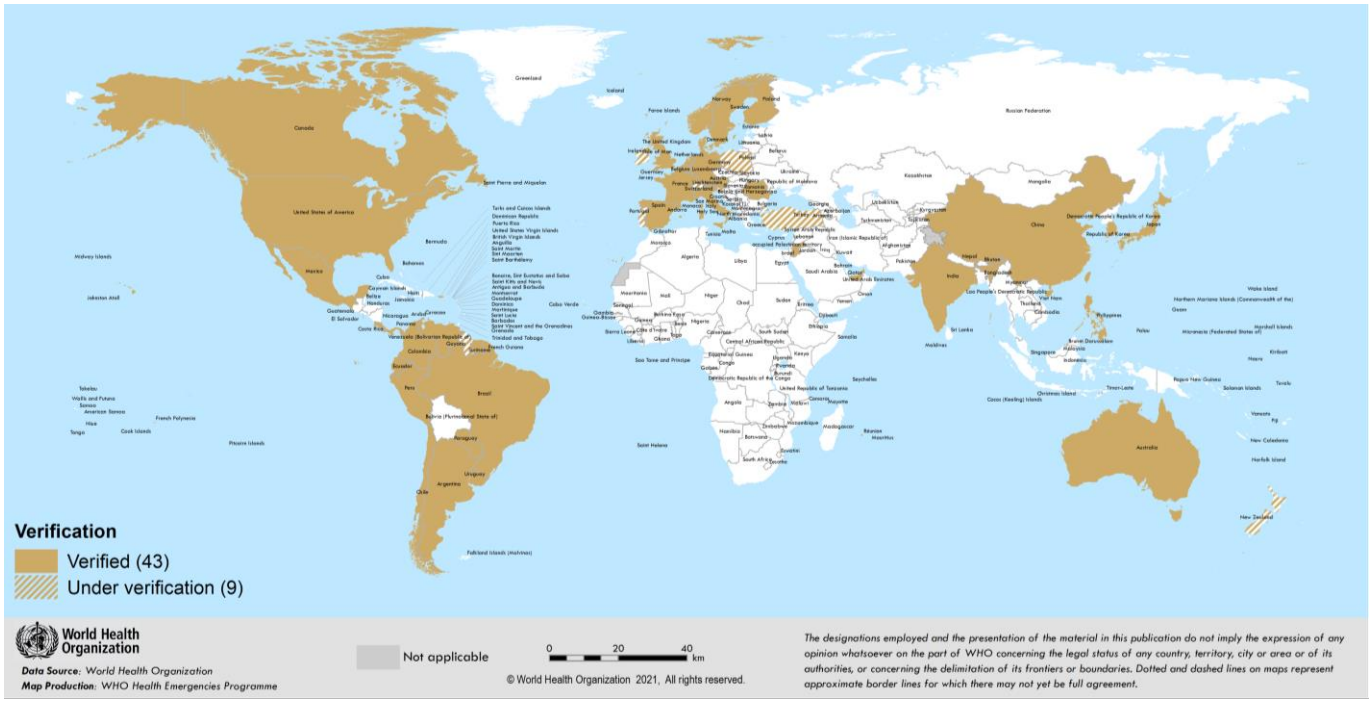


Figure 6. Countries, territories and areas reporting SARS-CoV-2 variant P.1, as of 20 April 2021



WHO recommendations

The chances of SARS-CoV-2 mutating increases with its frequency of human and animal infections. Hence, reducing transmission of SARS-CoV-2 through established disease control methods as well as avoiding introductions into animal populations are crucial aspects of the global strategy to reduce the occurrence of mutations that have negative public health implications. PHSM remain critical to curb the spread of SARS-CoV-2 and its variants. Evidence from multiple countries with extensive transmission of VOCs has indicated that the implementation of PHSM and infection prevention and control (IPC) measures in health facilities has been effective in reducing COVID-19 case incidence, which has led to a reduction in hospitalizations and deaths among COVID-19 patients. National and local authorities are encouraged to continue strengthening existing PHSM, IPC and disease control activities. Authorities are also encouraged to strengthen surveillance and sequencing capacities and apply a systematic approach to provide a representative indication of the extent of transmission of SARS-CoV-2 variants based on the local context, and the detection of unusual events.

Additional resources

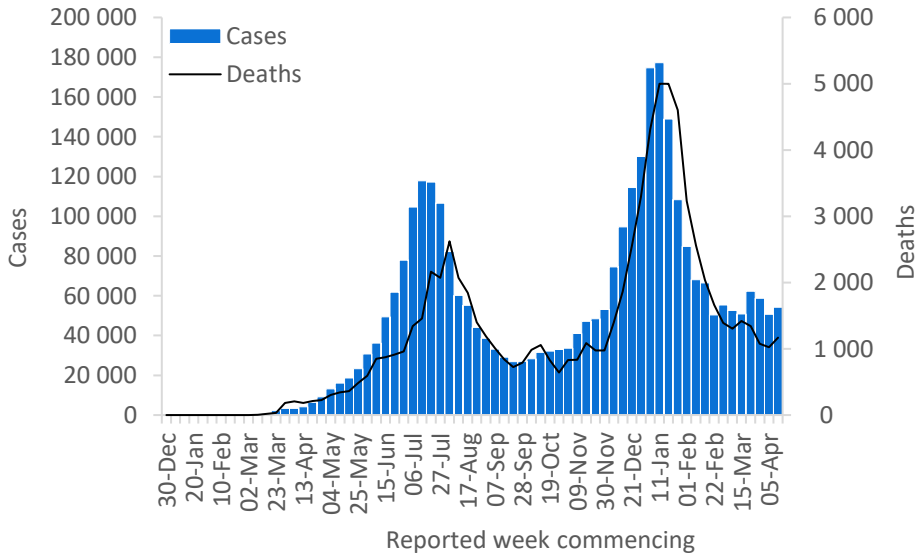
- Proposed working definitions of SARS-CoV-2 Variants of Interest and Variants of Concern
- COVID-19 new variants: Knowledge gaps and research
- PAHO Epidemiological Update: Variants of SARS-CoV-2 in the Americas - 24 March 2021
- PAHO COVID-19 Situation Reports
- WPRO COVID-19 Situation Reports
- SEARO COVID-19 Situation Reports
- EMRO COVID-19 Situation Reports
- Joint ECDC-WHO/EURO weekly surveillance report
- Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health
- Considerations for implementing and adjusting PHSM in the context of COVID-19
- Disease Outbreak News on SARS-CoV-2 Variants, 31 December 2020

WHO regional overviews

African Region

The Africa Region reported over 54 000 new cases and over 1100 new deaths, a 7% and a 14% increase respectively compared to the previous week. The number of weekly cases continues to fluctuate over the last eight weeks, with no clear trend, while weekly deaths increased last week reflecting a large increase in deaths reported by South Africa. The highest numbers of new cases were reported from Ethiopia (12 981 new cases; 11.3 new cases per 100 000 population; a 7% decrease), South Africa (8153 new cases; 13.7 new cases per 100 000; a 35% increase), and Kenya (6103 new cases; 11.3 new cases per 100 000; a 14% decrease).

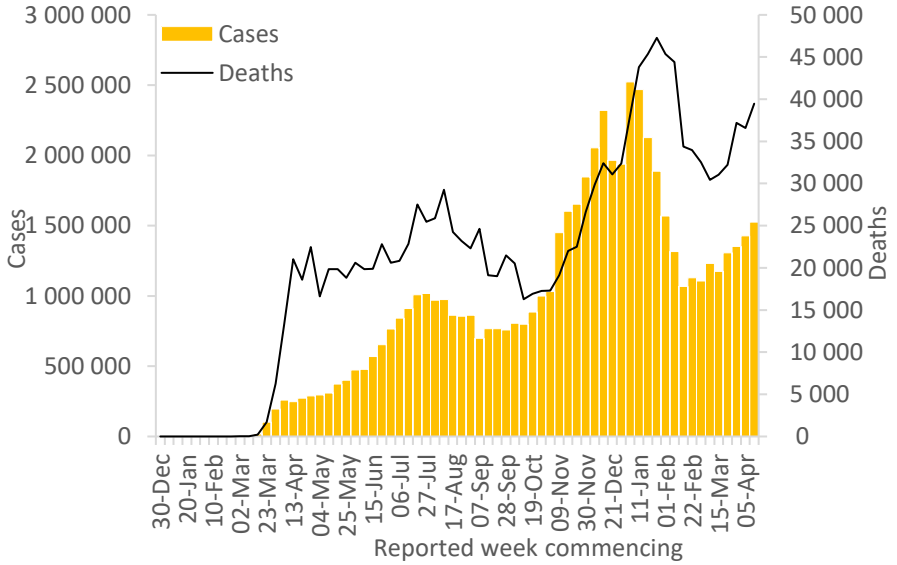
The highest numbers of new deaths were reported from South Africa (455 new deaths; 0.8 new deaths per 100 000 population; a 51% increase), Ethiopia (182 new deaths; 0.2 new deaths per 100 000; a 13% decrease), and Kenya (133 new deaths; 0.2 new deaths per 100 000; a 7% increase).



Region of the Americas

The Region of the Americas reported over 1.5 million new cases and over 39 000 new deaths, a 7% and an 8% increase respectively compared to the previous week. The region has reported an overall increasing trend in new cases for the last eight weeks and new deaths for the last five weeks. The highest numbers of new cases were reported from the United States of America (477 778 new cases; 144.3 new cases per 100 000; a 2% increase), Brazil (459 281 new cases; 216.1 new cases per 100 000; a 1% decrease), and Argentina (160 747 new cases; 355.7 new cases per 100 000; a 29% increase).

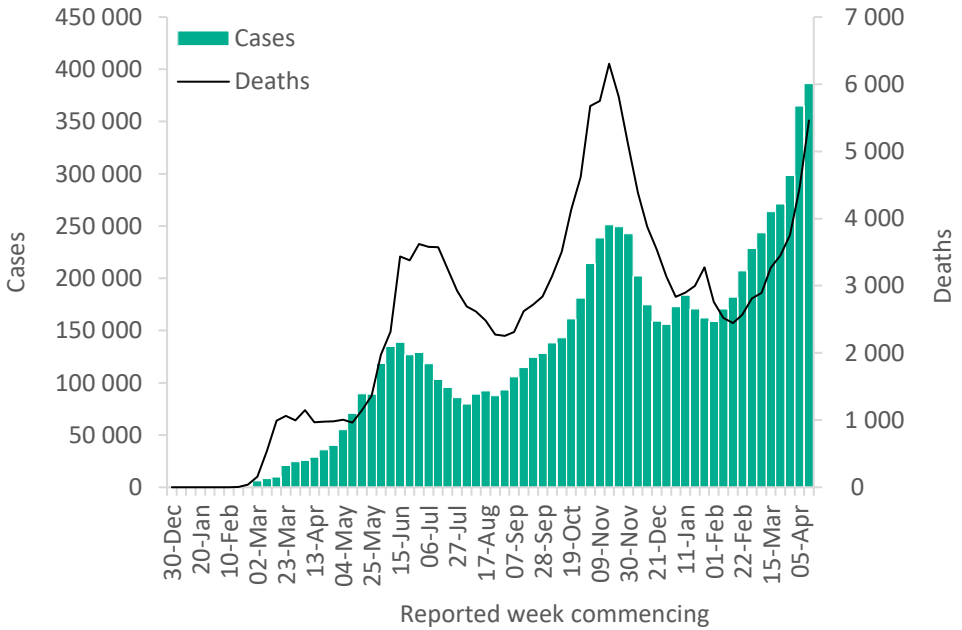
The highest numbers of new deaths were reported from Brazil (20 031 new deaths; 9.4 new deaths per 100 000; a 2% decrease), the United States of America (5146 new deaths; 1.6 new deaths per 100 000; a 1% decrease), and Mexico (4673 new deaths; 3.6 new deaths per 100 000; a 48% increase).



Eastern Mediterranean Region

The Eastern Mediterranean Region reported over 386 000 new cases and over 5400 new deaths, a 6% and a 23% increase respectively compared to the previous week. The upward trend in cases and deaths reported since February 2021 continues, with a sharper increase in new deaths the last two weeks. The highest numbers of new cases were reported from the Islamic Republic of Iran (166 367 new cases; 198.1 new cases per 100 000; a 29% increase), Iraq (52 832 new cases; 131.3 new cases per 100 000; a 6% increase), and Pakistan (34 190 new cases; 15.5 new cases per 100 000; a 3% increase).

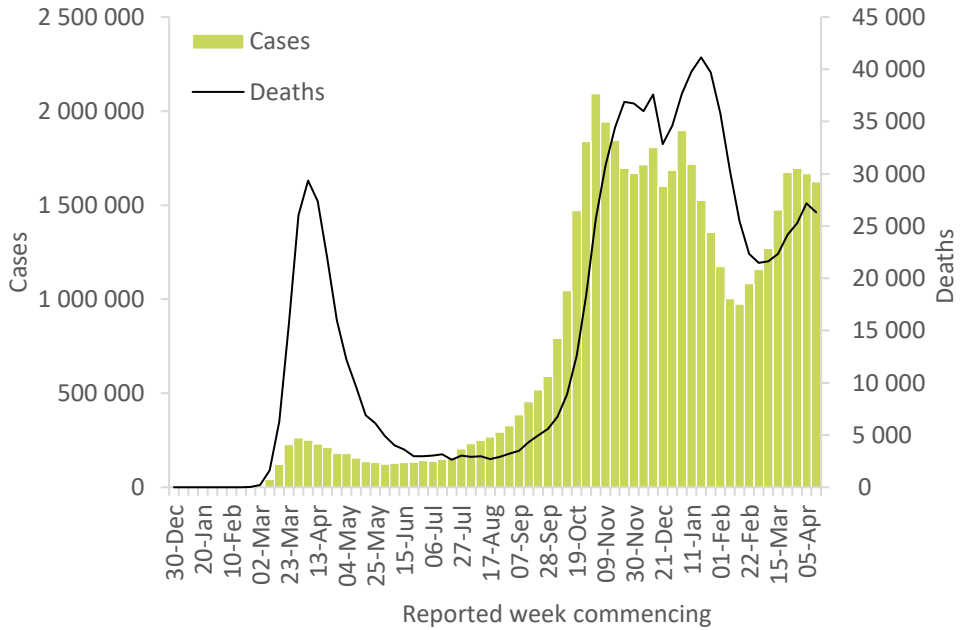
The highest numbers of new deaths were reported from the Islamic Republic of Iran (2095 new deaths; 2.5 new deaths per 100 000; a 70% increase), Pakistan (765 new deaths; 0.3 new deaths per 100 000; a 21% increase), and Tunisia (482 new deaths; 4.1 new deaths per 100 000; a 59% increase).



European Region

The European Region reported over 1.6 million new cases and over 26 000 new deaths. The region reported a slight decrease in new cases (3%) for the second week in a row, a sign that transmission in the region may be slowing as the number of new deaths also decreased (3%) for the first time following a five-week increasing trend. The highest numbers of new cases were reported from Turkey (414 312 new cases; 491.2 new cases per 100 000; a 17% increase), France (233 275 new cases; 358.7 new cases per 100 000; a 12% decrease), and Germany (143 994 new cases; 173.1 new cases per 100 000; a 28% increase).

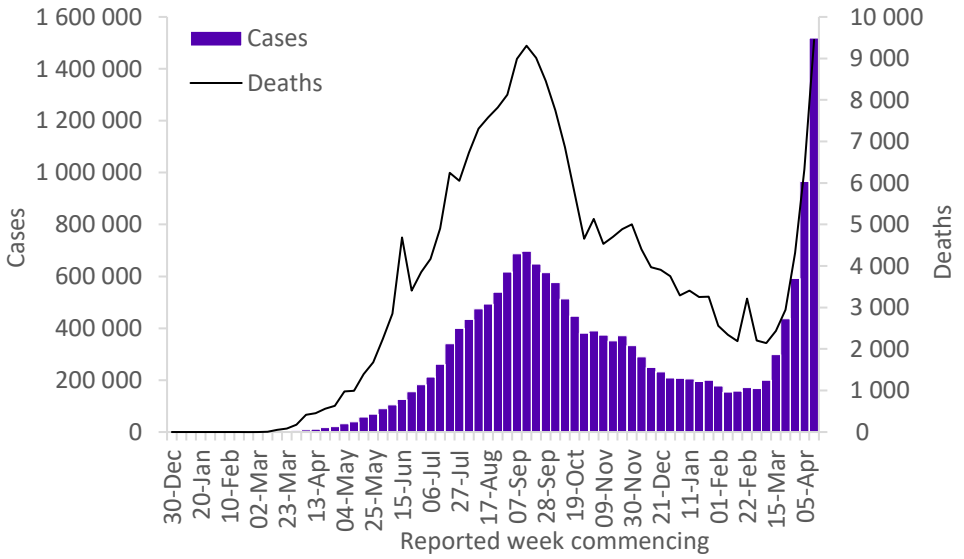
The highest numbers of new deaths were reported from Poland (3611 new deaths; 9.5 new deaths per 100 000; a 4% increase), Ukraine (2772 new deaths; 6.3 new deaths per 100 000; a 3% increase), and Italy (2753 new deaths; 4.6 new deaths per 100 000; a 14% decrease).



South-East Asia Region

The South-East Asia Region reported over 1.5 million new cases and over 9400 new deaths, a 57% and a 49% increase respectively compared to the previous week. The increasing trend in new cases and deaths, which appears to be accelerating, continued last week, with weekly cases rising sharply for the sixth consecutive week while weekly deaths rose for the fifth consecutive week. The trend in the region continues to be driven largely by the trajectory of the outbreak in India which reported the highest numbers of new cases (1 429 304 new cases; 103.6 new cases per 100 000; a 64% increase), followed by Indonesia (36 895 new cases; 13.5 new cases per 100 000; a 4% increase), and Bangladesh (36 315 new cases; 22.1 new cases per 100 000; a 25% decrease).

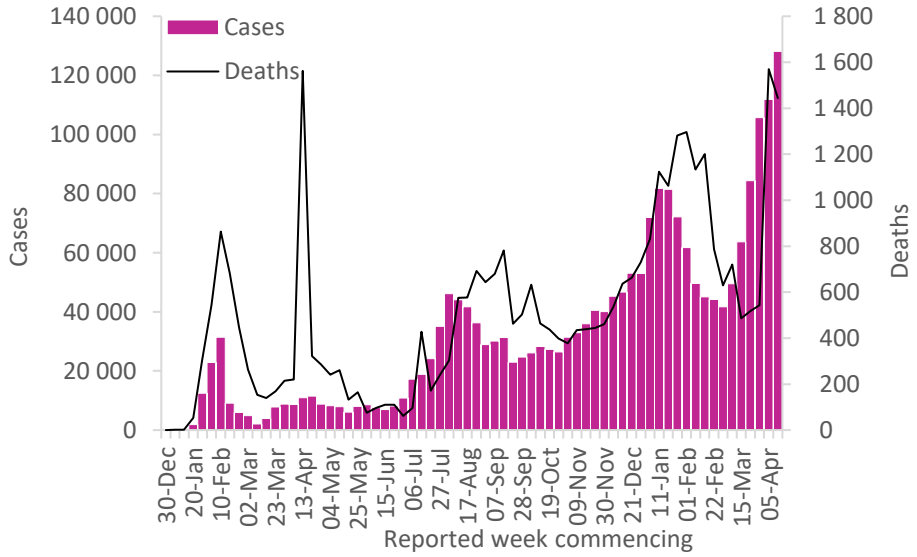
The highest numbers of new deaths were reported from India (7875 new deaths; 0.6 new deaths per 100 000; a 69% increase), Indonesia (885 new deaths; 0.3 new deaths per 100 000; a 26% decrease), and Bangladesh (622 new deaths; 0.4 new deaths per 100 000; a 39% increase).



Western Pacific Region

The Western Pacific Region reported over 128 000 new cases and over 1400 new deaths, a 15% increase and an 8% decrease respectively compared to the previous week. Cases increased for the sixth consecutive week, while deaths decreased after rising for three weeks, continuing to largely reflect the trajectory of deaths reported by the Philippines, the most affected country in the region. The highest numbers of new cases were reported from the Philippines (72 848 new cases; 66.5 new cases per 100 000; a 5% increase), Japan (26 426 new cases; 20.9 new cases per 100 000; a 29% increase), and Malaysia (13 742 new cases; 42.5 new cases per 100 000; a 45% increase).

The highest numbers of new deaths were reported from the Philippines (1066 new deaths; 1.0 new deaths per 100 000; a 19% decrease), Japan (240 new deaths; 0.2 new deaths per 100 000; a 49% increase), and Malaysia (49 new deaths; 0.2 new deaths per 100 000; a 40% increase).



Key weekly updates

WHO Director-General's key message

Opening remarks at the media briefing on COVID-19 – 19 April 2021:

- More than 3 million deaths have been reported to WHO. It took 9 months to reach 1 million deaths; 4 months to reach 2 million, and 3 months to reach 3 million. Big numbers can make us numb, but each one of these deaths is a tragedy for families, communities and nations.
- Greta Thunberg has become the powerful voice of a younger generation demanding climate action. Greta announced a donation of 100 000 Euros from the Greta Thunberg Foundation in support of COVAX to provide vaccines to people in need.
- WHO has partnered with an alliance of the six largest youth development organizations in the world to form the Global Youth Mobilization, to empower young people to respond to the challenges created by the pandemic in their local communities.

Updates and publications

- Statement on the seventh meeting of the International Health Regulations (2005) Emergency Committee regarding the coronavirus disease (COVID-19) pandemic
- Global Advisory Committee on Vaccine Safety (GACVS) review of latest evidence of rare adverse blood coagulation events with AstraZeneca COVID-19 Vaccine (Vaxzevria and Covishield)
- Pfizer BioNTech COVID-19 vaccine: What you need to know
- COVID-19 News updates: Latest news from WHO on COVID-19 and other breaking health stories

Technical guidance and other resources

- Technical guidance
- WHO Coronavirus Disease (COVID-19) Dashboard
- Weekly COVID-19 Operational Updates
- WHO COVID-19 case definitions
- COVID-19 Supply Chain Inter-Agency Coordination Cell Weekly Situational Update
- Research and Development
- Online courses on COVID-19 in official UN languages and in additional national languages
- The Strategic Preparedness and Response Plan (SPRP) outlining the support the international community can provide to all countries to prepare and respond to the virus
- Updates from WHO regions:
  - African Region
  - Region of the Americas
  - Eastern Mediterranean Region
  - South-East Asia Region
  - European Region
  - Western Pacific Region
- Recommendations and advice for the public:
  - Protect yourself
  - Questions and answers
  - Travel advice
- EPI-WIN: tailored information for individuals, organizations and communities
- WHO Academy COVID-19 mobile learning app

Annex

Annex 1. COVID-19 confirmed cases and deaths reported in the last seven days by countries, territories and areas, and WHO Region, as of 18 April 2021**

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Africa	**54 297**	**3 225 261**	**287.5**	**1 170**	**80 715**	**7.2**	
Ethiopia	12 981	240 236	209.0	182	3 328	2.9	Community transmission
South Africa	8 153	1 565 680	2 639.9	455	53 711	90.6	Community transmission
Kenya	6 103	151 287	281.4	133	2 463	4.6	Community transmission
Cameroon	4 394	61 731	232.5	68	919	3.5	Community transmission
Madagascar	4 069	31 617	114.2	45	538	1.9	Community transmission
Botswana	1 401	44 075	1 874.2	35	671	28.5	Community transmission
Cabo Verde	1 346	19 975	3 592.7	12	189	34.0	Community transmission
Mali	1 275	12 980	64.1	24	429	2.1	Community transmission
Gabon	1 222	21 858	982.1	6	133	6.0	Community transmission
Namibia	1 192	46 515	1 830.6	38	602	23.7	Community transmission
Algeria	1 108	119 486	272.5	26	3 152	7.2	Community transmission
Eswatini	1 042	18 415	1 587.3	2	671	57.8	Community transmission
Angola	969	24 300	73.9	11	561	1.7	Community transmission
Zambia	926	90 844	494.1	8	1 234	6.7	Community transmission
Guinea	653	21 460	163.4	5	138	1.1	Community transmission
Mozambique	556	69 134	221.2	9	798	2.6	Community transmission
Togo	549	12 496	150.9	3	119	1.4	Community transmission
Rwanda	523	23 866	184.3	8	322	2.5	Community transmission
Burundi	458	3 612	30.4	0	6	0.1	Community transmission
Nigeria	411	164 147	79.6	1	2 061	1.0	Community transmission
Ghana	403	91 663	295.0	17	771	2.5	Community transmission
Zimbabwe	396	37 669	253.4	14	1 552	10.4	Community transmission
Côte d'Ivoire	374	45 519	172.6	13	274	1.0	Community transmission
Senegal	367	39 731	237.3	13	1 090	6.5	Community transmission

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Democratic Republic of the Congo	352	28 894	32.3	0	745	0.8	Community transmission
Seychelles	344	4 834	4 915.2	1	25	25.4	Community transmission
Central African Republic	322	5 787	119.8	1	75	1.6	Community transmission
Uganda	227	41 340	90.4	1	338	0.7	Community transmission
Burkina Faso	158	13 114	62.7	2	154	0.7	Community transmission
Gambia	131	5 733	237.2	2	170	7.0	Community transmission
Malawi	129	33 934	177.4	11	1 138	5.9	Community transmission
Mauritania	116	18 121	389.7	2	452	9.7	Community transmission
Benin	96	7 611	62.8	3	96	0.8	Community transmission
South Sudan	92	10 432	93.2	0	114	1.0	Community transmission
Mauritius	91	1 203	94.6	3	15	1.2	Clusters of cases
Chad	75	4 691	28.6	1	168	1.0	Community transmission
Eritrea	44	3 491	98.4	0	10	0.3	Community transmission
Niger	42	5 114	21.1	2	190	0.8	Community transmission
Equatorial Guinea	40	7 259	517.4	0	106	7.6	Community transmission
Guinea-Bissau	32	3 710	188.5	0	66	3.4	Community transmission
Sierra Leone	27	4 020	50.4	0	79	1.0	Community transmission
Comoros	26	3 815	438.7	0	146	16.8	Community transmission
Sao Tome and Principe	12	2 275	1 038.1	0	35	16.0	Community transmission
Liberia	5	2 071	40.9	0	85	1.7	Community transmission
Lesotho	2	10 709	499.9	0	315	14.7	Community transmission
Congo	0	10 084	182.7	0	137	2.5	Community transmission
United Republic of Tanzania	0	509	0.9	0	21	0.0	Pending
Territories[iii]							
Réunion	917	18 425	2 057.9	12	135	15.1	Community transmission
Mayotte	146	19 789	7 253.6	1	168	61.6	Community transmission
Americas	**1 525 505**	**59 551 000**	**5 822.5**	**39 482**	**1 444 736**	**141.3**	
United States of America	477 778	31 250 635	9 441.2	5 146	560 858	169.4	Community transmission

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Brazil	459 281	13 832 455	6 507.6	20 031	368 749	173.5	Community transmission
Argentina	160 747	2 658 628	5 882.5	1 734	59 084	130.7	Community transmission
Colombia	115 216	2 619 422	5 147.9	2 281	67 564	132.8	Community transmission
Canada	60 784	1 106 062	2 930.6	290	23 541	62.4	Community transmission
Peru	60 532	1 689 051	5 122.7	2 169	56 454	171.2	Community transmission
Chile	48 826	1 117 348	5 845.0	842	25 055	131.1	Community transmission
Mexico	27 875	2 299 939	1 783.8	4 673	211 693	164.2	Community transmission
Uruguay	21 623	159 569	4 593.6	425	1 788	51.5	Community transmission
Paraguay	14 664	246 806	3 460.3	479	5 177	72.6	Community transmission
Ecuador	13 280	358 157	2 030.0	366	17 641	100.0	Community transmission
Guatemala	9 667	212 307	1 185.0	189	7 190	40.1	Community transmission
Venezuela (Bolivarian Republic of)	8 148	180 609	635.1	131	1 870	6.6	Community transmission
Cuba	6 902	92 474	816.4	59	512	4.5	Community transmission
Bolivia (Plurinational State of)	6 711	287 360	2 461.7	197	12 625	108.2	Community transmission
Costa Rica	6 033	228 577	4 487.1	53	3 071	60.3	Community transmission
Honduras	5 134	199 682	2 016.1	168	4 934	49.8	Community transmission
Dominican Republic	3 441	260 627	2 402.6	29	3 414	31.5	Community transmission
Panama	2 151	360 249	8 349.2	29	6 185	143.3	Community transmission
El Salvador	1 913	67 404	1 039.2	24	2 072	31.9	Community transmission
Jamaica	1 565	43 684	1 475.2	52	721	24.3	Community transmission
Guyana	684	11 642	1 480.1	15	267	33.9	Clusters of cases
Trinidad and Tobago	419	8 742	624.7	5	150	10.7	Community transmission
Bahamas	279	9 696	2 465.6	5	194	49.3	Clusters of cases
Suriname	231	9 496	1 618.7	9	187	31.9	Clusters of cases
Haiti	78	12 918	113.3	0	251	2.2	Community transmission
Saint Lucia	69	4 398	2 395.1	1	65	35.4	Community transmission
Barbados	65	3 773	1 312.9	0	44	15.3	Community transmission
Belize	51	12 538	3 153.2	0	318	80.0	Community transmission

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Nicaragua	41	5 407	81.6	1	180	2.7	Community transmission
Antigua and Barbuda	31	1 213	1 238.7	1	31	31.7	Clusters of cases
Saint Vincent and the Grenadines	29	1 819	1 639.6	0	10	9.0	Community transmission
Dominica	7	172	238.9	0	0	0.0	Clusters of cases
Grenada	2	159	141.3	0	1	0.9	Sporadic cases
Saint Kitts and Nevis	0	44	82.7	0	0	0.0	Sporadic cases
Territories[iii]							
Puerto Rico	7 371	120 571	4 214.5	42	2 194	76.7	Community transmission
Curaçao	1 042	11 674	7 114.3	20	80	48.8	Community transmission
Martinique	871	9 758	2 600.3	7	66	17.6	Community transmission
Guadeloupe	623	12 927	3 230.7	5	194	48.5	Community transmission
French Guiana	532	18 081	6 053.6	1	95	31.8	Community transmission
Aruba	323	10 219	9 571.4	0	92	86.2	Community transmission
Bermuda	287	2 060	3 308.0	3	17	27.3	Community transmission
United States Virgin Islands	57	3 028	2 899.7	0	26	24.9	Community transmission
Bonaire	36	1 511	7 224.5	0	14	66.9	Community transmission
Sint Maarten	28	2 202	5 135.0	0	27	63.0	Community transmission
Saint Barthélemy	26	954	9 651.0	0	1	10.1	Clusters of cases
Turks and Caicos Islands	25	2 369	6 118.6	0	17	43.9	Clusters of cases
British Virgin Islands	9	187	618.4	0	1	3.3	Clusters of cases
Cayman Islands	9	525	798.8	0	2	3.0	Sporadic cases
Saint Martin	7	1 710	4 423.3	0	13	33.6	Community transmission
Falkland Islands (Malvinas)	2	62	1 780.1	0	0	0.0	Sporadic cases
Anguilla	0	29	193.3	0	0	0.0	Sporadic cases
Montserrat	0	20	400.1	0	1	20.0	No cases
Saba	0	6	310.4	0	0	0.0	No cases
Saint Pierre and Miquelon	0	25	431.4	0	0	0.0	Sporadic cases
Sint Eustatius	0	20	637.1	0	0	0.0	No cases

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Eastern Mediterranean	**386 176**	**8 444 694**	**1 155.5**	**5 460**	**170 580**	**23.3**	
Iran (Islamic Republic of)	166 367	2 215 445	2 637.7	2 095	66 327	79.0	Community transmission
Iraq	52 832	970 987	2 414.0	270	14 948	37.2	Community transmission
Pakistan	34 190	750 158	339.6	765	16 094	7.3	Community transmission
Jordan	21 071	683 466	6 698.6	470	8 178	80.2	Community transmission
Lebanon	13 870	508 503	7 450.1	256	6 886	100.9	Community transmission
Tunisia	13 679	283 976	2 402.8	482	9 717	82.2	Community transmission
United Arab Emirates	13 287	495 224	5 007.1	21	1 550	15.7	Clusters of cases
Kuwait	10 156	255 860	5 991.2	37	1 440	33.7	Community transmission
Oman	8 663	176 668	3 459.6	74	1 821	35.7	Community transmission
Bahrain	7 711	163 113	9 586.0	34	588	34.6	Community transmission
Qatar	6 693	195 757	6 794.6	45	376	13.1	Community transmission
Saudi Arabia	6 418	404 054	1 160.6	63	6 810	19.6	Community transmission
Egypt	5 807	215 484	210.6	289	12 694	12.4	Community transmission
Libya	4 243	171 131	2 490.5	75	2 882	41.9	Community transmission
Morocco	3 759	505 447	1 369.4	53	8 944	24.2	Community transmission
Syrian Arab Republic	886	21 004	120.0	69	1 437	8.2	Community transmission
Djibouti	690	10 412	1 053.8	21	114	11.5	Community transmission
Afghanistan	633	57 793	148.5	18	2 539	6.5	Community transmission
Somalia	566	12 837	80.8	51	656	4.1	Community transmission
Yemen	494	5 774	19.4	88	1 120	3.8	Community transmission
Sudan	221	33 022	75.3	35	2 208	5.0	Clusters of cases
Territories[iii]							
occupied Palestinian territory	13 940	308 579	6 048.9	149	3 251	63.7	Community transmission
Europe	**1 624 060**	**49 208 464**	**5 273.8**	**26 302**	**1 035 294**	**111.0**	
Kosovo[1]	3 686	101 110		85	2 051		Community transmission
Turkey	414 312	4 212 645	4 994.9	1 906	35 608	42.2	Community transmission
France	233 275	5 178 513	7 962.1	1 965	99 921	153.6	Community transmission

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Germany	143 994	3 142 262	3 778.3	1 561	79 914	96.1	Community transmission
Poland	113 394	2 688 025	7 081.6	3 611	62 032	163.4	Community transmission
Italy	103 366	3 857 443	6 467.7	2 753	116 676	195.6	Clusters of cases
Ukraine	93 261	1 946 510	4 450.8	2 772	39 786	91.0	Community transmission
Russian Federation	60 711	4 702 101	3 222.1	2 596	105 582	72.3	Clusters of cases
Netherlands	52 986	1 395 233	8 015.1	152	16 904	97.1	Community transmission
Sweden	35 133	900 138	8 715.9	28	13 788	133.5	Community transmission
Spain	31 084	3 396 685	7 176.2	176	76 882	162.4	Community transmission
Hungary	30 344	750 508	7 682.1	1 767	25 184	257.8	Community transmission
Romania	24 174	1 027 039	5 313.5	1 066	26 072	134.9	Community transmission
Belgium	23 034	949 994	8 244.7	252	23 741	206.0	Community transmission
Serbia	20 823	660 299	9 532.7	254	5 954	86.0	Community transmission
Czechia	20 158	1 600 347	14 965.0	618	28 426	265.8	Community transmission
Greece	19 681	313 444	2 924.3	564	9 397	87.7	Community transmission
Kazakhstan	18 391	341 599	1 819.3	194	4 157	22.1	Clusters of cases
The United Kingdom	17 893	4 385 942	6 460.7	180	127 260	187.5	Community transmission
Austria	16 296	588 101	6 607.1	223	9 616	108.0	Community transmission
Croatia	15 274	307 790	7 584.5	254	6 562	161.7	Community transmission
Azerbaijan	14 943	298 522	2 944.2	228	4 107	40.5	Clusters of cases
Bulgaria	14 432	385 963	5 552.2	787	15 138	217.8	Clusters of cases
Switzerland	9 883	629 507	7 273.7	20	9 815	113.4	Community transmission
Belarus	8 060	342 923	3 629.1	69	2 413	25.5	Community transmission
Lithuania	7 458	233 631	8 361.6	73	3 760	134.6	Community transmission
Bosnia and Herzegovina	7 171	190 296	5 800.3	479	7 837	238.9	Community transmission
Georgia	6 962	295 358	7 404.0	62	3 939	98.7	Community transmission
Armenia	5 703	208 520	7 036.9	143	3 878	130.9	Community transmission
Slovenia	5 645	231 599	11 050.3	26	4 460	212.8	Clusters of cases
North Macedonia	5 576	146 733	7 043.0	237	4 419	212.1	Community transmission

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Slovakia	4 912	375 974	6 888.7	541	11 106	203.5	Clusters of cases
Denmark	4 630	241 731	4 151.5	13	2 452	42.1	Community transmission
Republic of Moldova	4 608	245 494	6 085.7	179	5 548	137.5	Community transmission
Cyprus	4 372	55 407	6 239.5	16	288	32.4	Clusters of cases
Norway	4 264	106 223	1 979.0	24	708	13.2	Community transmission
Latvia	3 757	110 997	5 818.4	62	2 048	107.4	Community transmission
Portugal	3 632	830 560	8 066.9	32	16 942	164.6	Clusters of cases
Estonia	3 380	117 554	8 845.5	72	1 092	82.2	Clusters of cases
Ireland	2 595	243 238	4 899.6	52	4 835	97.4	Community transmission
Finland	1 926	83 633	1 513.6	19	887	16.1	Community transmission
Uzbekistan	1 758	86 680	259.0	3	637	1.9	Clusters of cases
Kyrgyzstan	1 656	91 883	1 408.3	27	1 549	23.7	Clusters of cases
Albania	1 301	129 456	4 498.4	30	2 340	81.3	Clusters of cases
Montenegro	1 130	95 548	15 213.1	61	1 434	228.3	Clusters of cases
Israel	1 113	836 926	9 669.3	42	6 334	73.2	Community transmission
Luxembourg	1 096	64 746	10 341.0	17	785	125.4	Community transmission
Malta	379	29 927	5 816.0	7	409	79.5	Clusters of cases
Andorra	274	12 771	16 528.8	3	123	159.2	Community transmission
San Marino	54	5 010	14 762.2	1	86	253.4	Community transmission
Liechtenstein	51	2 892	7 463.8	0	54	139.4	Sporadic cases
Iceland	28	6 286	1 726.3	0	29	8.0	Community transmission
Monaco	22	2 395	6 102.8	0	31	79.0	Sporadic cases
Holy See	0	26	3 213.8	0	0	0.0	Sporadic cases
Tajikistan	0	13 714	143.8	0	91	1.0	Pending
Territories[iii]							
Gibraltar	14	4 291	12 736.3	0	94	279.0	Clusters of cases
Jersey	2	3 232	2 998.3	0	69	64.0	Community transmission
Faroe Islands	1	662	1 354.8	0	1	2.0	Sporadic cases

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Guernsey	1	822	1 275.1	0	14	21.7	Community transmission
Isle of Man	1	1 575	1 852.2	0	29	34.1	No cases
Greenland	0	31	54.6	0	0	0.0	No cases
South-East Asia	**1 518 708**	**17 696 534**	**875.5**	**9 447**	**237 832**	**11.8**	
India	1 429 304	14 788 109	1 071.6	7 875	177 150	12.8	Clusters of cases
Indonesia	36 895	1 599 763	584.9	885	43 328	15.8	Community transmission
Bangladesh	36 315	715 252	434.3	622	10 283	6.2	Community transmission
Thailand	9 727	42 352	60.7	4	101	0.1	Clusters of cases
Nepal	3 933	283 658	973.5	36	3 075	10.6	Clusters of cases
Sri Lanka	1 591	96 439	450.4	22	617	2.9	Clusters of cases
Maldives	621	26 145	4 836.8	2	69	12.8	Clusters of cases
Timor-Leste	228	1 236	93.7	1	2	0.2	Clusters of cases
Myanmar	52	142 628	262.1	0	3 206	5.9	Clusters of cases
Bhutan	42	952	123.4	0	1	0.1	Sporadic cases
Western Pacific	**128 176**	**2 205 688**	**112.3**	**1 444**	**34 918**	**1.8**	
Philippines	72 848	926 035	845.1	1 066	15 810	14.4	Community transmission
Japan	26 426	529 829	418.9	240	9 622	7.6	Clusters of cases
Malaysia	13 742	372 859	1 152.0	49	1 370	4.2	Community transmission
Mongolia	6 472	20 655	630.1	21	41	1.3	Clusters of cases
Republic of Korea	4 560	114 114	222.6	29	1 797	3.5	Clusters of cases
Cambodia	2 151	6 389	38.2	14	43	0.3	Sporadic cases
Papua New Guinea	1 296	9 738	108.8	21	89	1.0	Community transmission
China	190	103 273	7.0	3	4 856	0.3	Clusters of cases
Singapore	175	60 808	1 039.4	0	30	0.5	Sporadic cases
Australia	109	29 505	115.7	1	910	3.6	Clusters of cases
Viet Nam	89	2 781	2.9	0	35	0.0	Clusters of cases
New Zealand	20	2 238	46.4	0	26	0.5	Clusters of cases
Lao People's Democratic Republic	9	58	0.8	0	0	0.0	Sporadic cases

Reporting Country/Territory/Area[i]	New cases in last 7 days	Cumulative cases	Cumulative cases per 100 thousand population	New deaths in last 7 days	Cumulative deaths	Cumulative deaths per 100 thousand population	Transmission classification[ii]
Fiji	4	72	8.0	0	2	0.2	Sporadic cases
Brunei Darussalam	2	221	50.5	0	3	0.7	Sporadic cases
Solomon Islands	0	20	2.9	0	0	0.0	No cases
Territories[iii]							
French Polynesia	44	18 696	6 655.6	0	141	50.2	Sporadic cases
Guam	29	7 654	4 535.0	0	136	80.6	Clusters of cases
Wallis and Futuna	6	447	3 974.7	0	5	44.5	Sporadic cases
New Caledonia	2	123	43.1	0	0	0.0	Sporadic cases
Northern Mariana Islands (Commonwealth of the)	2	162	281.5	0	2	3.5	Pending
Marshall Islands	0	4	6.8	0	0	0.0	No cases
Samoa	0	4	2.0	0	0	0.0	No cases
Vanuatu	0	3	1.0	0	0	0.0	No cases
Global	**5 236 922**	**140 332 386**		**83 305**	**3 004 088**		

*See *Annex: Data, table and figure notes*

Annex 2. List of countries/territories/areas reporting variants of concern as of 20 April 2021**

Country/Territory/Area	VOC 202012/01 (B.1.1.7)	501Y.v2 (B.1.351)	P.1 (B.1.1.28)
Afghanistan	Verified*		
Albania	Not Verified		
Algeria	Verified		
Angola	Verified	Verified	
Argentina	Verified		Verified
Armenia	Not Verified*		
Aruba	Verified	Verified	Verified
Australia	Verified	Verified	Verified
Austria	Verified	Verified	Verified
Azerbaijan	Verified		
Bahrain	Verified		
Bangladesh	Verified	Not Verified	
Barbados	Verified		
Belarus	Verified		
Belgium	Verified	Verified	Verified
Belize	Verified		
Bonaire	Verified		
Bosnia and Herzegovina	Not Verified		
Botswana		Verified	
Brazil	Verified	Verified	Verified
Brunei Darussalam	Verified	Verified	
Bulgaria	Verified		
Cabo Verde	Verified		
Cambodia	Verified		
Cameroon		Verified	
Canada	Verified	Verified	Verified
Cayman Islands	Verified		
Chile	Verified	Verified*	Verified
China	Verified	Verified	Verified
Colombia	Verified*		Verified
Comoros		Verified	
Costa Rica	Verified	Verified	Verified
Croatia	Verified	Not Verified	
Cuba	Verified	Verified	
Curaçao	Verified		
Cyprus	Verified		
Czechia	Verified	Not Verified	
Democratic Republic of the Congo	Verified	Verified	
Denmark	Verified	Verified	Verified
Dominican Republic	Verified		
Ecuador	Verified		Verified*
Estonia	Verified	Not Verified	
Eswatini		Verified	
Faroe Islands			Verified
Finland	Verified	Verified	Verified
France	Verified	Verified	Verified
French Guiana	Verified	Verified*	Verified
French Polynesia	Verified		Verified
Gambia	Verified		
Georgia	Verified		
Germany	Verified	Verified	Verified
Ghana	Verified	Verified	
Gibraltar	Not Verified		
Greece	Verified	Verified	
Grenada	Verified		
Guadeloupe[†]	Verified		

Country/Territory/Area	VOC 202012/01 (B.1.1.7)	501Y.v2 (B.1.351)	P.1 (B.1.1.28)
Guyana			Not Verified
Hungary	Verified	Not Verified	
Iceland	Verified		
India	Verified	Verified	Verified
Indonesia	Verified		
Iran (Islamic Republic of)	Verified		
Iraq	Verified		
Ireland	Verified	Verified	Not Verified
Israel	Verified	Verified	
Italy	Verified	Not Verified	Verified
Jamaica	Verified		
Japan	Verified	Verified	Verified
Jordan	Verified	Verified*	Verified*
Kazakhstan	Not Verified	Not Verified	
Kenya	Not Verified	Verified	
Kosovo[1]	Verified		
Kuwait	Verified		
Latvia	Verified	Verified	
Lebanon	Verified		
Lesotho		Verified	
Libya	Verified	Verified	
Liechtenstein	Verified		
Lithuania	Verified	Verified	
Luxembourg	Verified	Verified	Not Verified
Malawi	Verified	Verified	
Malaysia	Verified	Verified	
Malta	Verified	Not Verified	
Martinique†	Verified		

Country/Territory/Area	VOC 202012/01 (B.1.1.7)	501Y.v2 (B.1.351)	P.1 (B.1.1.28)
Mauritius	Not Verified		
Mayotte	Verified	Verified	
Mexico	Verified		Verified
Monaco	Verified	Not Verified	
Montenegro	Verified		
Morocco	Verified		
Mozambique		Verified	
Namibia		Verified	
Nepal	Verified		
Netherlands	Verified	Verified	Verified
New Caledonia	Verified		
New Zealand	Verified	Verified	Not Verified
Nigeria	Verified		
North Macedonia	Verified		
Norway	Verified	Verified	Verified
occupied Palestinian territory	Verified	Verified	
Oman	Verified		
Pakistan	Verified		
Panama	Verified*	Verified	Verified
Paraguay			Verified
Peru	Verified		Verified
Philippines	Verified	Verified	Verified
Poland	Verified	Not Verified	Not Verified
Portugal	Verified	Verified	Not Verified
Puerto Rico	Verified		Verified
Qatar	Verified	Verified	
Republic of Korea	Verified	Verified	Verified

Country/Territory/Area	VOC 202012/01 (B.1.1.7)	501Y.v2 (B.1.351)	P.1 (B.1.1.28)
Republic of Moldova	Not Verified		
Réunion	Verified	Verified	Verified
Romania	Verified	Verified	Verified
Russian Federation	Verified	Not Verified	
Rwanda	Not Verified	Not Verified	
Saint Barthélemy	Verified		
Saint Lucia	Verified		
Saint Martin	Verified	Verified	Verified
Saudi Arabia	Verified		
Senegal	Verified		
Serbia	Verified		
Singapore	Verified	Not Verified	
Sint Maarten	Verified		
Slovakia	Verified	Not Verified	
Slovenia	Verified	Verified	Not Verified
South Africa	Verified	Verified	
Spain	Verified	Verified	Verified
Sri Lanka	Verified	Verified	
Suriname	Verified	Verified	Verified
Sweden	Verified	Verified	Verified
Switzerland	Verified	Verified	Not Verified
Syrian Arab Republic	Not Verified*		
Thailand	Verified	Verified	
The United Kingdom	Verified	Verified	Verified
Togo	Verified		
Trinidad and Tobago	Verified		
Tunisia	Verified		
Turkey	Verified	Not Verified	Not Verified
Turks and Caicos Islands	Verified		
Uganda		Not Verified	
Ukraine	Not Verified	Not Verified*	
United Arab Emirates	Verified	Verified	Verified
United Republic of Tanzania		Verified	
United States of America	Verified	Verified	Verified
Uruguay	Verified		Verified
Uzbekistan	Verified	Not Verified*	
Venezuela (Bolivarian Republic of)			Verified
Viet Nam	Verified	Verified	
Wallis and Futuna	Not Verified		
Zambia		Verified	
Zimbabwe		Verified	

*New country added in this update.

†Variants 501Y.V2 and P.1 for Guadeloupe and Martinique were removed based on further information received.

**See *Annex : Data, table and figure notes*

Annex 3. Data, table and figure notes

Data presented are based on official laboratory-confirmed COVID-19 case and deaths reported to WHO by country/territories/areas, largely based upon WHO case definitions and surveillance guidance. While steps are taken to ensure accuracy and reliability, all data are subject to continuous verification and change, and caution must be taken when interpreting these data as several factors influence the counts presented, with variable underestimation of true case and death incidence, and variable delays to reflecting these data at global level. Case detection, inclusion criteria, testing strategies, reporting practices, and data cut-off and lag times differ between countries/territories/areas. A small number of countries/territories/areas report combined probable and laboratory-confirmed cases. Differences are to be expected between information products published by WHO, national public health authorities, and other sources. Due to public health authorities conducting data reconciliation exercises which remove large numbers of cases or deaths from their total counts, negative numbers may be displayed in the new cases/deaths columns as appropriate. When additional details become available that allow the subtractions to be suitably apportioned to previous days, graphics will be updated accordingly. A record of historic data adjustment made is available upon request by emailing epi-data-support@who.int. Please specify the country(ies) of interest, time period(s), and purpose of the request/intended usage. Prior situation reports will not be edited; see covid19.who.int for the most up-to-date data. Global totals include 745 cases and 13 deaths reported from international conveyances.

The designations employed, and the presentation of these materials do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement. Countries, territories and areas are arranged under the administering WHO region. The mention of specific companies or of certain manufacturers' products does not imply that they are endorsed or recommended by WHO in preference to others of a similar nature that are not mentioned. Errors and omissions excepted, the names of proprietary products are distinguished by initial capital letters.

[1] All references to Kosovo should be understood to be in the context of the United Nations Security Council resolution 1244 (1999). In the map, number of cases of Serbia and Kosovo (UNSCR 1244, 1999) have been aggregated for visualization purposes.

[i] Excludes countries, territories, and areas that have never reported a confirmed COVID-19 case (Annex 1), or the detection of a variant of concern (Annex 2).

[ii] Transmission classification is based on a process of country/territory/area self-reporting. Classifications are reviewed on a weekly basis and may be revised as new information becomes available. Differing degrees of transmission may be present within countries/territories/areas. For further information, please see: Considerations for implementing and adjusting public health and social measures in the context of COVID-19:

- No (active) cases: No new cases detected for at least 28 days (two times the maximum incubation period), in the presence of a robust surveillance system. This implies a near-zero risk of infection for the general population.
- Imported / Sporadic cases: Cases detected in the past 14 days are all imported, sporadic (e.g., laboratory acquired or zoonotic) or are all linked to imported/sporadic cases, and there are no clear signals of further locally acquired transmission. This implies minimal risk of infection for the general population.
- Clusters of cases: Cases detected in the past 14 days are predominantly limited to well-defined clusters that are not directly linked to imported cases, but which are all linked by time, geographic location and common

exposures. It is assumed that there are a number of unidentified cases in the area. This implies a low risk of infection to others in the wider community if exposure to these clusters is avoided.

- Community transmission: Which encompasses a range of levels from low to very high incidence, as described below and informed by a series of indicators described in the aforementioned guidance. As these subcategorization are not currently collated at the global level, but rather intended for use by national and sub-national public health authorities for local decision-making, community transmission has not been disaggregated in this information product.
    - CT1: Low incidence of locally acquired, widely dispersed cases detected in the past 14 days, with many of the cases not linked to specific clusters; transmission may be focused in certain population sub-groups. Low risk of infection for the general population.
    - CT2: Moderate incidence of locally acquired, widely dispersed cases detected in the past 14 days; transmission less focused in certain population sub-groups. Moderate risk of infection for the general population.
    - CT3: High incidence of locally acquired, widely dispersed cases in the past 14 days; transmission widespread and not focused in population sub-groups. High risk of infection for the general population.
    - CT4: Very high incidence of locally acquired, widely dispersed cases in the past 14 days. Very high risk of infection for the general population.
- Pending: transmission classification has not been reported to WHO.

[iii] "Territories" include territories, areas, overseas dependencies and other jurisdictions of similar status.

This is **"Exhibit J"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

A Commissioner, etc.

World Health Organization

Search by Country, Territory, or Area

Covid-19 Response Fund

Donate

WHO Coronavirus (COVID-19) Dashboard

Overview | Data Table | Explore

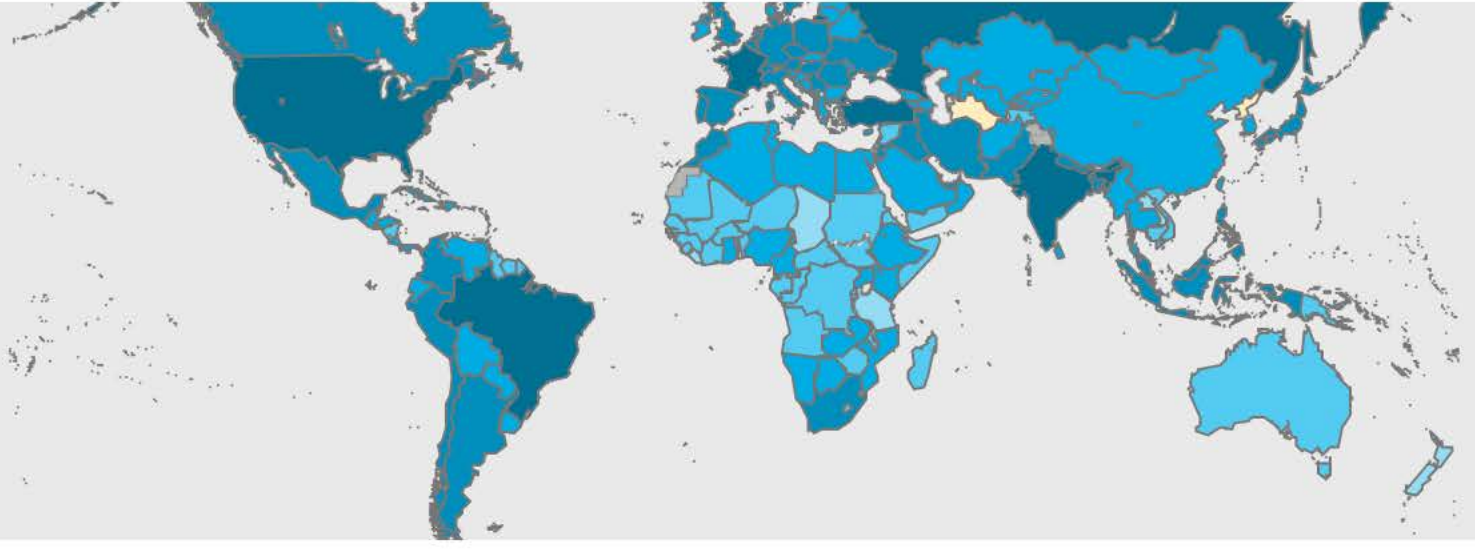
Total

437,764
new cases

179,686,071
confirmed cases

3,899,172
deaths

2,624,733,776
vaccine doses administered



Download Map Data

Globally, as of **4:12pm CEST, 25 June 2021**, there have been **179,686,071 confirmed cases** of COVID-19, including **3,899,172 deaths**, reported to WHO. As of **24 June 2021**, a total of **2,624,733,776 vaccine doses** have been administered.

This is **"Exhibit K"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

A Commissioner, etc.

SCIENCE BRIEFS

COVID-19 Hospitalizations, ICU Admissions and Deaths Associated with the New Variants of Concern

Ashleigh R. Tuite, David N. Fisman, Ayodele Odutayo, Pavlos Bobos, Vanessa Allen, Isaac I. Bogoch, Adalsteinn D. Brown, Gerald A. Evans, Anna Greenberg, Jessica Hopkins, Antonina Maltsev, Douglas G. Manuel, Allison McGeer, Andrew M. Morris, Samira Mubareka, Laveena Munshi, V. Kumar Murty, Samir N. Patel, Fahad Razak, Robert J. Reid, Beate Sander, Michael Schull, Brian Schwartz, Arthur S. Slutsky, Nathan M. Stall, Peter Jüni on behalf of the Ontario COVID-19 Science Advisory Table

Version 1.0

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Author Affiliations: The affiliations of the members of the Ontario COVID-19 Science Advisory Table can be found at https://covid19-sciencetable.ca/.

Declarations of Interest: The declarations of interest of the members of the Ontario COVID-19 Science Advisory Table, its Working Groups, or its partners can be found at https://covid19-sciencetable.ca/.

About Us: The Ontario COVID-19 Science Advisory Table is a group of scientific experts and health system leaders who evaluate and report on emerging evidence relevant to the COVID-19 pandemic, to inform Ontario's response. Our mandate is to provide weekly summaries of relevant scientific evidence for the COVID-19 Health Coordination Table of the Province of Ontario, integrating information from existing scientific tables, Ontario's universities and agencies, and the best global evidence. The Science Table summarizes its findings for the Health Coordination Table and the public in Science Briefs.

Correspondence to: Secretariat of the Ontario COVID-19 Science Advisory Table (info@covid19-sciencetable.ca)

The views and findings expressed in this Science Brief are those of the authors and do not necessarily reflect the views of all of the members of the Ontario COVID-19 Science Advisory Table, its Working Groups, and its partners.

Key Message

New variants of concern (VOCs) now account for 67% of all Ontario SARS-CoV-2 infections. Compared with early variants of SARS-CoV-2, VOCs are associated with a 63% increased risk of hospitalization, a 103% increased risk of intensive care unit (ICU) admission and a 56% increased risk of death due to COVID-19.

VOCs are having a substantial impact on Ontario's healthcare system. On March 28, 2021, the daily number of new SARS-CoV-2 infections in Ontario reached the daily number of cases observed near the height of the second wave, at the start of the province-wide lockdown, on December 26, 2020.

The number of people hospitalized with COVID-19 is now 21% higher than at the start of the province-wide lockdown, while ICU occupancy is 28% higher (Figure 1). The percentage of COVID-19 patients in ICUs who are younger than 60 years is about 50% higher now than it was prior to the start of the province-wide lockdown.

Because the increased risk of COVID-19 hospitalization, ICU admission and death with VOCs is most pronounced 14 to 28 days after diagnosis, there will be significant delays until the full burden to the health care system becomes apparent.

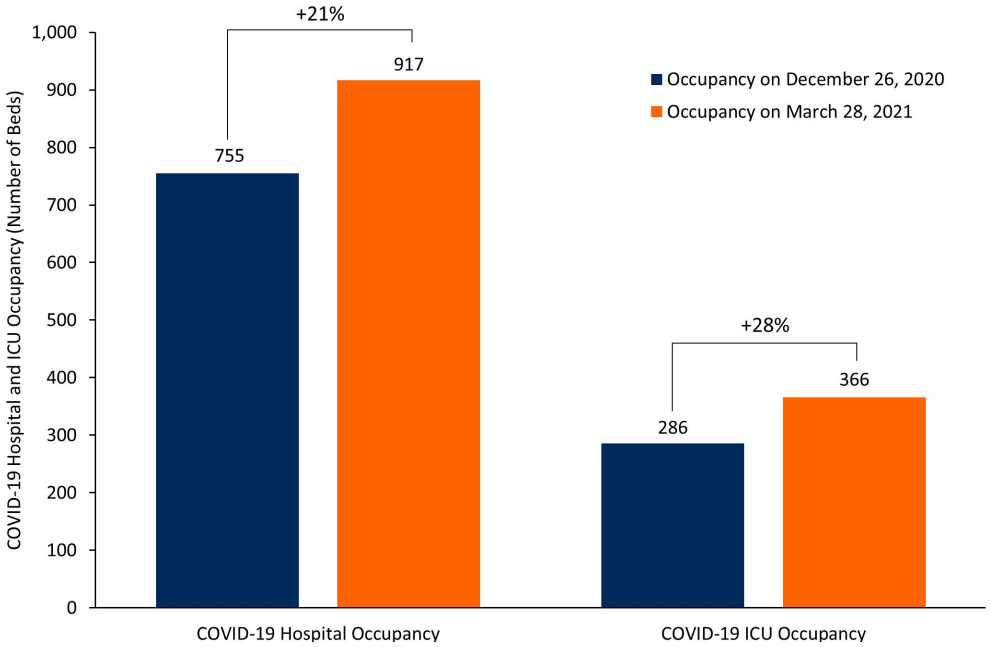

Figure 1. COVID-19 Hospital and ICU Occupancy on March 28, 2021 Compared with December 26, 2020
Bar graphs showing the COVID-19 hospital and ICU occupancy in Ontario. The relative increase between March 28,

2021 and December 26, 2020 is indicated above the corresponding bars for hospital and ICU occupancy. ICU, intensive care unit.

Summary

Background

As of March 28, 2021 new variants of concern (VOCs) account for 67% of all Ontario SARS-CoV-2 infections. The B.1.1.7 variant originally detected in Kent, United Kingdom accounts for more than 90% of all VOCs in Ontario, with emerging evidence that it is both more transmissible and virulent.

Questions

What are the risks of COVID-19 hospitalization, ICU admission and death caused by VOCs as compared with the early variants of SARS-CoV-2?

What is the early impact of new VOCs on Ontario's healthcare system?

Findings

A retrospective cohort study of 26,314 people in Ontario testing positive for SARS-CoV-2 between February 7 and March 11, 2021, showed that 9,395 people (35.7%) infected with VOCs had a 62% relative increase in COVID-19 hospitalizations (odds ratio [OR] 1.62, 95% confidence interval [CI] 1.41 to 1.87), a 114% relative increase in ICU admissions (OR 2.14, 95% CI 1.52 to 3.02), and a 40% relative increase in COVID-19 deaths (OR 1.40, 95% CI 1.01 to 1.94), after adjusting for age, sex and comorbidities.

A meta-analysis including the Ontario cohort study and additional cohort studies in the United Kingdom and Denmark showed that people infected with VOCs had a 63% higher risk of hospitalization (RR 1.63, 95% CI 1.44 to 1.83), a doubling of the risk of ICU admission (RR 2.03, 95% CI 1.69 to 2.45), and a 56% higher risk of all-cause death (RR 1.56, 95% CI 1.30 to 1.87). Estimates observed in different studies and regions were completely consistent, and the B.1.1.7 variant was dominant in all three jurisdictions over the study periods.

The number of people hospitalized with COVID-19 on March 28, 2021, is 21% higher than at the start of the province-wide lockdown during the second wave on December 26, 2020, while ICU occupancy is 28% higher.

Between December 14 to 20, 2020, there were 149 new admissions to ICU; people aged 59 years and younger accounted for 30% of admissions. Between March 15, 2021 and March 21, 2021, there were 157 new admissions to ICU; people aged 59 years and younger accounted for 46% of admissions.

Interpretation

The new VOCs will result in a considerably higher burden to Ontario's health care system during the third wave compared to the impact of early SARS-CoV-2 variants during Ontario's second wave.

Since the start of the third wave on March 1, 2021, the number of new cases of SARS-CoV-2 infection, and the COVID-19 hospital and ICU occupancies have surpassed prior thresholds at the start of the province-wide lockdown on December 26, 2020.

Background

Around March 1, 2021, Ontario entered the third wave of the COVID-19 pandemic, with the slope of the epidemic curve driven by the increasing number of VOCs since March 3, 2021 (Figure 2).[1] As of March 28, 2021, there were an estimated total of

107.1 new SARS-CoV-2 infections per 100,000 persons per week, with 35.7 new SARS-CoV-2 infections per 100,000 Ontarians per week caused by early variants of SARS-CoV-2 (non-VOCs), and 71.4 new SARS-CoV-2 infections per 100,000 Ontarians per week caused by new VOCs. The VOCs accounted for an estimated 67% of new cases of SARS-CoV-2 infections.[1] VOCs are now the dominant source of SARS-CoV-2 infection in Ontario.

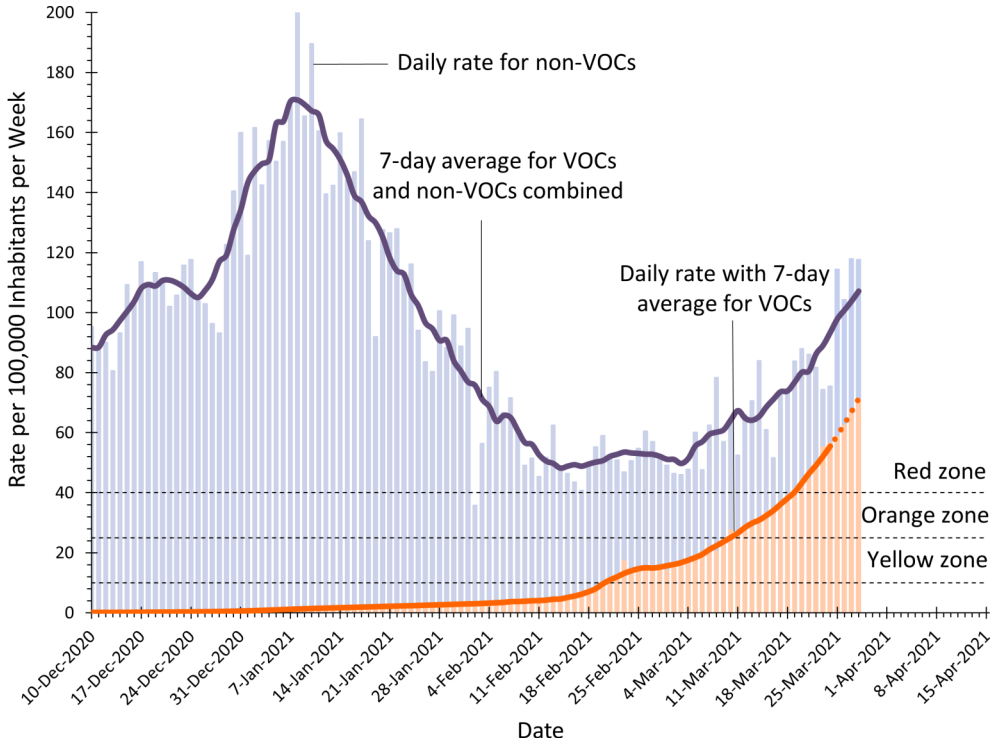

Figure 2. Rate of New SARS-CoV-2 Infections in Ontario

Seven-day moving averages of confirmed new SARS-CoV-2 infections overall in Ontario per 100,000 inhabitants per week (purple line), and infections caused by new VOCs in Ontario per 100,000 inhabitants per week (orange line). The daily rate per 100,000 inhabitants per week is represented by blue and orange bars. The incidence of new infections related to VOCs from March 24th 2021 and onwards is predicted (dashed orange line). The color-coded zones are the zones of public health measures established by Ontario's COVID-19 response framework: grey/red zone = weekly SARS-CoV-2 incidence of ≥40 per 100,000; orange zone = weekly incidence 25 to 39.9 per 100,000; and yellow zone = weekly incidence of 10 to 24.9 per 100,000. VOC, variant of concern. Graph adapted from Ontario COVID-19 Science Advisory Table.[1]

The B.1.1.7 variant, which was originally detected in Kent, United Kingdom, currently accounts for more than 90% of all VOCs in Ontario. The B.1.351 and P.1 variants originally detected in South Africa and Brazil, respectively, account for the remaining VOCs.[2] The B.1.1.7 variant which is dominant in Ontario, is at least 40% more transmissible than early variants of SARS-CoV-2,[3] and emerging evidence suggests it may be more virulent.[4]

Questions

What are the risks of COVID-19 hospitalization, ICU admission and death caused by VOCs as compared with the early variants of SARS-CoV-2?

What is the early impact of new VOCs on Ontario's healthcare system?

Findings

Table 1 presents the results of a retrospective cohort study of 26,314 people in Ontario who were PCR-positive for SARS-CoV-2 between February 7 and March 11, 2021, with 9,395 people (35.7%) having an infection caused by a VOC. After adjusting for age, sex and comorbidities, infections due to VOCs were associated

with a 62% relative increase in COVID-19 hospitalizations (odds ratio [OR] 1.62, 95% confidence interval [CI] 1.41 to 1.87), a 114% relative increase in ICU admissions (OR 2.14, 95% CI 1.52 to 3.02), and a 40% relative increase in COVID-19 deaths (OR 1.40, 95% CI 1.01 to 1.94). These risk elevations for COVID-19 hospitalization, ICU admission and death were consistent across all age groups.

	Adjusted odds ratio (95% CI)
COVID-19 Hospitalizations	1.62 (1.41 to 1.87)
COVID-19 ICU admissions	2.14 (1.52 to 3.02)
COVID-19 Deaths	1.40 (1.01 to 1.94)

Table 1. Risk of COVID-19 Hospitalization, Intensive Care Unit Admission and Death Associated with VOCs Compared to Early Variants in Ontario, Canada

Adjusted odds ratios and 95% confidence intervals for the risk of COVID-19 hospitalizations, intensive care unit admissions and deaths associated with new VOCs compared to early variants. VOC, variant of concern; CI, confidence interval; ICU, intensive care unit.

Figure 3 presents the results a meta-analysis of cohort studies in Ontario (Table 1, above), the United Kingdom[5,6] and Denmark[7] comparing new VOCs with early variants, again with the dominant VOC being B.1.1.7 in all three jurisdictions over the study periods.[3] Pooling adjusted estimates of relative risks (RRs), people infected with VOCs had a 63% higher risk of hospitalization (RR 1.63, 95% CI 1.44 to 1.83), a doubling of the risk of ICU admission (RR 2.03, 95% CI 1.69 to 2.45), and a 56% higher risk of all-cause death (RR 1.56, 95% CI 1.30 to 1.87). Estimates observed in different studies and regions were completely consistent.

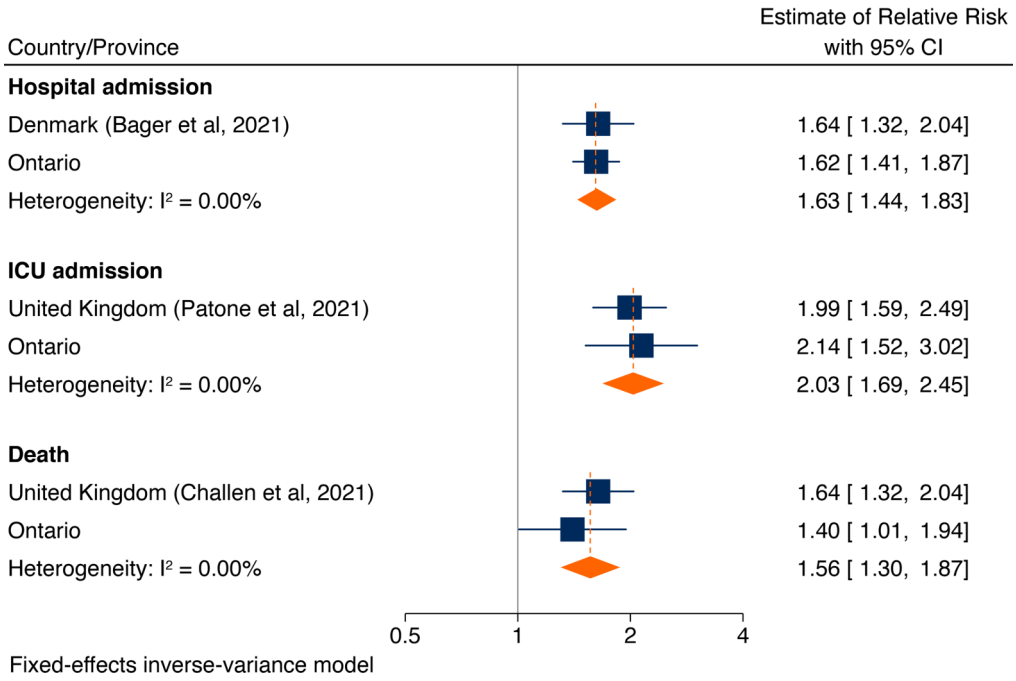

Figure 3. Meta-Analysis of the Risk of COVID-19 Hospitalization, Intensive Care Unit Admission and Death Associated with new VOCs Compared to Early Variants

Each square presents the results of an individual cohort study, with the size of the square being proportional to the weights used in the meta-analysis and the horizontal lines indicating the 95% confidence intervals. The solid vertical line at 1 indicates that there is no difference in prognosis between new VOCs and early variants. The diamond indicates the pooled estimate of the relative risk combining individual studies from different regions. Estimates for Ontario and Denmark are odds ratios; estimates for the United Kingdom are hazard ratios. The retrospective cohort study in Ontario included 26,314 participants in Ontario with PCR confirmed SARS-CoV-2 infection between February 7 and March 11, 2021, of whom 9,395 were infected with new VOCs. The retrospective cohort study by Bager et al. included 18,449 participants in Denmark with PCR confirmed SARS-CoV-2 infection between January 1 and February 9, 2021 with 2,155 infected with new VOCs.[7] Estimates were adjusted for age, sex, calendar period, region, and number of comorbidities during the past 5 years. The retrospective cohort study by Patone et al. included 198,420 individuals in the United Kingdom with PCR confirmed SARS-CoV-2 infection between November 1, 2020 and January 27, 2021, of whom 80,494 were infected with new VOCs. Relative risk estimates were adjusted for age, sex, region, socio-demographic factors and comorbidities, including asthma, chronic obstructive pulmonary disease, diabetes

and hypertension.[5] The retrospective cohort study by Challen et al. included 109,812 individuals in the United Kingdom with PCR confirmed SARS-CoV-2 infection between October 1, 2020 and January 29, 2021, with 54,906 participants with new VOCs matched to 54,906 participants with early variants.[6] Participants were matched on age, sex, date of specimen collection, ethnicity, geographical location, and index of multiple deprivation, which is a marker for socioeconomic status; estimates were subsequently adjusted for age. VOC, variant of concern; CI, confidence interval; ICU, intensive care unit.

Figure 4 shows the time to death observed in a retrospective cohort study by Challen et al. in the United Kingdom involving 109,812 participants with positive PCR tests for SARS-CoV-2 between October 1, 2020, to January 29, 2021, with 54,906 participants infected with new VOCs matched to 54,906 participants infected with the early variant.[6] The curves overlap until day 12 after diagnosis, at which point the curves start to separate, with a higher risk of death among participants infected with new VOCs compared with participants infected with early variants.

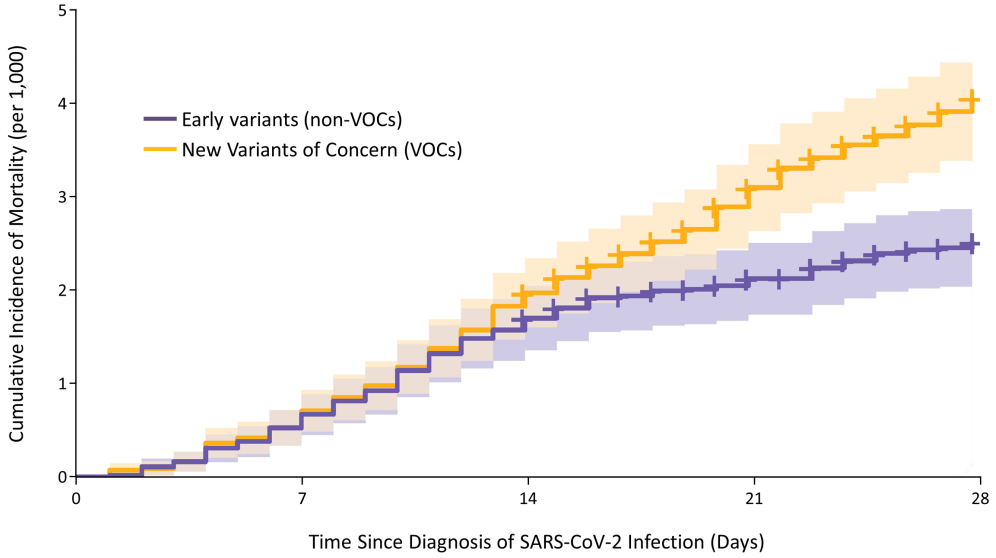

Figure 4. Time to Death Following SARS-CoV-2 Infection with New VOCs Compared with Early Variants
Curves describing the time to death from first PCR confirmation of SARS-CoV-2 infection among individuals in the United Kingdom infected with new VOCs versus early SARS-CoV-2 variants. Participants were matched on age, sex, date of specimen collection, ethnicity, geographical location, and index of multiple deprivation, which is a marker for socioeconomic status, and estimates were subsequently adjusted for age. Data from Challen et al.[6] VOC, variant of concern.

Figure 5 shows the risk of death associated with new VOCs compared with early SARS-CoV-2 variants from days 0 to 14 and days 15 to 28 after diagnosis of SARS-CoV-2 infection. Results are adapted from the aforementioned retrospective cohort study of people with PCR confirmed SARS-CoV-2 infection in the United Kingdom by Challen et al.[6] Between days 0 and 14 after diagnosis, there was only a minimal difference in the risk of death (RR 1.23, 95% CI 0.92 to 1.64) associated with the new VOCs compared with early variants. However, between days 15 and 28, the risk of death was more than doubled (RR 2.40, 95% CI 1.66 to 3.47).

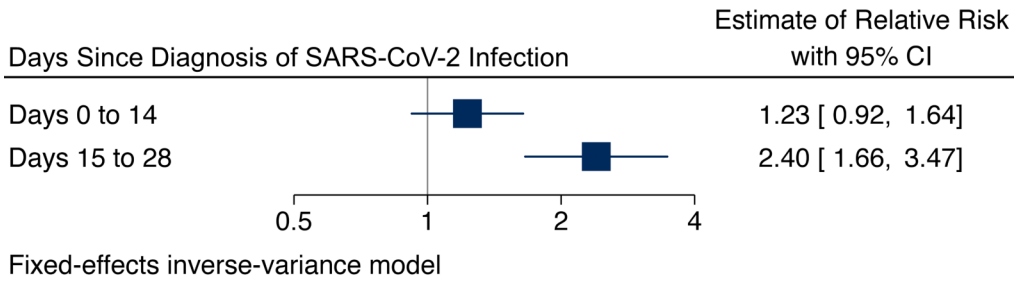

Figure 5. Risk of COVID-19 Death Associated with new VOCs Compared with Early Variants by Time Since Diagnosis of SARS-CoV-2 Infection
Adapted from a retrospective cohort study by Challen et al. which included 109,812 individuals in the United Kingdom with PCR-confirmed SARS-CoV-2 infection between October 2020 to 29 January 2021, with 54,906 individuals with new VOCs matched to 54,906 individuals with the early variant.[6] Individuals were matched on age, sex, date of specimen

collection, ethnicity, geographical location, and index of multiple deprivation, which is a marker for socioeconomic status. Each square presents the relative risk for death with the new VOCs versus early variants. The horizontal lines indicate the 95% confidence intervals. The solid vertical line at 1 indicates that there is no difference in prognosis between new VOCs and early SARS-CoV-2 variants. VOC, variant of concern; CI, confidence interval.

Figure 6 shows the risk of ICU admission associated with new VOCs versus early SARS-CoV-2 variants at days 1, 5, 10 and 15 after diagnosis of SARS-CoV-2 infection in a retrospective cohort study by Patone et al. The study involved 198,420 individuals in the United Kingdom with PCR-confirmed SARS-CoV-2 infection, of whom 80,494 were infected with new VOCs.[5] On day 1, there was a minimal difference in the risk of ICU admission between people infected with new VOCs and those infected with early variants (RR 1.20, 95% CI 0.58 to 2.48). Subsequently, there was a progressive, lagged increase in the risk of ICU admission associated with new VOCs, with a 58% increase at day 5 and a near fourfold increase at day 10.

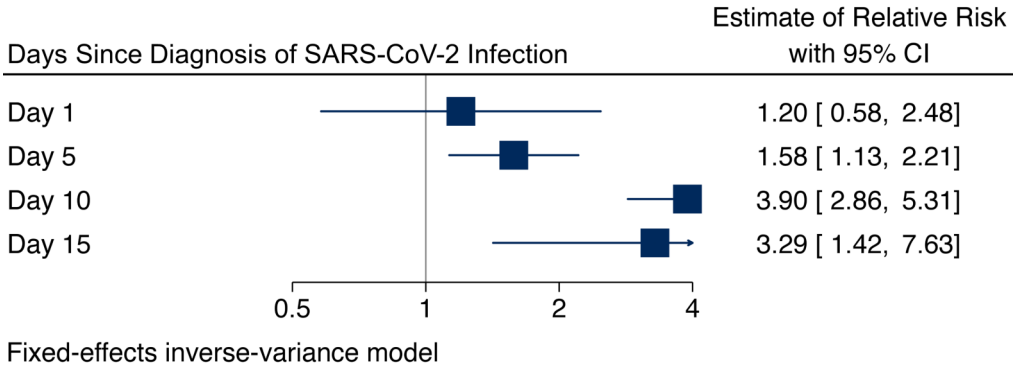

Figure 6. Risk of COVID-19 ICU Admission Associated with New VOCs Compared with Early Variants by Time Since Diagnosis of SARS-CoV-2 Infection

Adapted from a retrospective cohort study by Patone et al.[5] The study involved 198,420 individuals in the United Kingdom with PCR-confirmed SARS-CoV-2 infection, of whom 80,494 were infected with new VOCs. Relative risk estimated were adjusted for age, sex, region, socio-demographic factors and comorbidities including asthma, chronic obstructive pulmonary disease, diabetes and hypertension. Each square represents the relative risk for ICU admission with the new VOCs versus early variants. The horizontal lines indicate the 95% confidence intervals. The solid vertical line at 1 indicates that there is no difference in prognosis between new VOCs and early variants. VOC, variant of concern; CI, confidence interval.

Figure 7 shows the 7-day moving average of daily SARS-CoV-2 infections, and daily COVID-19 hospital and ICU occupancy in Ontario. At the time of the province-wide lockdown near the height of Ontario's second wave on December 26, 2020, there were 2,236 new infections per day, 755 people were hospitalized due to COVID-19, and 286 in ICU due to COVID-19.

Since the start of the third wave around March 1, 2021, the number of new cases, as well as hospital and ICU occupancy have surpassed prior thresholds seen at the start of the province-wide lockdown on December 26, 2020. The threshold of 286 COVID-19 cases in ICUs at the time of the lockdown on December 26, 2020, was reached on March 9, 2021. Likewise, COVID-19 hospital occupancy of 755 people was reached on March 16, 2021. Finally, the threshold of 2,236 new SARS-CoV-2 infections per day was reached on March 28, 2021.

We project a 2 to 4 week time lag between daily SARS-CoV-2 cases and COVID-19 hospitalizations and ICU admissions, with lagging risk increases due to the new VOCs (see Figures 3 to 5). Therefore, hospital and ICU occupancies due to COVID-19 will continue to increase considerably over time, and would so even if SARS-CoV-2 case numbers were to remain at the current level seen on March 28, 2021.

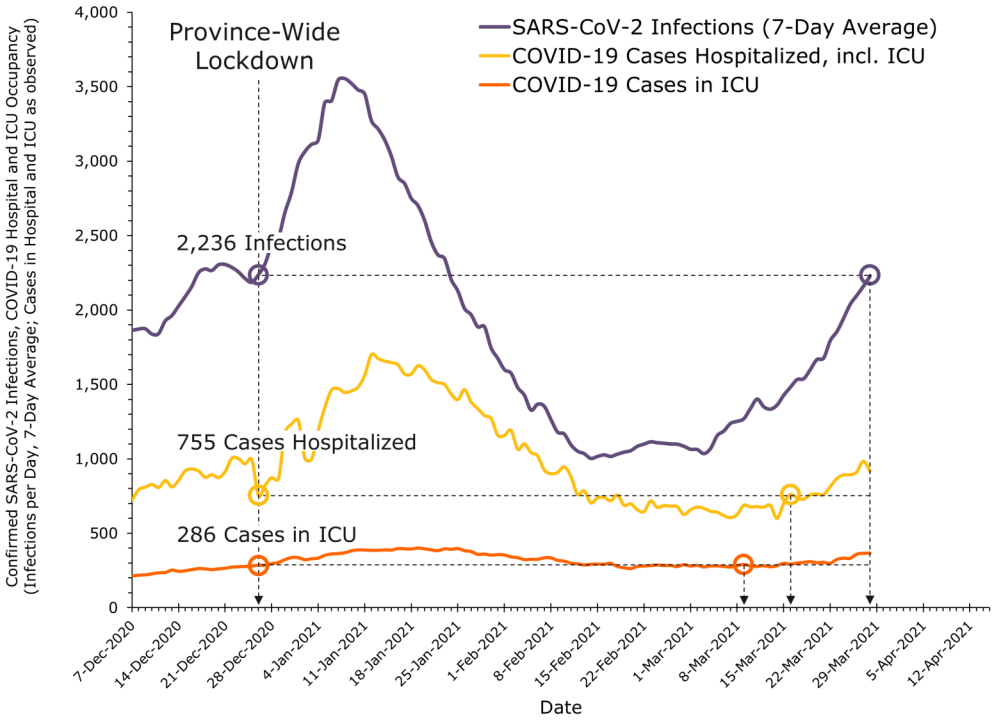

Figure 7. Number of New SARS-CoV-2 Infections, COVID-19 Hospital, and ICU Occupancy in Ontario
7-day moving averages of confirmed new SARS-CoV-2 infections in Ontario per week, number of people hospitalized with COVID-19, and number of ICU beds in Ontario occupied by COVID-19 patients. VOC, variant of concern; ICU, intensive care unit.

Table 2 presents a comparison of the number of new SARS-CoV-2 infections and COVID-19 hospital and ICU occupancy for key dates during the third wave compared with the start of the province-wide lockdown on December 26, 2020 during the second wave. As of March 28, 2021, the predicted 7-day average of SARS-CoV-2 infections during the third wave reached the 7-day midpoint average seen at the start of the province-wide lockdown on December 26, 2020.

Key	Date	SARS-CoV-2 Infections	Hospital Occupancy	ICU Occupancy
A	26-Dec-20	**2,236**	**755**	**286**
B	9-Mar-21	1,269	689	**290**
C	16-Mar-21	1,480	**761**	292
D	28-Mar-21	**2,236**	917	366

Table 2. Comparison of Key Dates During the Third Wave in Ontario with the Start of the Province-Wide Lockdown During the Second Wave on December 26, 2020
A, December 26, 2020, was the start date of the province-wide lockdown during the second wave; B, March 9, 2021 is the date when the COVID-19 ICU occupancy during the third wave reached COVID-19 ICU occupancy seen on December 26, 2020; C, March 16, 2021 is the date when COVID-19 hospital occupancy during the third wave reached COVID-19 hospital occupancy seen on December 26, 2020; D, March 28, 2021 is the date when the predicted 7-day average of SARS-CoV-2 infections during the third wave reached the 7-day midpoint average seen on December 26, 2020. ICU, intensive care unit. Second wave, September 1, 2020 to February 28, 2021. Third wave, March 1, 2020 to ongoing.

Figure 1 above presents a comparison of COVID-19 hospital occupancy and ICU occupancy in Ontario on March 28, 2021, compared with the start of the province-wide lockdown on December 26, 2020. The number of people hospitalized with COVID-19 on March 28, 2021, is 21% higher than on December 26, 2020, while ICU occupancy is 28% higher.

Figure 8 presents the percentage of COVID-19 ICU admissions in Ontario by age group in the week prior to the lockdown during the second wave (December 14 to 20, 2020) with the last available week of ICU admission data during the third wave (March 15 to 21, 2021). Between December 14 to 20, 2020, there were 149 new admissions to ICU; people aged 59 years and younger accounted for 30% of admissions. Between March 15, 2021 and March 21, 2021, there were 157 new admissions to ICU; people aged 59 years and younger accounted for 46% of admissions.

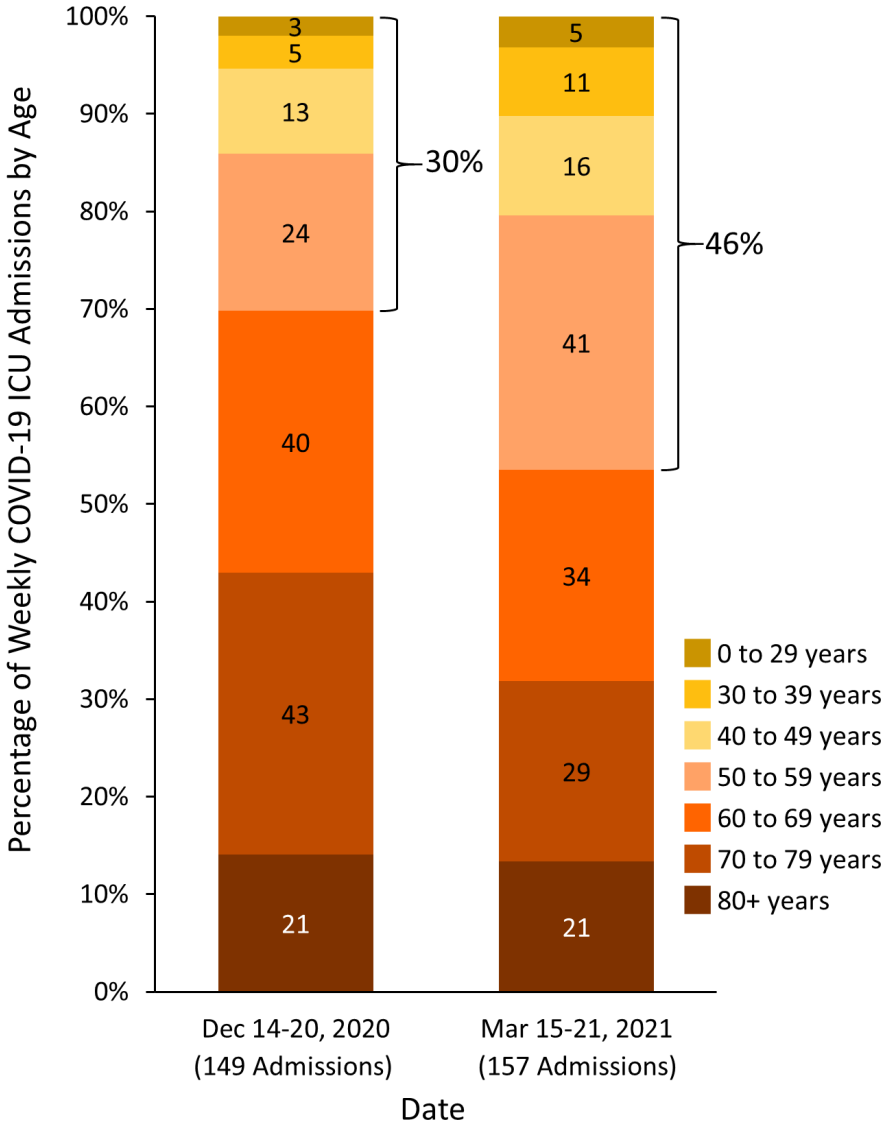

Figure 8. Weekly COVID-19 ICU Admissions in Ontario by Age
December 14 to 20, 2020 corresponds to the week prior to lockdown during the second wave, March 15 to 21, 2021 corresponds to the last available week of ICU admission data during the third wave. Data sourced from the Critical Care Information System (CCIS).

Interpretation

Compared with early variants of SARS-CoV-2, new VOCs are associated with a 103% increase in the risk of hospitalization, a 63% increase in the risk of ICU admission and a 56% increase in the risk of death due to COVID-19, which will result in a considerably higher burden to the health care system than observed with early variants during the second wave. The risk increase is particularly pronounced 14 to 28 days after a diagnosis of SARS-CoV-2 infection, which in turn will result in delays until the full burden to the health care system becomes apparent.

Since the start of the third wave around March 1, 2021, the number of new cases of SARS-CoV-2 infection, and the COVID-19 hospital and ICU occupancies have surpassed prior thresholds at the start of the province-wide lockdown on December 26, 2020. As of March 28, 2020, hospital occupancy was 21% higher and ICU occupancy 28% higher than at the start of the province-wide lockdown.

Currently, patients aged 59 years and younger make up 46% of new COVID-19 admissions to ICUs, compared with 30% in the week prior to the start of the province-wide lockdown on December 26, 2020.

Methods Used for This Science Brief

We conducted a retrospective cohort study using cases of SARS-CoV-2 infection reported in CCM/iPHIS with a case report date between Feb 7 and March 11, 2021. We restricted the analysis to cases that were tested for variants of concern. As Ontario's long-term care population was highly vaccinated with SARS-CoV-2 vaccines as of February 2021, and were unlikely to become critically ill and require intensive care, long term care residents were excluded from the analysis. A total of 26,314 individuals were included in the analysis, of whom 9,395 had a detected SARS-CoV-2 infection with a VOC. Associations between VOC SARS-CoV-2 infection and COVID-19 outcomes were evaluated by constructing logistic regression models with the following prespecified covariates: age (by 10-year age categories), sex, obesity, and any of the following medical comorbidities: asthma, immunocompromise, COPD, hematological disease, renal disease, neurological condition, diabetes, or liver disease. Time (date of case report) was included as a linear trend term. To account for geographic variability in the fraction of infections caused by VOCs, public health units were included as indicator variables. The analysis of the age distribution in Figure 8 is based on all cases, without exclusion of long-term care residents.

We searched PubMed, Google Scholar, the COVID-19 Rapid Evidence Reviews, the Joanna Briggs Institute's COVID-19 Special Collection, LitCovid in PubMed, the Oxford COVID-19 Evidence Service, the World Health Organization's Global Literature on Coronavirus Disease, and other COVID-19 specific resources listed by the Guidelines International Network and the McMaster Health Forum for studies on the prognosis associated with new VOCs compared with early variants. In addition, we retrieved reports citing relevant articles through Google Scholar and reviewed references from identified articles for additional studies. The search was last updated on March 26, 2021. For the United Kingdom, the analysis by Challen et al[6] was selected for extraction of mortality data rather than the analysis by Davies et al[4] since Challen et al.'s analysis was considered to have a lower risk of confounding.

We used an inverse-variance fixed-effects meta-analysis to combine adjusted estimates from individual studies. Analyses were done in R (R Foundation, Vienna, Austria) and STATA (StataCorp LLC, College Station, TX).

Author Contributions

PJ conceived the Science Brief. ART, AO and PJ wrote the first draft. ART, DNF, PB and PJ performed analyses. All authors revised the Science Brief critically for important intellectual content and approved the final version.

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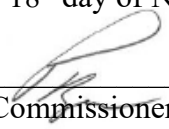
This is **"Exhibit L"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



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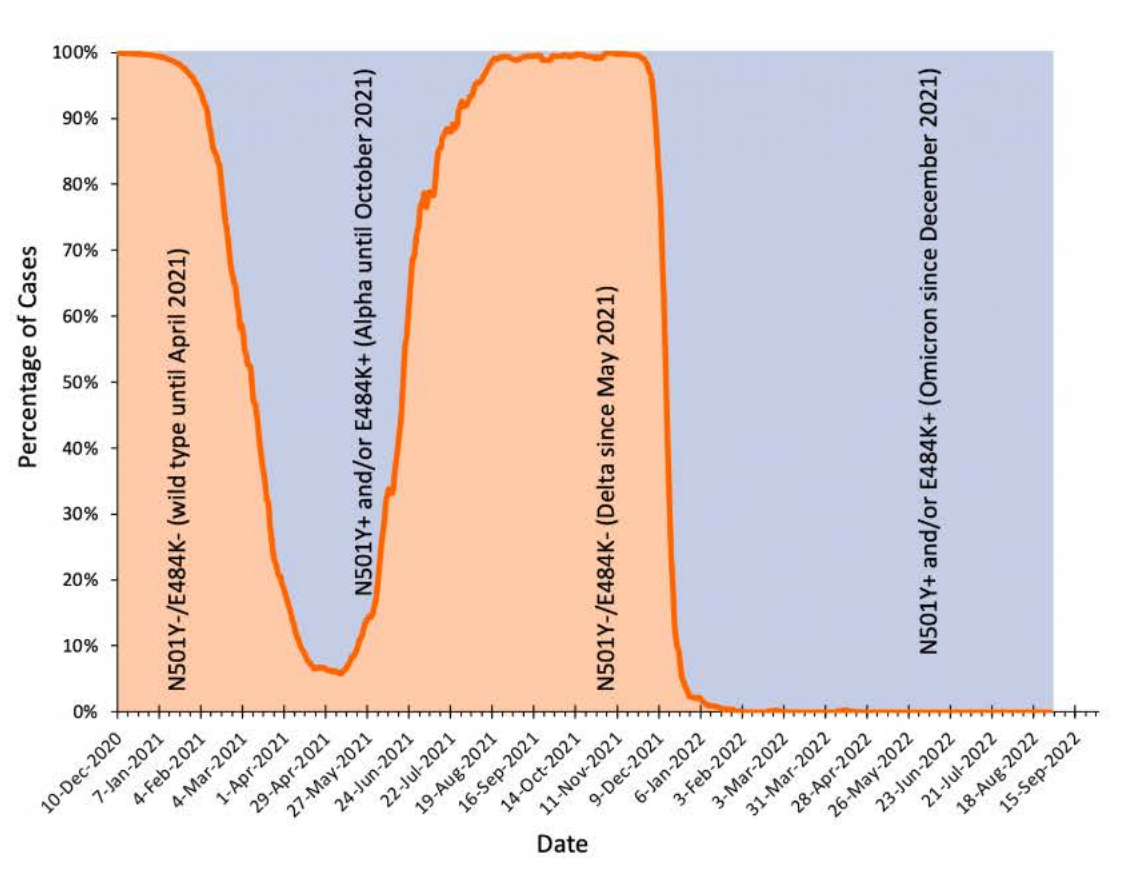
Percentage of Cases Caused by Different Variants in Ontario



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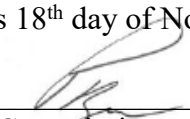
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



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Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study

Katherine A Twohig, Tommy Nyberg*, Asad Zaidi, Simon Thelwall, Mary A Sinnathamby, Shirin Aliabadi, Shaun R Seaman, Ross J Harris, Russell Hope, Jamie Lopez-Bernal, Eileen Gallagher, Andre Charlett, Daniela De Angelis, the COVID-19 Genomics UK (COG-UK) consortium†, Anne M Presanis, Gavin Dabrera*

Summary

Background The SARS-CoV-2 delta (B.1.617.2) variant was first detected in England in March, 2021. It has since rapidly become the predominant lineage, owing to high transmissibility. It is suspected that the delta variant is associated with more severe disease than the previously dominant alpha (B.1.1.7) variant. We aimed to characterise the severity of the delta variant compared with the alpha variant by determining the relative risk of hospital attendance outcomes.

Methods This cohort study was done among all patients with COVID-19 in England between March 29 and May 23, 2021, who were identified as being infected with either the alpha or delta SARS-CoV-2 variant through whole-genome sequencing. Individual-level data on these patients were linked to routine health-care datasets on vaccination, emergency care attendance, hospital admission, and mortality (data from Public Health England's Second Generation Surveillance System and COVID-19-associated deaths dataset; the National Immunisation Management System; and NHS Digital Secondary Uses Services and Emergency Care Data Set). The risk for hospital admission and emergency care attendance were compared between patients with sequencing-confirmed delta and alpha variants for the whole cohort and by vaccination status subgroups. Stratified Cox regression was used to adjust for age, sex, ethnicity, deprivation, recent international travel, area of residence, calendar week, and vaccination status.

Findings Individual-level data on 43 338 COVID-19-positive patients (8682 with the delta variant, 34 656 with the alpha variant; median age 31 years [IQR 17–43]) were included in our analysis. 196 (2·3%) patients with the delta variant versus 764 (2·2%) patients with the alpha variant were admitted to hospital within 14 days after the specimen was taken (adjusted hazard ratio [HR] 2·26 [95% CI 1·32–3·89]). 498 (5·7%) patients with the delta variant versus 1448 (4·2%) patients with the alpha variant were admitted to hospital or attended emergency care within 14 days (adjusted HR 1·45 [1·08–1·95]). Most patients were unvaccinated (32 078 [74·0%] across both groups). The HRs for vaccinated patients with the delta variant versus the alpha variant (adjusted HR for hospital admission 1·94 [95% CI 0·47–8·05] and for hospital admission or emergency care attendance 1·58 [0·69–3·61]) were similar to the HRs for unvaccinated patients (2·32 [1·29–4·16] and 1·43 [1·04–1·97]; p=0·82 for both) but the precision for the vaccinated subgroup was low.

Interpretation This large national study found a higher hospital admission or emergency care attendance risk for patients with COVID-19 infected with the delta variant compared with the alpha variant. Results suggest that outbreaks of the delta variant in unvaccinated populations might lead to a greater burden on health-care services than the alpha variant.

Funding Medical Research Council; UK Research and Innovation; Department of Health and Social Care; and National Institute for Health Research.

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See Comment page 2

*Contributed equally

†Full list of consortium names and affiliations are in appendix pp 11–17

COVID-19 National Epidemiology Cell (K A Twohig MPH, A Zaidi MSc, S Thelwall PhD, M A Sinnathamby MPH, S Aliabadi PhD, R Hope PhD, G Dabrera FFPH), **Statistics, Modelling and Economics Department** (R J Harris PhD, A Charlett PhD, D De Angelis), **Immunisation and Countermeasures Division** (J Lopez-Bernal PhD), **COVID-19 Genomic Analysis Cell** (E Gallagher PhD), **and Joint Modelling Team** (A Charlett, D De Angelis, A M Presanis), **Public Health England, London, UK; MRC Biostatistics Unit, University of Cambridge, Cambridge, UK** (T Nyberg PhD, S R Seaman PhD, D De Angelis PhD, A M Presanis PhD)

Correspondence to: Ms Katherine Twohig, COVID-19 National Epidemiology Cell, Public Health England, London, NW9 5EQ, UK. **feedback.c19epi@phe.gov.uk**

See Online for appendix

Introduction

As SARS-CoV-2 evolves and new variants emerge worldwide, sustained monitoring and rapid assessment of genetic changes are required to inform the public health response and health-care management of COVID-19. WHO has outlined three key criteria to designate variants of concern (VOCs) in relation to global public health: increased transmissibility, increase in virulence or change in clinical disease presentation, and decrease in effectiveness of public health and social measures or available diagnostics, vaccines, and therapeutics.[1]

One of the first VOCs, alpha (B.1.1.7), was initially detected in England in November, 2020. Alpha had increased transmissibility compared with the previous wildtype lineage,[2,3] and became the predominant lineage accounting for 95% of cases in England by early February, 2021.[4] This variant has been identified in 154 countries and was until recently the most prevalent lineage in Europe and North America.[5]

The B.1.617 lineage was first reported in India in December, 2020.[6,7] Following previous waves of COVID-19, the number of confirmed cases and test positivity in India rapidly increased, with the latter

Research in context

Evidence before this study

We did a literature review to identify all publications on the severity of the SARS-CoV-2 delta variant (B.1.617.2). We searched PubMed on June 18, 2021, using the query: "((SARS-CoV-2) OR (COVID-19) OR (coronavirus disease 2019)) AND ((B.1.617.2) OR (Delta) OR (VOC-21APR-02)) AND ((severity) OR (hospitalisation) OR (hospital) OR (emergency care) OR (mortality) OR (lethality) OR (death))". The search was restricted to articles published from Dec 1, 2020, with no language restrictions. Only one relevant publication was found. Based on record linkage of data on 7723 delta and 11 820 alpha variant COVID-19 cases between April 1 and June 6, 2021, with routine health-care data, the EAVE II study in Scotland reported a higher risk of hospital admission within 14 days for patients with the delta variant compared with the alpha variant (hazard ratio [HR] 1·85 [95% CI 1·39–2·47]). The patients had been tested through PCR tests and variant status was determined based on S-gene positivity, a proxy test for SARS-CoV-2 variant.

Added value of this study

This study included data on 8682 patients with the delta variant and 34 656 patients with the alpha variant, confirmed by whole-genome-sequencing. Hence, to our knowledge, it is the largest study to date to report on hospitalisation risk for the delta variant compared with the alpha variant, and the first to do so based on sequencing-confirmed variants. The HR of hospital admission within 14 days was 2·26 (95% CI 1·32–3·89) after stratification and regression adjustment for confounders. We also believe this study is the first to estimate a risk for emergency care attendance or hospital admission within 14 days; the adjusted HR was 1·45 (1·08–1·95).

Implications of all the available evidence

The evidence from these two studies in Scotland and England consistently suggest that patients with COVID-19 who are infected with the delta variant have approximately two times the risk of hospital admission compared with patients with the alpha variant. These findings should be considered for resource and policy planning in secondary care, particularly in areas where the delta variant is increasing and is likely to become the dominant circulating SARS-CoV-2 variant.

reaching 30% by the end of April, 2021.[8] In Delhi, this coincided with the B.1.617 lineages overtaking the alpha lineage, accounting for 60% of all sequenced samples. During this increase, the sub-lineage delta (B.1.617.2) also increased to approximately 80% of B.1.617 cases.[8]

The delta variant was first detected in England in March, 2021, and was designated as a VOC on May 6, 2021.[9] The proportion of COVID-19 cases in England caused by the delta variant has rapidly increased, reaching more than 50% of sequenced isolates by May 25, 2021.[10] Studies in India have estimated that the delta variant could be up to 50% more transmissible than the alpha variant.[8] In England, the secondary attack rate for the delta variant was found to be nearly 3%, compared with less than 2% for the alpha variant.[10] In addition, there is evidence of modest reduction in vaccine effectiveness against infection with the delta variant.[11] However, among patients infected with the delta variant, previous vaccination has been reported to reduce the risk of hospital admission.[12]

To inform the public health response to the delta variant, we did two analyses. First, we characterised the severity of the delta variant compared with the alpha variant by determining the relative risk of hospital attendance or admission following infection using a stratified analysis. Second, we assessed whether associations with hospital attendance outcomes were modified by vaccination.

Methods

Data sources and definitions

This cohort study was done in England among individuals with laboratory confirmed COVID-19. COVID-19 is a notifiable disease and Public Health England collects data on all positive cases in England held within the Second Generation Surveillance System (SGSS).[13,14] Individual-level data on patients with laboratory-confirmed COVID-19 with first positive specimen dates between March 29 and May 23, 2021, were linked with sequencing data uploaded to the Cloud Infrastructure for Big Data Microbial Bioinformatics database.[15] Sampling for whole-genome sequencing mainly includes geographic-weighted population-level sampling of community cases, but can be supplemented by targeted selection such as recent international travellers, care homes, or National Health Service (NHS) diagnostic laboratories.[16] Variant classification was assigned on the basis of lineage definitions from Public Health England.[17] Patients with whole-genome-sequencing-confirmed alpha and delta variants were deterministically linked with data on vaccination,[18] hospital care,[19,20] and mortality using NHS number.[21] A full description of the data sources is in the appendix (p 1).

Potential cases of re-infection were removed to avoid misallocation of variants to different episodes of care by excluding observations for which the sequenced specimen collection date was more than 14 days after the specimen collection date of the individual's first recorded positive test. Observations without an NHS number could not be linked to health-care datasets and were excluded.

The surveillance activities within which this study was conducted are part of Public Health England's responsibility to monitor COVID-19 during the current pandemic. Public Health England has legal permission, provided by Regulation 3 of The Health Service (Control of

Patient Information) Regulations 2002 to process confidential patient information under Sections 3(i) a–c, 3(i) d(i and ii), and 3(iii) as part of its outbreak response activities. This study falls within the research activities approved by the Public Health England Research Ethics and Governance of Public Health Practice Group.

Hospital attendance categorisation

Hospital care data from the Emergency Care Data Set (ECDS) and Secondary Uses Service (SUS) were linked to data for patients with confirmed COVID-19 on June 7, 2021, thereby including data submitted by NHS Trusts up to June 5, 2021. Two outcomes of hospital attendance were defined: (1) hospital admission only, and (2) attendance to emergency care or hospital admission.

Due to a lag between an individual's hospital admission and submission of corresponding SUS data (up to 8 weeks), the definition of hospital admission was determined using a combination of ECDS and SUS variables, some of which exist in only one data source. Where ECDS data were available, hospital admissions were classified as COVID-19 related if a patient presented to emergency care between 1 and 14 days after the patient's first SARS-CoV-2-positive specimen date, there was no International Classification of Disease version 10 (ICD10) code indicating that the attendance was injury related, and the discharge status indicated transfer or admission.

Where SUS data were available, hospital admissions were defined using two sets of criteria. The first set of criteria defined if the hospital visit was related to COVID-19 infection and the second evaluated whether the hospital visit qualified as an admission. All hospital visits for which the attendance date was between 1 and 14 days after the first positive specimen date were considered COVID-19-related. If the admission date was the same as the specimen date, the visit was considered COVID-19 related if (1) the patient's symptom onset date recorded in the laboratory system at the time of test was reported between 1–7 days before the specimen was taken, or (2) if hospital records included ICD10 codes relevant to COVID-19 and the patient died in hospital. These criteria add the flexibility of including records with evidence of onset preceding hospital attendance and severe COVID-19 related outcomes, without including coincidental hospitalisations among infected individuals. Admissions were defined as those where the interval between admission and discharge was more than 0 days; or if the interval between admission and discharge was 0 days and either the hospital record included ICD10 codes relevant to COVID-19 symptoms, or the patient died in hospital, or both.

Attendances to emergency care were included in the second hospital attendance outcome category. A patient was defined as having a COVID-19-related emergency care attendance if ECDS data indicated presentation to emergency care between 1 and 14 days after the patient's first SARS-CoV-2-positive specimen date, there was no ICD10 code indicating that the attendance was injury-related, and discharge details did not indicate transfer or admission.

Unless meeting the criteria described in this section, individuals who first tested positive on the same date as their hospital admission or attendance date were excluded to reduce bias of routine testing at admission for non-COVID-19 related attendances.

Covariates and confounders

Age, sex, and area of residence were extracted from SGSS for patients with COVID-19. National-level Index of Multiple Deprivation (IMD) quintile groups were matched to the patient's lower super output area of residence. IMD is an area-level measure of relative socioeconomic deprivation. Ethnicity was determined from linkage to NHS England's Hospital Episodes Statistics data and through self-reported ethnicity at the COVID-19 test request.

Recent travel was defined as a record of travel outside of the UK within 14 days before the patient's positive COVID-19 test. This indicator was derived from five data sources: public health passenger locator forms, contact tracing of patients done by Public Health England and NHS Test and Trace, travel reported in the COVID-19 test request form, records from the International Arrival COVID-19 testing programme, and additional questionnaires completed through telephone interview for patients for whom no other travel information was available.

Confounder sets were chosen for either stratification or regression adjustment on the basis of the expected strength of the association with exposure or outcomes. The initial outbreaks of the delta variant were localised to northern England and observed in south Asian ethnic groups, and increasing prevalence of the delta variant coincided with the expansion of the COVID-19 vaccination programme to younger age groups.[9,22] Therefore, the set of most likely confounders included age (10-year age bands),[23] ethnicity (White; Asian; Black; and mixed, other, or unknown),[24] calendar week of specimen, area of residence (lower tier local authority [LTLA]: 314 areas), and vaccination status.[11]

Additional potential confounders included sex and socioeconomic deprivation (IMD quintiles) due to association with hospitalisation risk,[23,24] and international travel within 14 days of positive test, which was more common for patients with the delta variant when its incidence first began to increase in England.[9] There was no a-priori expectation that these variables would strongly confound the associations between variant and outcomes so they were considered for regression adjustment rather than stratification.

Statistical analysis

Patients were followed up for a maximum of 14 days from their earliest COVID-19-positive specimen until the hospital admission or emergency care attendance date. Patients were censored at the date of death if this occurred

without a previous hospital attendance event within the 14-day period.

In the primary analysis, stratified Cox regression was used to estimate hazard ratios (HRs) of the hospitalisation outcomes (hospital admission or emergency care attendance) for patients with the delta variant compared with patients with the alpha variant. Strata were created by intersecting the likely confounders. Additional potential confounders were included using main effects. Linear main effects terms for age and calendar date were used to adjust for residual confounding after stratification.

In the secondary analysis, the HRs of the hospitalisation outcomes by variant were estimated by vaccination status. The base models were refitted with an interaction term between variant and vaccination. Due to low numbers of patients with COVID-19 who had been vaccinated, and consequently low numbers within some vaccination categories, vaccination status was grouped into two categories: unvaccinated or less than 21 days since the first vaccination dose; and 21 days or more since the first vaccination dose, with or without the second dose.

In additional analyses, the proportional hazards assumption of the Cox regression model was graphically assessed using Schoenfeld residual plots and formally tested using the Schoenfeld test. Post-evaluations of the relative magnitudes of the confounders' contribution to the adjusted HRs were done by sequentially adding the adjustment variables in the order of the percentage change in the adjusted HRs for patients with the delta variant versus the alpha variant. To assess the impact of stratification versus regression modelling on the HRs and 95% CIs, the primary model was refitted with each stratification variable instead included as a regression variable.

HRs were assessed for sensitivity to stratification by alternative region or calendar period covariates, confounding due to recent international travel or symptomatic status subgroups, or to the precise outcome definitions. Details are shown in the appendix (p 8).

Data were prepared using Stata version 15.1. Statistical analyses were done in R version 4.1.0.

Role of the funding source

The funders of the study had no role in study design, data collection, data analysis, data interpretation, writing of the report, or in the decision to submit for publication.

Results

Of the 49 930 sequencing-confirmed cases of alpha and delta variants in England from March 29 to May 23, 2021, 43 338 were included in our analysis (appendix p 2). 5634 records were excluded due to missing NHS numbers (4240 [10·7%] of 39 677 patients with the alpha variant and 1394 [13·6%] of 10 253 patients with the delta variant). Missing NHS number occurred more frequently among Black and Asian individuals than White individuals (1512 [15·0%] of 10 075 Asian, 291 [19·3%] of 1508 Black, and 2574 [7·7%] of 33 306 White individuals), and among international travellers (871 [29·5%] of 2952 international travellers *vs* 4762 [10·1%] of 46 977 non-travellers).

34 656 patients were infected with the alpha variant and 8682 patients had the delta variant; the proportion of weekly cases by variant changed across the study period with alpha decreasing from 7593 (99·8%) of 7606 cases in the week of March 29, 2021, to 2117 (34·8%) of 6090 cases in the week of May 17, 2021. Patients with the delta variant were younger (median age 29 years [IQR 15–41]) than patients with the alpha variant (median age 31 years [17–43]). Compared with patients with the alpha variant, a greater proportion of patients with the delta variant were from an Asian background, or lived in the north west of England or London (table 1).

The results of the analysis of hospital attendance outcomes among patients with the alpha variant versus the delta variant are shown in table 2. The estimated risk for hospital admission within 14 days after the specimen was taken was higher among patients with the delta variant than the alpha variant. The estimated risk for hospital admission or emergency care within 14 days was also higher among patients with the delta variant than the alpha variant.

Table 3 shows the HRs of the hospital attendance outcomes for patients with the delta variant versus the alpha variant by vaccination status. Among patients who were unvaccinated or had less than 21 days since the first vaccination dose, patients with the delta variant had a higher estimated risk of hospital admission and a higher risk of either hospital admission or emergency care attendance than patients with the alpha variant. In the subgroup of vaccinated patients (≥21 days after first vaccination dose, with and without a second dose), no significant difference was detected in the estimated risk for either hospital attendance outcome between patients with the delta variant and patients with the alpha variant. The risk estimates for the delta versus the alpha variant among vaccinated patients were limited by low precision and wide CIs. There were no significant interactions when comparing the HRs in the vaccinated versus unvaccinated subgroups (table 3).

The Schoenfeld residuals and test showed no significant deviation from the proportional hazards assumption (appendix p 3). The post-evaluations of the confounders showed that adjusted HRs of both categories of hospital attendance outcome (hospital admission, hospital admission or emergency care attendance) changed the most when adjusted for calendar week (83% change for hospital admission, 39% change for hospital admission or emergency care attendance; appendix p 4). When including one or all stratification variables as regression variables instead, the estimated risk for both hospital attendance outcomes were consistently greater for patients with the delta variant than for patients with the alpha variant (appendix p 7). The sensitivity analyses in which the impact on the results was assessed after adjustment for alternative

region or calendar period variables, symptomatic status, analyses of subgroups, or after varying the outcome definitions are shown in the appendix (pp 8–9). The estimated risk for both categories of hospital attendance outcomes was higher for patients with the delta variant than for patients with the alpha variant in all sensitivity analyses. The differences were consistently statistically significant, except the subgroup analysis by symptom status, in which the CIs were wider, and in some instances included 1.

Discussion

New SARS-CoV-2 infections in England are increasingly caused by the delta variant. Although the proportion of cases caused by the delta variant was 20% overall during the study period, this increased to 74% of new sequenced cases in the week starting May 31, 2021.[9] To our knowledge, this study provides the largest whole-genome-sequencing dataset for SARS-CoV-2 in a high-income country to date, enabling the assessment of hospitalisation risk for the delta variant compared with the alpha variant using linked administrative data. The results suggest that patients with the delta variant had more than two times the risk of hospital admission compared with patients with the alpha variant. Emergency care attendance combined with hospital admission was also higher for patients with the delta variant, showing increased use of emergency care services as well as inpatient hospitalisation. Similar results were observed for the subgroup of unvaccinated patients when comparing risks of both hospital care outcomes between the two variants. In the subgroup of patients who had received at least one vaccine dose (≥21 days since their first dose), the precision was too low to determine whether the risks of the outcomes were higher or similar for patients with the delta variant compared with patients with the alpha variant. It has previously been reported that vaccination leads to a similar relative reduction in the risk of hospitalisation for patients with the delta variant or the alpha variant.[12] This is consistent with the findings in the present study: overall, the number of hospital attendances were low in the vaccinated subgroup resulting in low-precision relative risk estimates.

This analysis is strengthened by using national, timely datasets on COVID-19 cases, hospital care episodes, and vaccinations. The individual-level data included all laboratory-confirmed COVID-19 cases, up to 98% of hospital activity, and all vaccinated individuals registered with a general practitioner in England,[14,18,25] with these data updated daily. Whole-genome sequencing coverage in England increased throughout the study period: for new positive tests between April 23 and May 24, 2021, more than 60% were successfully sequenced.[9]

Compared with a matched study design, the stratified Cox regression method offers the advantage of using all potential matches rather than a fixed number of patients with the alpha variant per patient with the delta variant. Confounders such as changing demographic profiles of

	Overall (n=43 338)	Alpha variant (B.1.1.7; n=34 656)	Delta variant (B.1.617.2; n=8682)
Age, years			
<10	3564 (8·2%)	2671 (7·7%)	893 (10·3%)
10–19	9462 (21·8%)	7373 (21·3%)	2089 (24·1%)
20–29	7636 (17·6%)	6183 (17·8%)	1453 (16·7%)
30–39	9157 (21·1%)	7364 (21·2%)	1793 (20·7%)
40–49	6885 (15·9%)	5588 (16·1%)	1297 (14·9%)
50–59	3916 (9·0%)	3196 (9·2%)	720 (8·3%)
60–69	1681 (3·9%)	1375 (4·0%)	306 (3·5%)
70–79	584 (1·3%)	495 (1·4%)	89 (1·0%)
≥80	453 (1·0%)	411 (1·2%)	42 (0·5%)
Sex			
Female	22 162 (51·1%)	17 913 (51·7%)	4249 (48·9%)
Male	21 176 (48·9%)	16 743 (48·3%)	4433 (51·1%)
Ethnicity			
White	30 152 (69·6%)	25 940 (74·8%)	4212 (48·5%)
Black	1183 (2·7%)	854 (2·5%)	329 (3·8%)
Asian	8416 (19·4%)	5130 (14·8%)	3286 (37·8%)
Mixed, other, or unknown	3587 (8·3%)	2732 (7·9%)	855 (9·8%)
Region of residence within England			
London	3854 (8·9%)	2601 (7·5%)	1253 (14·4%)
East midlands	5021 (11·6%)	4309 (12·4%)	712 (8·2%)
East of England	3808 (8·8%)	2771 (8·0%)	1037 (11·9%)
North east	2519 (5·8%)	2385 (6·9%)	134 (1·5%)
North west	10 561 (24·4%)	6354 (18·3%)	4207 (48·5%)
South east	2381 (5·5%)	1933 (5·6%)	448 (5·2%)
South west	723 (1·7%)	573 (1·7%)	150 (1·7%)
West midlands	4135 (9·5%)	3645 (10·5%)	490 (5·6%)
Yorkshire and Humber	10 336 (23·8%)	10 085 (29·1%)	251 (2·9%)
Index of multiple deprivation, quintile*			
1	14 480 (33·4%)	11 476 (33·1%)	3004 (34·6%)
2	9474 (21·9%)	7517 (21·7%)	1957 (22·5%)
3	7326 (16·9%)	5997 (17·3%)	1329 (15·3%)
4	6737 (15·5%)	5413 (15·6%)	1324 (15·2%)
5	5321 (12·3%)	4253 (12·3%)	1068 (12·3%)
Calendar week of specimen in 2021			
March 29–April 4	7606 (17·6%)	7593 (21·9%)	13 (0·1%)
April 5–April 11	5635 (13·0%)	5568 (16·1%)	67 (0·8%)
April 12–April 18	4806 (11·1%)	4673 (13·5%)	133 (1·5%)
April 19–April 25	4774 (11·0%)	4431 (12·8%)	343 (4·0%)
April 26–May 2	4690 (10·8%)	4058 (11·7%)	632 (7·3%)
May 3–May 9	4985 (11·5%)	3608 (10·4%)	1377 (15·9%)
May 10–May 16	4752 (11·0%)	2608 (7·5%)	2144 (24·7%)
May 17–May 23	6090 (14·1%)	2117 (6·1%)	3973 (45·8%)
Vaccination status at date of specimen			
Unvaccinated	32 078 (74·0%)	25 823 (74·5%)	6255 (72·0%)
<21 days after first vaccination dose	2632 (6·1%)	2206 (6·4%)	426 (4·9%)
≥21 days after first vaccination dose	7834 (18·1%)	6172 (17·8%)	1662 (19·1%)
≥14 days after second vaccination dose	794 (1·8%)	455 (1·3%)	339 (3·9%)
Recent international travel within 14 days before specimen			
No	41 435 (95·6%)	33 218 (95·9%)	8217 (94·6%)
Yes	1903 (4·4%)	1438 (4·1%)	465 (5·4%)

(Table 1 continues on next page)

	Overall (n=43 338)	Alpha variant (B.1.1.7; n=34 656)	Delta variant (B.1.617.2; n=8682)
(Continued from previous page)			
Symptom status at the time of specimen			
Asymptomatic	18 593 (42·9%)	14 934 (43·1%)	3659 (42·1%)
Symptomatic	22 091 (51·0%)	17 757 (51·2%)	4334 (49·9%)
Unknown	2654 (6·1%)	1965 (5·7%)	689 (7·9%)

Data are n (%). *Quintiles are ranked from most deprived (quintile 1) to least deprived (quintile 5).

Table 1: **Observed number and proportion of cases by variant and patient characteristics**

	Alpha variant (B.1.1.7)	Delta variant (B.1.617.2)	HR (95% CI), delta variant *vs* alpha variant	
			Unadjusted	Adjusted*
Hospital admission within 14 days after specimen	764/34 656 (2·2%)	196/8682 (2·3%)	1·03 (0·88–1·21)	2·26 (1·32–3·89)
Hospital admission or emergency care attendance within 14 days after specimen	1448/34 656 (4·2%)	498/8682 (5·7%)	1·39 (1·25–1·53)	1·45 (1·08–1·95)

Data are n/N (%) except where otherwise stated. HR=hazard ratio. *Stratification for age group, ethnicity, lower-tier local authority, calendar week of specimen, vaccination status; regression adjustment for age (linear), date (linear), sex, index of multiple deprivation, and international traveller status.

Table 2: **Hospitalisation outcomes for patients with the delta variant compared with patients with the alpha variant**

	Alpha variant*	Delta variant*	Adjusted HR (95% CI)†, delta variant *vs* alpha variant	p value‡
Hospital admission				
Unvaccinated or <21 days after first vaccination dose	536/28 029 (1·9%)	149/6681 (2·2%)	2·32 (1·29–4·16)	..
≥21 days after first vaccination dose with or without second vaccination dose	228/6627 (3·4%)	47/2001 (2·3%)	1·94 (0·47–8·05)	0·82
Hospital admission or emergency care attendance				
Unvaccinated or <21 days after first vaccination dose	1095/28 029 (3·9%)	369/6681 (5·5%)	1·43 (1·04–1·97)	..
≥21 days after first vaccination dose with or without second vaccination dose	353/6627 (5·3%)	129/2001 (6·4%)	1·58 (0·69–3·61)	0·82

Data are n/N (%) except where otherwise stated. HR=hazard ratio. *These crude descriptive frequencies are unadjusted for age and other confounders, and so they are not directly comparable between the groups. †Stratification for age group, ethnicity, lower-tier local authority, calendar week, vaccination status; regression adjustment for age, sex, index of multiple deprivation, specimen date, and international travel status. ‡p values are for tests for interaction between vaccination status and variant.

Table 3: **Hospitalisation outcomes for patients with the delta variant compared with patients with the alpha variant, by vaccination status**

patients by variant or local interventions over time are accounted for. However, this method results in a loss of informative observations when stratifying by many covariates, reducing precision compared with estimates based on adjustment through regression modelling.

Administrative data have several limitations in this context. First, hospital admission data received via SUS can have a reporting delay due to monthly submission periods, which could lead to confounding. This delay and potential confounding was mitigated by both using more rapid ECDS data to identify hospital admissions via presentation to emergency care and stratification by calendar time. The confounder post-evaluation found that the HRs were most changed by adjustment for calendar week, indicating that the unadjusted estimates were indeed confounded by registration delays or other calendar-period-specific factors. Also, given regression adjustment on specific calendar date, residual confounding due to registration delays seems unlikely and is expected to affect the more recent delta cases primarily, causing a slight underestimation of the HRs. Second, there was suboptimal information on the reason for a hospital visit, preventing conclusive attribution of attendance or admission to COVID-19. However, some data flags such as injury-related attendance and ICD10 codes were used as proxies to define outcomes in the primary analysis. Nevertheless, non-COVID-19-related visits might have been included, resulting in a slight underestimate of the HRs because this misclassification is not expected to differ by variant. A strength of considering alternative outcomes is that different categories of hospital use, which could indicate levels of disease severity, have been assessed; these sensitivity analyses showed some variation in HRs but estimated risks were consistently higher for patients with the delta variant than with the alpha variant. Finally, there were no available data on comorbidities, which are known to contribute to hospitalisation risk.[24] This study instead indirectly accounted for comorbidities using related covariates, including age, sex, ethnicity, and deprivation.[26]

Linkage was not possible for all sequenced cases due to missing NHS numbers. 5634 (11·3%) of 49 930 sequenced cases during the study period were excluded for this reason. International travellers and minority ethnic groups were overrepresented among patients with missing NHS numbers. These groups were also overrepresented in the delta variant group compared with the alpha variant group. Although there are no data to suggest that the hospital attendance or admission risk would systematically differ for the excluded individuals compared with their included peers, this cannot be ruled out.

Hospital use and admission risk might be influenced by heterogenous health-care-seeking behaviour and transmission across the variants, ethnic groups, and particularly over time and area. Changes over time in hospital admission policy might have occurred—eg, due to local hospital burden or increased use of at-home pulse oximeter monitoring.[27] Such changes might have resulted in reduced length of stay, with shorter stays less affected by reporting delays in more recent weeks. However, stratification for calendar week and area of residence should account for such differences.

The conditions for whole-genome-sequencing selection and successful sequencing might restrict the generalisability of the study findings. Samples that test positive by PCR are most likely to be successfully sequenced if they have a low enough cycle threshold value (<30), which might be more likely in patients with a high viral load. In addition, when comparing sequenced and non-sequenced samples in the study period, there was an overrepresentation in sequenced samples from patients in younger age groups and from areas in northern England. This is likely to be due to geographic area-based increases in sequencing to understand the initial outbreaks of the delta variant. There was also a higher proportion of pillar 2 (ie, community-based) samples that were sequenced compared with samples taken through pillar 1 (public health and hospital testing and routine screening).[28] Despite the potential that a higher proportion of delta variant samples might have been sequenced due to increased regional coverage, slightly higher ascertainment is not likely to have significantly reduced detection of the alpha variant because alpha was the most prevalent variant throughout March and April, 2021. The same sequence-quality metrics were also applied across all samples and the area-level sampling would have included a mixture of individuals with the alpha variant and individuals with the delta variant. There was no expected sample prioritisation by variant based on clinical status, particularly as most sequenced samples were from community testing.

During the study period, the incidence of the delta variant in England was increasing, and so individuals with shorter times from infection to positive test (ie, more recent infections) might be overrepresented among those who tested positive. By contrast, the incidence of the alpha variant was decreasing during the study period, and so individuals with longer times to positive test (ie, less recent infections) are likely to be overrepresented.[29] Time from infection to testing positive among the patients in this study might be dependent on symptoms that prompt someone to be tested, because most the study population had community (pillar 2) testing, rather than routine testing in hospital or for screening (pillar 1). People who test quickly might be more likely to have earlier or more symptoms than people who test less quickly, suggesting that their disease progression might have been both faster and more severe. This differential selection of patients with potentially more severe symptoms from the delta variant and patients with less severe symptoms from the alpha variant might result in an overestimation of the HRs. However, this bias might be mitigated by the overall preferential selection of patients with low cycle threshold values (higher viral load), that might affect the alpha and delta variant groups similarly. Furthermore, the estimated HRs were similar for patients who were asymptomatic at the time the specimen was taken, for whom the time from infection to test is unlikely to reflect differences in test-seeking behaviour. To address this bias, incidence would need to be modelled jointly with severity.

The impact of the delta variant within India has been substantial. Alongside high infection incidence, major cities also experienced overwhelming hospital burden leading to shortages of supplies and life-saving equipment.[6] However, there has been little research done to quantify the hospitalisation risk for patients with this variant. The EAVE II study is a recent, large-scale study reporting on the hospital admission risk for patients with the delta variant in Scotland.[30] Based on record-linkage of routine health-care data, it used S-gene target detection through diagnostic tests as a proxy for delta compared with the alpha profile that includes S-gene target failure. Their results showed an adjusted HR of hospital admission of 1·85 (95% CI 1·39–2·47), which is consistent with the HR of 2·26 (1·32–3·89) estimated in this study.

Supplementary sensitivity analyses provide assurance regarding the robustness of outcomes; however, future work should include metrics based on richer but less timely data on severe COVID-19 outcomes, such as length of hospital stay, admission to intensive care, or indicators of critical illness. Further work is also needed to measure the risk of mortality due to the delta variant, as a large proportion of the cohort included in this study was still within the 28-day follow-up period when analysis was done.

To our knowledge, this study is the largest assessment of hospitalisation risk for the delta variant using cases confirmed by whole-genome sequencing, providing important foundational evidence of increased risk compared with the alpha variant. Before the emergence of the delta variant, the evidence base largely focused on the alpha variant and its higher transmissibility and severity when compared with previous wildtype strains.[2,3,31–33] Further research is needed to clarify if the hospitalisation risks differ in vaccinated individuals infected with the delta variant compared with the alpha variant; however, a previous study has estimated low hospitalisation risks for vaccinated individuals after infection with either variant.[12] Together, these two studies suggest that outbreaks of the delta variant in unvaccinated populations might lead to a higher health-care burden, particularly compared with the previous prevalent SARS-CoV-2 strains. The findings are key for resource planning and policy decisions to mitigate the impact of the delta variant in the UK, where the delta variant now dominates, and in other high-income countries where the rapid spread of the delta variant might occur.

Contributors

KAT, TN, AZ, ST, MAS, SA, RJH, AC, DDA, AMP, and GD designed the study. RH, JL-B, and EG contributed to data collection and creation of data resources. KAT and AZ checked and verified the dataset and prepared it for analysis. TN did the statistical analysis, with support from SRS, KAT, ST, RJH, DDA, and AMP. AMP, AC, and DDA acquired funding. KAT, TN, AZ, ST, MAS, SA, AMP, and GD wrote the manuscript. SRS, RJH, RH, JL-B, EG, AC, and DDA reviewed and edited the manuscript. AMP and GD supervised the work. All authors had full access to all the data in the study and had final responsibility for the decision to submit for publication.

Declaration of interests
GD's employer, Public Health England, has received funding from GlaxoSmithKline for a research project related to seasonal influenza and antiviral treatment; this project preceded and had no relation to COVID-19, and GD had no role in and received no funding from the project. All other authors declare no competing interests.

Data sharing
This analysis was based on routine health-care data, which cannot be made available to others by the study authors. Requests to access these non-publicly available data are handled by the Public Health England Office for Data Release.

For the **Public Health England Office for Data Release** see https://www.gov.uk/government/publications/accessing-public-health-england-data/about-the-phe-odr-and-accessing-data

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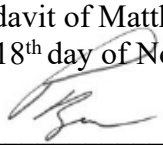
This is **"Exhibit N"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



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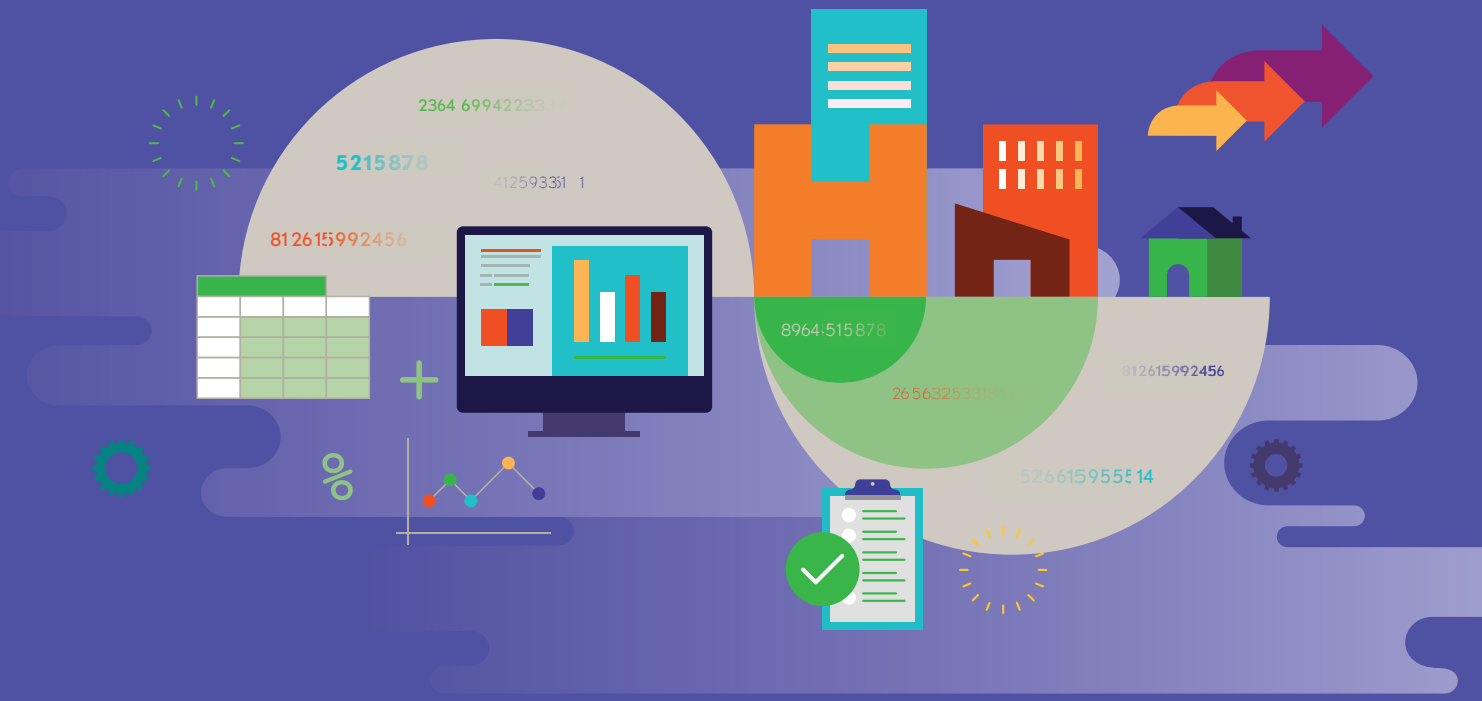
A Commissioner, etc.

Ontario Hospitals - Leaders in Efficiency

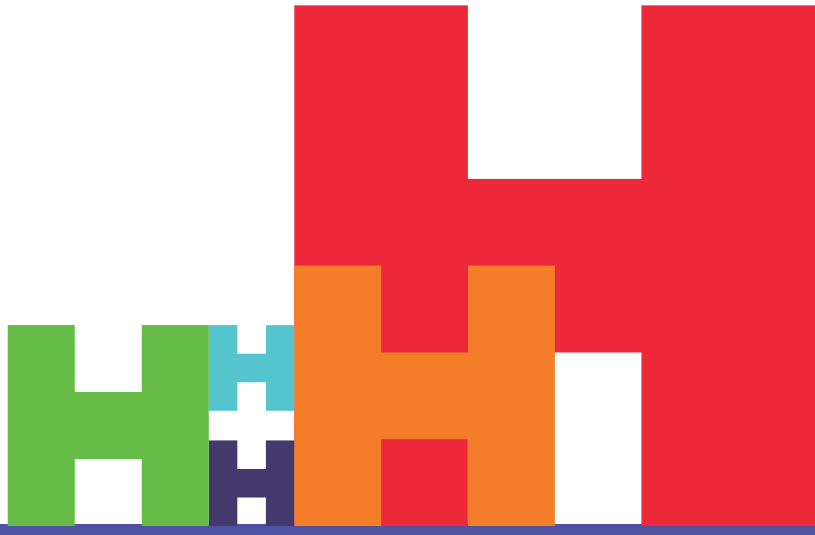
DECEMBER 2019



Ontario Hospital Association

This report provides key information and context regarding Ontario hospitals' long track record of efficiency as well as the significant pressures they are facing today.

Through a brief narrative, together with supporting evidence in the form of a series of descriptive charts, the report offers a wider-lens view of the hospital sector's past and present state.



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Hospital Efficiency in Context

Health care reform paired with fiscal restraint presents a challenge

Ontario's health care system has entered a new period of major reform, which will require years to complete. All providers will be impacted as the system continues to change to become more patient-focused, better integrated and even more efficient in serving a growing and aging population. At the same time, Ontario is facing a new cycle of fiscal restraint as the provincial government aims to eliminate the current $9 billion budget deficit by 2023-24[1]. This new budgetary plan falls on the heels of the previous decade of restraint that was sparked by the 2008 financial crisis. Continued financial challenges will potentially be faced across a full range of provincial programs, including the health care sector.

Hospitals have always been at the forefront of efficiency and improvement efforts

With pressure to find short-term financial savings, there will be a heightened interest in focusing on hospitals. This has always been the case. Hospitals comprise the single largest sector within health care, which itself is the largest government budget item. In past decades, during times of fiscal challenge, Ontario hospitals have been at the forefront of efforts to 'bend the cost curve' — efforts that were over and above ongoing work to continuously improve patient care and operational performance. It could be argued that no other public sector — in health care or otherwise — has been more frequently or consistently at the centre of performance improvement work. Ontario hospitals' embrace of the Quality Management movement in combination with funding methods that promote efficiency have been important factors in achievements throughout the years.

Ontario hospitals are the most efficient in Canada

Because of these efforts, several key performance measures show clearly that Ontario hospitals have long been the most efficient in Canada. If Ontario were to fund hospitals at the average rate per capita for all other provinces, it would cost the province an additional $4 billion[2]. In fact, Ontario's overall health system was recently recognized by the Blue Ribbon Panel on Alberta's Finances[3] as a model to emulate due to the significantly lower cost of providing high quality care — owing in large part to the hospital component of health spending.

Despite several years of funding restraint, hospitals continue to uphold and streamline services in every possible way in order to maintain and meet increasing demand for care. Hospitals face daily challenges of crowded emergency departments (EDs), high occupancy and difficulties in discharging Alternate Level of Care (ALC) patients who are waiting for more appropriate services provided in a different setting. These challenges are not surprising given that Ontario (in a tie with Mexico) has the fewest acute care hospital beds per capita in the world.

Hospitals are meeting increased demand despite capacity and inflationary cost pressures

In addition to physical capacity limitations, hospitals face cost pressures and constraints over which they have little control. Wage settlements (with labour comprising almost 70% of hospital costs) and other inflationary pressures continue to increase. Hospitals have managed these pressures through responsible collective bargaining both in terms of process and results. Hospitals have developed a province-wide central bargaining process that avoids having to conduct almost 400 separate negotiations, which would otherwise cost hospitals approximately $33 million. Further, this efficient approach has also resulted in collective bargaining outcomes consistently below broader public sector wage trends.

Despite these moderate labour cost increases, hospitals have found ways to address their collective situation using innovation, new technologies and new ways to deliver care. In addition, and for good reason, hospitals must comply with many regulatory and other responsibilities that span a range from essential health and safety requirements all the way through to a variety of mandatory policies and practices which may no longer hold value.

Further hospital budget tightening will cause significant strain unless overall system capacity is addressed first

Given the current state, the prospect of achieving significant further improvement in the hospital sector without **first addressing** issues outside the sector is slim. While the ALC issue — representing 17% of beds — is an inefficient use of hospitals, it stems from overall health system issues. The lack of alternatives to hospital care for ALC patients — that are less costly and better for patients — has led to severe hospital capacity pressures. Accordingly, attempts to squeeze out any more perceived hospital inefficiencies — **with existing system structure and capacity** — will likely worsen hallway health care. The very real risk is that access to hospital care will become even more difficult and wait times will continue to rise.

Ontario hospitals have been voicing this concern for several years under relatively flat funding increases. (In some years, mid-year funding relief was necessary to support hospitals in meeting unprecedented surges in patient demand.) Hospitals' current pressures and high level of efficiency is the reality and is borne out by the evidence presented below. There is clearly no significant 'low-hanging fruit' to be found in the hospital sector alone. Much greater gains can be realized by addressing system organization and capacity as a whole. In doing so, proper timing and sequencing of events will be critical.

The benefits of structural change will take years to realize

As stated, health care reform is just beginning and will take years. At the same time, as Ontario Health Teams are announced, hospitals will need to be bolstered in order to "protect what matters most." It will be critical to shield hospitals and the broader health system from further financial erosion until key transformative change and potentially new investments have occurred. These changes and investments must have actual realized benefits — in terms of patient outcomes, patient experience, cost-savings (or cost-avoidance) and greater efficiency.

Ontario has been here before. In the early 1990s, a severe economic recession led to a decline in government revenues. For the first time ever, in 1993-94, provincial government expenditure on hospitals declined from the previous year. As cuts continued for several more years, hospitals rose to the challenge. Hospital bed numbers were cut by a third, innovation fostered a switch to more day procedures, lengths of stay were shortened and other general operational efficiencies occurred.

Ontario's experience with restructuring and budget tightening in the 1990s

In late 1995, the Ontario government announced the creation of the Health Services Restructuring Commission (HSRC) which would formally reorganize hospitals and services over four years. **At the same time**, a total of $1.3 billion in hospital funding cuts over three years were announced which represented 5% ($365 million), 6% ($435 million) and 7% ($507 million) each year starting in 1996/97.[4] Given the efficiencies already achieved, only the first two years of cuts could be made, and the third year was cancelled in order to both protect patient care and maintain hospital financial stability. At the time of the HSRC, there was the ability to consolidate and reduce the number of hospital corporations from 225 to 156. (Presently in 2019 there are 141 hospital corporations led by 126 CEOs.) However, the efficiencies that were sought through mergers and clinical program shifts were not realized until future years. The original restructuring budget of $450 million was increased to $880 million by 1997.[5] A key lesson was that a coordinated strategy for restructuring and cost cutting — as well setting realistic time lines — was essential to system stability and access to care.

Ontarians need a strong and stable hospital and health care system

In summary, Ontario hospitals are fiscally responsible and have always strived to maintain access to high quality care for the communities they serve. Ontario hospitals lead the country with their long-standing, lean operational performance. However, they are clearly showing the strain of a combination of years of funding restraint, significant demographic growth and a shortage of capacity in other health sectors. Hallway health care and record-high levels of ALC patients and ED wait times are among the most visible signs of a hospital system under severe pressure and are directly experienced by individual patients and their families. The current situation cannot realistically be sustained. As the Ontario government aims to achieve dual goals of deficit elimination by 2023 and initiation of important health system change, it will be critical to ensure that the necessary supports are in place to uphold hospital and health system stability — and ultimately, access to high quality care for Ontarians.

The Evidence

The section that follows offers key evidence of Ontario hospitals' current and past record of high performance as well as that of the pressures that have been building over the past few years.

Ontario Hospitals are Fiscally Responsible

SAVINGS

Ontario hospital budgets reflect the **lowest hospital expenditure per capita by a provincial government.** If Ontario were to fund hospitals at the average rate per capita for all other provinces it would cost the province an **additional $4 billion**; if funded like Alberta, **$7.1 billion**.

Ontario hospitals contribute to the:

- **Second-lowest** health care expenditure per capita by a province; and the
- **Lowest** provincial program expenditure per capita by a province

How Ontario Hospitals Have Done This

CLINICAL INNOVATION

Continuous improvement has led to Ontario having the:

- **Shortest** average length of stay in acute care hospitals in Canada
- **Lowest** hospitalization rate in Canada

Which results in the:

- **Lowest** number of beds per 1,000 population than any other province or country
- **Lowest** cost of a hospital inpatient stay in Canada

Hospital bed numbers have not changed in two decades although:

- Ontario population has increased 27%
- Population aged 65 and older has increased 75%

LEADERS

Hospitals have achieved these results while:

- **Increasing** volumes year-over-year despite inflation not being fully funded
- **Maintaining** the lowest cost per hospital stay
- **Maintaining** quality over time

System Capacity Issues

EVEN IN DIFFICULT TIMES

Hospitals face **record-setting**:

- Emergency department wait times
- Number of patients waiting in emergency to be admitted
- Number of ALC patients waiting in hospital for more appropriate services

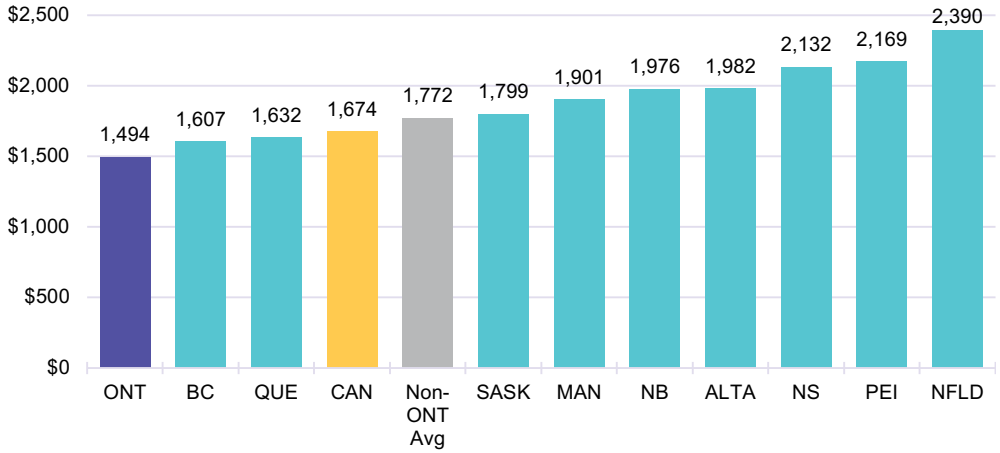
Ontario Government Hospital and Health Spending in Context

Hospital Expenditure

Per capita hospital expenditure by provincial governments is lowest in Ontario

Provincial government expenditure on hospitals is lower in Ontario than in any other province at $1,494 per capita for 2019. If Ontario were to fund hospitals at the average rate per capita for all other provinces ($1,772) it would cost the province an additional $4 billion. This is the Ontario hospital efficiency dividend.

Figure 1a
Hospital Expenditure, $ per Capita by Provincial Governments, 2019

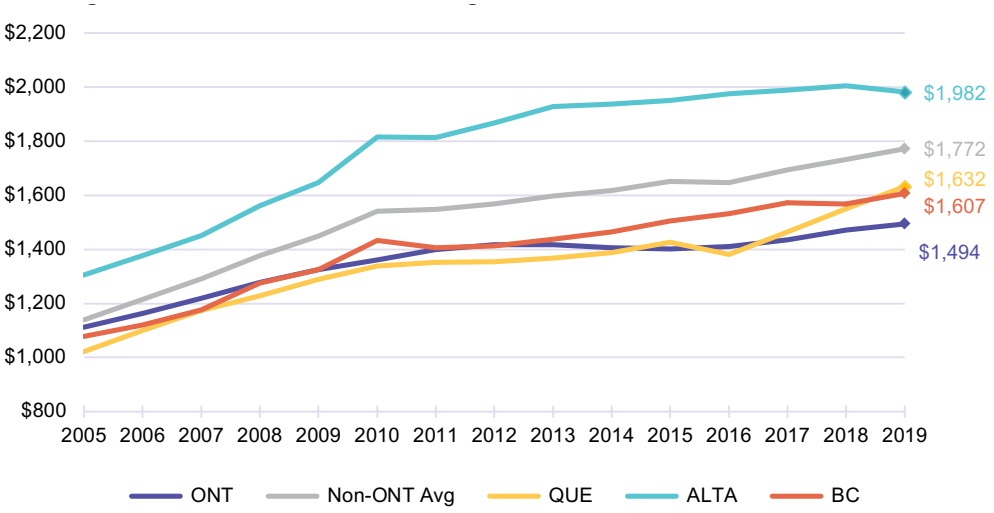


Source: CIHI National Health Expenditure Database, 2019 forecast, Canada includes Territories

Per capita hospital expenditure in Ontario has been far lower than in most other provinces for many years

For many years, Ontario's hospital expenditure has been very low. In comparison, Quebec's ability to keep expenditure low has been attributed to overall lower hourly rates for nurses which are also lower than in Ontario.

Figure 1b
Hospital Expenditure, $ per Capita by Provincial Governments, 2005-2019
Four Largest Provinces & Non-Ontario Average



Source: CIHI National Health Expenditure Database, 2018 & 19 are forecast

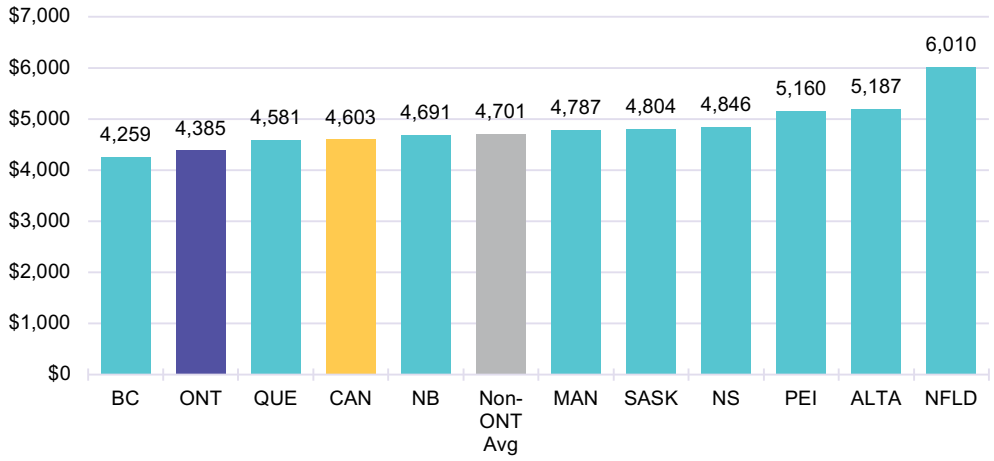
Health Care Expenditure

Per capita health care expenditure by provincial governments is second-lowest in Ontario

Ontario's provincial government total health care expenditure for all sectors combined is the second-lowest of all the provinces at $4,385 per capita for 2019. If Ontario were to fund health care at the average rate per capita for all other provinces ($4,701), it would cost the province an additional $4.6 billion. This is the Ontario health care efficiency dividend.

Sectors include: hospitals, physicians, drugs, public health, other institutions, other professionals, home care, capital, research, health system administration and other.

Figure 2a
Health Care Expenditure, $ per Capita by Provincial Governments, 2019

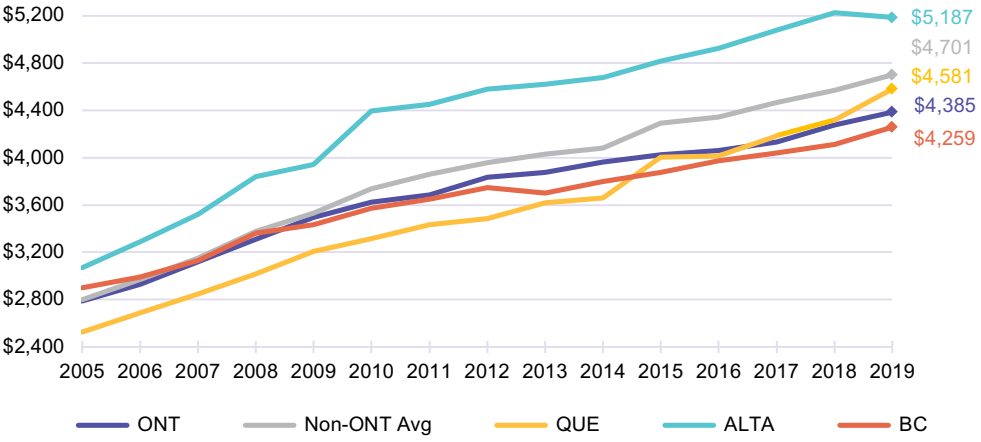


Source: CIHI National Health Expenditure Database, 2019 forecast, Canada includes Territories

Per capita health care expenditure in Ontario has been in the lowest range in Canada for many years

Ontario has been the second-lowest for total health care expenditure for the past three years and has been below the average for all other provinces since 2005.

Figure 2b
Health Care Expenditure, $ per Capita by Provincial Governments, 2005-2019
Four Largest Provinces & Non-Ontario Average



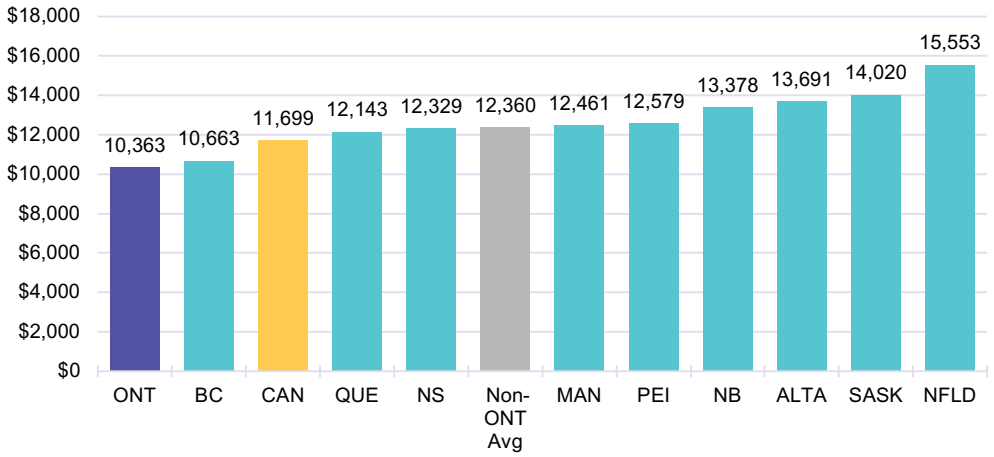
Source: CIHI National Health Expenditure Database, 2018 & 19 are forecast

Provincial Government Program Expenditure

Per capita provincial government program expenditure is lowest in Ontario

Provincial government expenditure for all programs combined (e.g., health, education, transportation, social services, justice and others) is lower in Ontario than in any other province at $10,363 per capita for 2017 (latest year available). If Ontario were to fund provincial programs at the average per capita rate for all the other provinces ($12,360) it would cost the province an additional $28 billion.

Figure 3a
Provincial Government Program Expenditure, $ per Capita, 2017

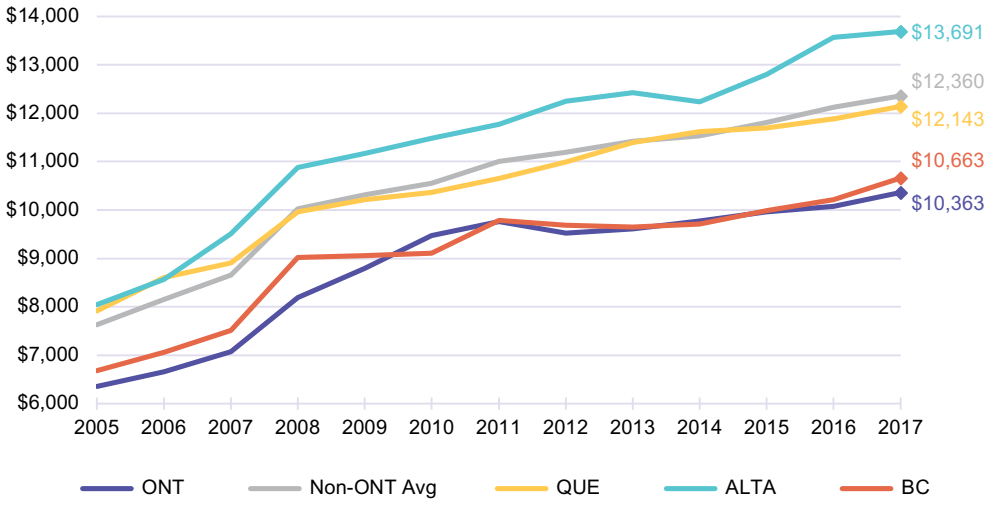


Source: CIHI National Health Expenditure Database, 2017 (latest year available) Canada includes Territories

Per capita provincial government program expenditure in Ontario has been the lowest in Canada over many years

From 2005 to present, provincial government expenditure on all programs combined has been the lowest in Ontario in all but two years (including provinces not shown).

Figure 3b
Provincial Government Program Expenditure, $ per Capita, 2005 to 2017
Four Largest Provinces & Non-Ontario Average



Source: CIHI National Health Expenditure Database, 2017 (latest year available)

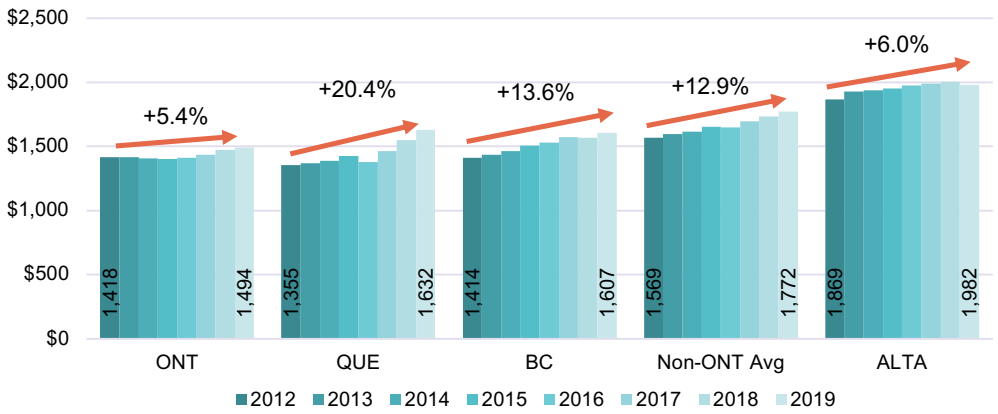
Hospital Funding, Cost Pressures and Hospital Unit Cost

Ontario's constrained hospital funding has been outpaced by inflation and population pressures

A closer review of provincial government hospital funding over recent years reveals hospital financial pressures and lean operations. During a decade of restraint, Ontario hospitals faced four consecutive years of 0% increases in base operating funding from 2012/13 to 2015/16. (Base funding is the main funding envelope supporting basic requirements and excludes specialized programs or specific targeted funding.)

The overall seven-year, per-capita increase in government funding to hospitals between 2012 and 2019 was 5.4%. Within this 5.4% increase, Ontario hospitals absorbed inflationary costs due to labour agreements plus rising costs of supplies, medications and equipment. The per capita calculation does not take into account the impact of population aging which has further increased the pressure on hospitals.

Figure 4
Hospital Expenditure, $ per Capita – Seven-year Trend, 2012 to 2019
Four Largest Provinces & Non-Ontario Average

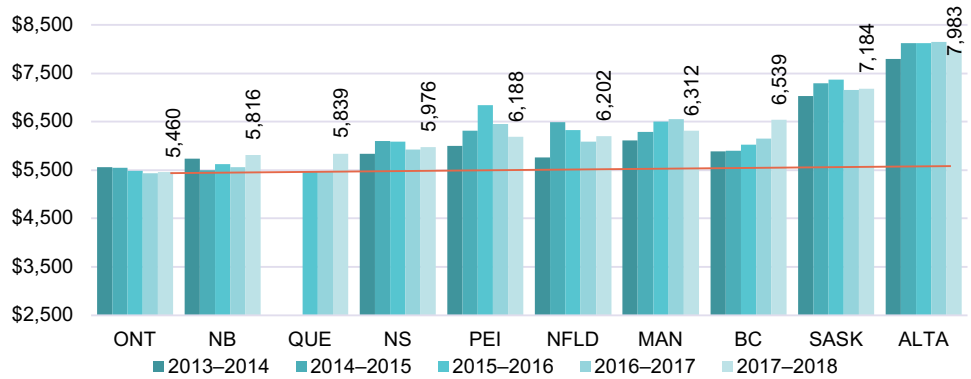


Source: CIHI National Health Expenditure Database, 2018 & 19 are forecast

Ontario has the lowest-cost hospital inpatient stay of all the provinces

Further, in comparison to all other provinces, Ontario has the lowest cost of an inpatient hospital stay, which has been getting lower over the years.

Figure 5
Cost of a Hospital Inpatient Stay in $, by Province, 2013-14 to 2017-18



Source: CIHI Your Health System - In Depth

Hospital Wage Settlements

Ontario hospitals have taken a responsible approach to compensation

Recent Collective Bargaining Outcomes

The provision of health care is labour-intensive. With approximately 70% of hospital costs attributed to labour, collective bargaining outcomes have a large impact on future hospital cost pressures.

The highly efficient central bargaining process for Ontario hospitals has resulted in recent wage settlements at levels that are below those experienced in the broader public sector.

Figure 6
Recent Collective Bargaining Outcomes (Hospitals) Compared to Relevant Average Outcomes of Other Major Ontario Broader Public Sector (BPS) Employers

Year	Hospital Average	Major BPS Average
2016	1.03%	1.33%
2017	1.40%	1.39%
2018	1.40%	1.85%
2019	1.68%	1.75%
Average over Four Years	1.38%	1.58%

Source: Ontario Hospital Association

Ontario Hospital Bed Capacity and Usage

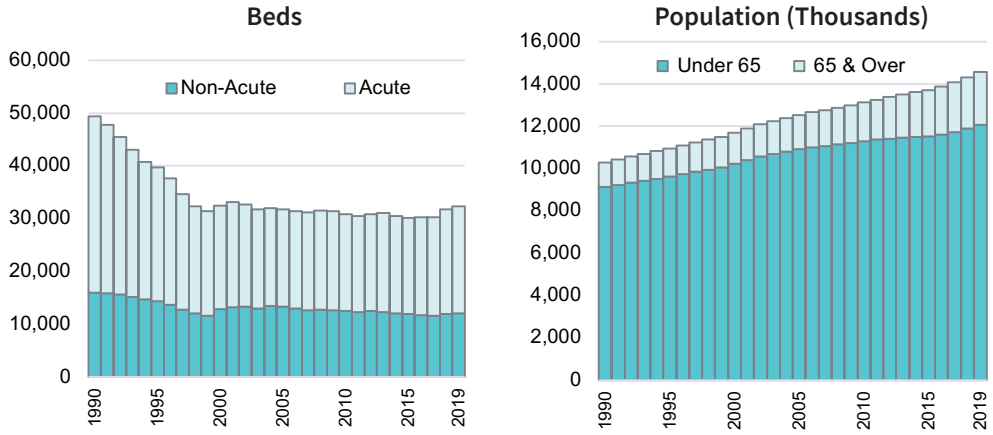
Beds vs. Population

Ontario hospital bed capacity has not changed over the past two decades although the population has increased 27%

An overall per capita bed reduction has been observed worldwide over two decades. In Ontario, beds declined sharply through the 1990s in response to fiscal restraint, hospital restructuring and technological change. Since 1999, overall bed capacity has been virtually constant although the population has increased by 27%. In the past two years, a small increase in beds occurred in order to relieve extreme occupancy pressures. Recently, new strategies to manage tight capacity have been adopted that involve ground-breaking methods to specifically improve patient flow and surgical scheduling processes.

The population aged 65+ has increased 75%

Figure 7
Ontario Hospital Bed Capacity vs. Population, 1990 to 2019

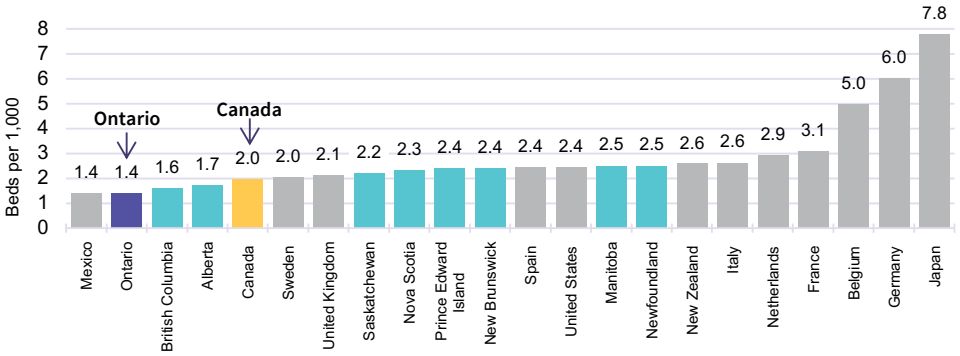


Sources: Ontario Ministry of Health and Long-Term Care Daily Census Data; Statistics Canada Population Data

Ontario is tied with Mexico for the lowest number of acute care beds per 1,000 population

Ontario has fewer acute hospital beds per 1,000 population than any other province and fewer beds than any other country in the world (tied with Mexico) that is tracked by the Organization for Economic Co-operation and Development (OECD). Ontario has 1.4 acute beds per 1,000 and 2.2 total beds per 1,000.

Figure 8
Acute Hospital Beds per 1,000 Population, 2015, 2016, 2017, 2018
Ontario vs. Other Provinces and Other Countries (Quebec data not available)



Sources: OECD Health Statistics; CIHI Hospital Beds; Statistics Canada Population Data; Ontario Ministry of Health and Long-Term Care Daily Census Data. Most recent year available for each jurisdiction shown.

How Hospitals have Managed — Shorter Stays, Fewer Hospitalizations

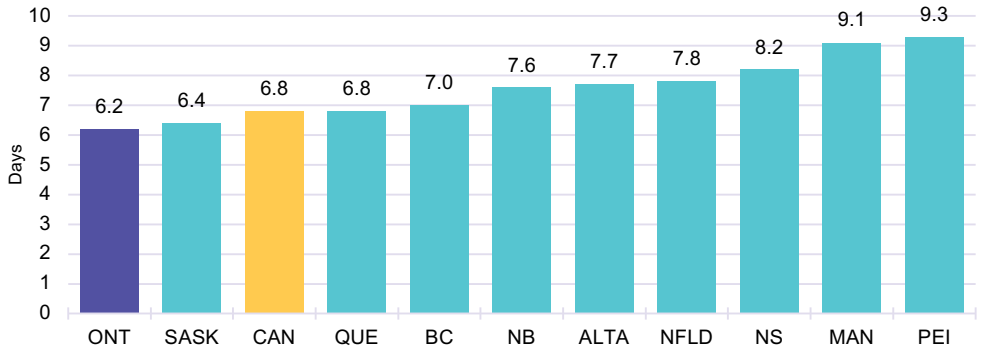
For many years, Ontario acute care hospitals have had the shortest average length of stay

Over time, hospitals have accommodated population growth and aging with fewer beds by: working to shorten hospital stays; working to reduce the need for hospitalizations (through greater use of same-day procedures and outpatient services) and; a host of other innovative quality and operational improvement efforts.

Figure 9a

Inpatient Average Length of Stay in Days, by Province, 2017-18

Acute Care Hospitals, Age Standardized



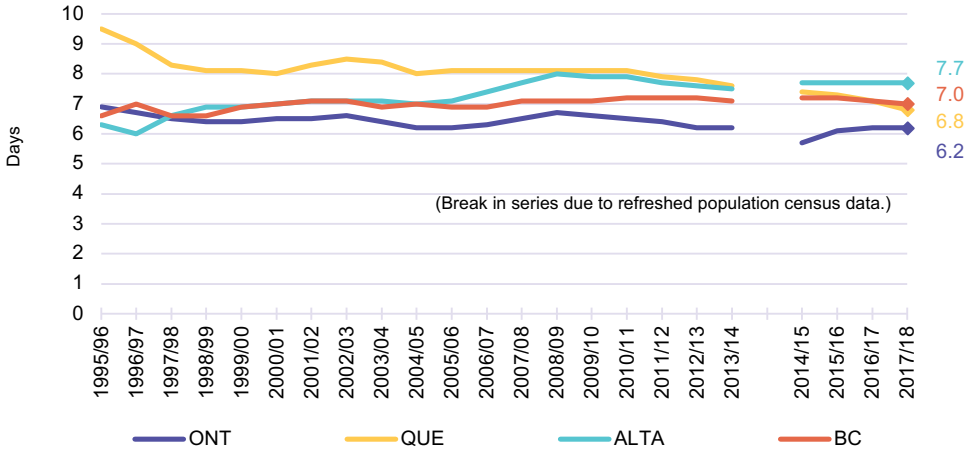
Source: CIHI Quick Stats

There are limits to how much and how fast lengths of stay can be reduced. For some types of patients, the average stay may even be longer today than it was in the past (if preventive care or outpatient care is more available, only the most acutely ill will need to be admitted to hospital). Among the four largest provinces, Ontario has had the shortest average length of stay since 1997/98. Compared to all other provinces (not shown), Ontario has had the lowest rate since 2010.

Figure 9b

Inpatient Average Length of Stay in Days, by Province, 1995-96 to 2017-18

Acute Care Hospitals, Age Standardized, Four Largest Provinces

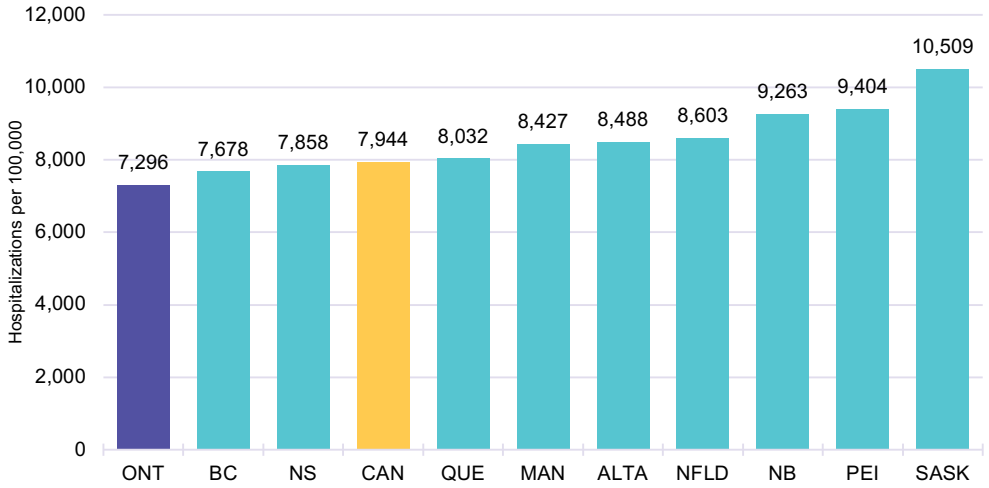


Source: CIHI Quick Stats

Ontario has had the lowest hospitalization rate in all years but one since 1995

Ontario has also had the lowest hospitalization rate among all provinces almost every year since 1995.

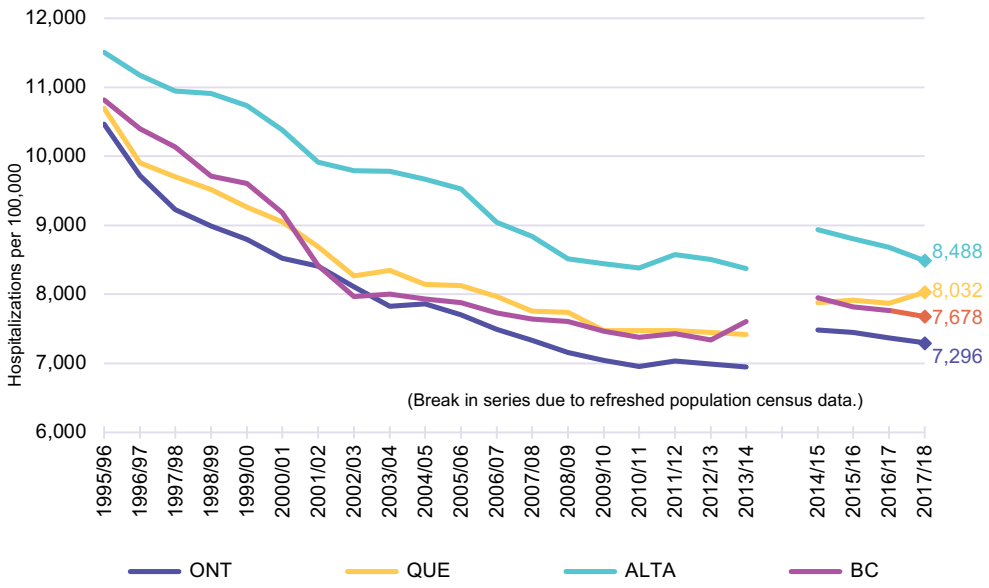
Figure 10a
Inpatient Hospitalization Rate per 100,000, by Province, 2017-18
Acute Care Hospitals, Age-Sex Standardized



Source: CIHI Quick Stats

The hospitalization rate has been dropping steadily since at least 1995.

Figure 10b
Inpatient Hospitalization Rate per 100,000, by Province, 1995-96 to 2017-18
Acute Care Hospitals, Age-Sex Standardized, Four Largest Provinces



Source: CIHI Quick Stats

Signs of Capacity Pressure

Alternate Level of Care

As system capacity pressures rise, timely access to care becomes more difficult

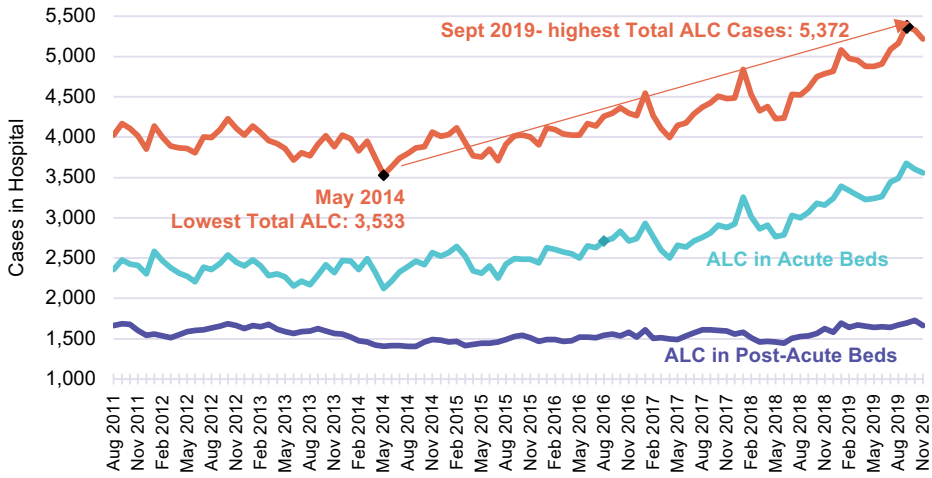
There are record-high numbers of ALC patients in Ontario hospitals. ALC is a major long-standing issue reflecting sub-optimal care and an inefficient use of hospital resources. The ALC problem reflects a lack of system capacity and lack of access to services outside the hospital.

In September 2019, there were 5,372 ALC patients — accounting for 17% of hospital beds — waiting for a different level of care that was not available when needed. The total number of days of stay in hospital for the patients waiting as of September 2019 was approximately 750,00 days which is a 25% increase from the almost 600,000 days for all ALC patients waiting in September 2018.

ALC cases are at record highs

A majority of ALC patients are waiting for a place in a long-term care facility while others are waiting for home care services, supervised or assisted living, rehabilitation, palliative care, mental health services or other services. Some ALC patients wait significantly longer for placement in an appropriate care setting due to the nature of their care needs.

Figure 11
Ontario ALC Cases (Total, Acute and Post-Acute), 2011-2019



Source: CCO

High ALC rates have a ripple effect: long ED wait times and high numbers of patients in ED waiting for a regular bed

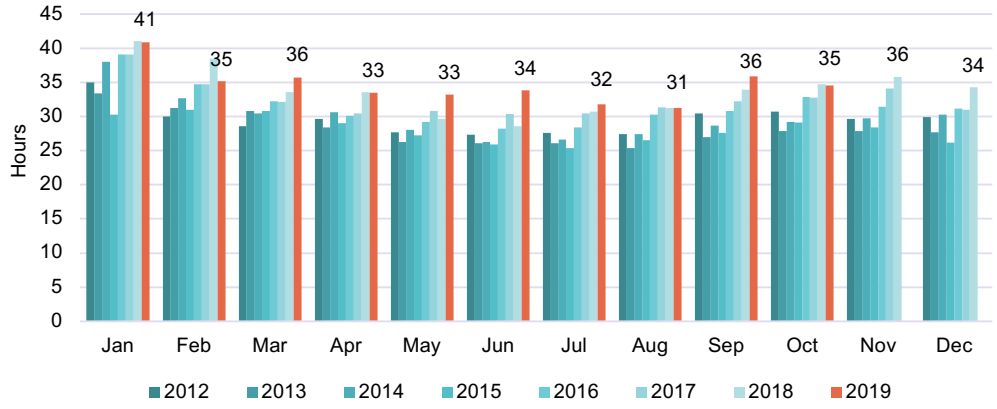
With more beds occupied by ALC patients, emergency department (ED) 'backups' worsen and become more frequent. Patients waiting in the ED face very long waits to be transferred to an appropriate patient care unit. Due to lack of physical capacity in the ED patients must often wait in a hallway bed or in another 'unconventional' location. In some severe cases, bed shortages may lead to cancelled elective surgeries.

Emergency Department

Long ED wait times are getting even longer

Long ED wait times are getting even longer. In Ontario in January 2019, 10% of patients waiting to be admitted as an inpatient waited over 41 hours while 90% waited under 41 hours. (This is called the '90th percentile' wait time.) Wait times vary depending on seasonal illness such as the flu. The Canadian Institute for Health Information (CIHI) tracks annual ED wait times (using a comparable measure) for four provinces: Ontario, Alberta, Quebec and B.C. Each province has seen an increase over time. In 2018-19, Ontario's 90th percentile wait time was 33.3 hours which is higher than Alberta's (at 27.1 hours) and lower than B.C.'s (at 42.4 hours) and Quebec's (at 39.9 hours).[6]

Figure 12
Ontario ED Wait Times in Hours for Admitted Patients, by Month, 90th percentile (90% of patients waited fewer hours, 10% waited more hours), 2012 to 2019

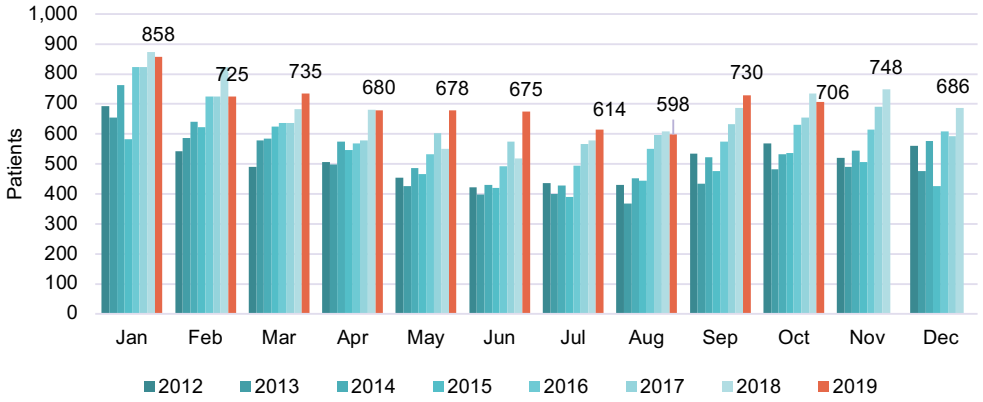


Source: CCO

Ontario EDs are busier than ever with higher numbers of patients waiting for inpatient beds

Over time, there have been increasingly higher numbers of patients waiting at 8 a.m. in the ED for an inpatient bed. This measure reflects the fact that patients are not being 'cleared out' of the ED fast enough — due to lack of beds and due to increased ED volumes overall — relating to population growth and aging. The provincial volume of ED patients has been growing at approximately 2.5% annually over the past decade — faster than population growth, to a current level of almost 6 million visits per year.

Figure 13
Ontario Daily Average Number of Patients Waiting for a bed at 8 a.m., 2012 to 2019



Source: CCO

Quality of Care — Broad Measures

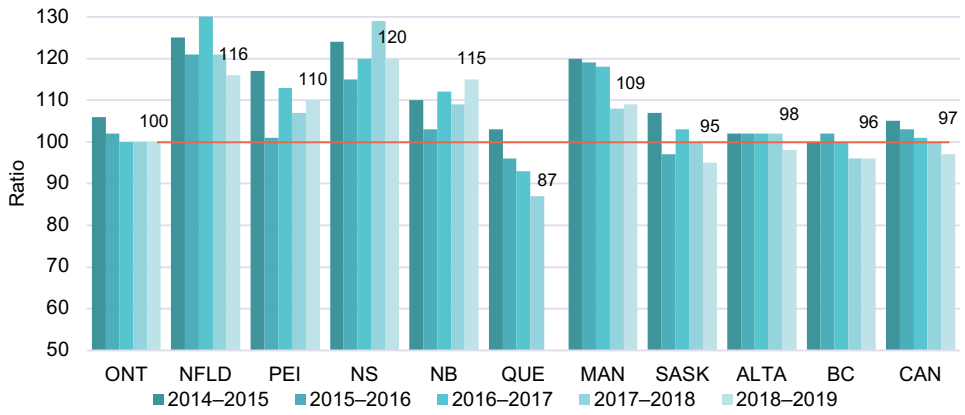
Hospital Standardized Mortality Ratio (HSMR)

Over three broad quality measures, Ontario hospitals' results have been stable over time

One important hospital quality indicator is the Hospital Standardized Mortality Ratio. CIHI states: "This indicator of health care quality measures whether the number of deaths at a hospital is higher or lower than you would expect, based on the average experience of Canadian hospitals (set at 100 in 2017-18). When tracked over time, this measure can indicate whether hospitals have been successful in reducing patient deaths and improving care."[7] Ontario's Hospital Standardized Mortality Ratio (HSMR) has remained unchanged for three years, and for 2018-19 is effectively at the national average.

Ontario's HSMR is effectively at the national average and is stable

Figure 14
Hospital Standardized Mortality Ratio (HSMR), by Province, 2014-15 to 2018-19 (Lower is Better)



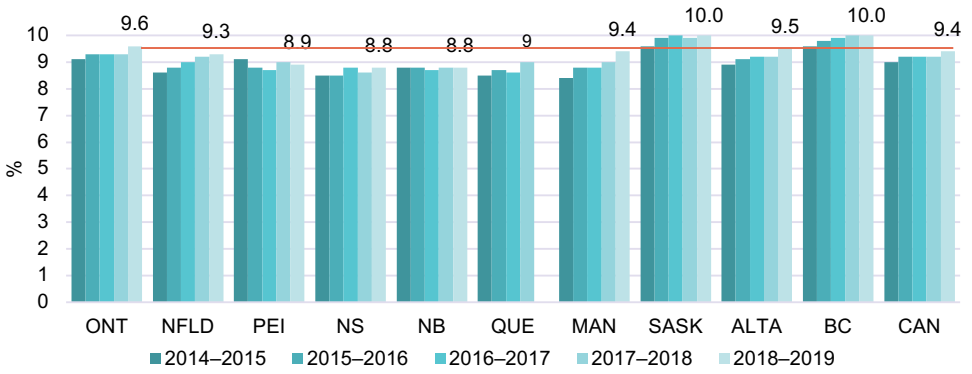
Source: CIHI Your Health System - In Depth

Hospital Readmission Rate

Another key quality indicator is the Hospital Readmission Rate (risk- adjusted to account for the range of severity of illness across patient types). Ontario's rate increased slightly in 2018-19 after holding steady for the previous three years. Ontario's 2018-19 rate is slightly higher than the average rate for Canada.

Ontario's readmission rate is slightly above the national average and has been stable

Figure 15
Percentage of Patients Readmitted within 30 Days, by Province, 2014-15 to 2018-19 (Lower is better)



Source: CIHI Your Health System - In Depth

Timeliness of Hip Fracture Surgery

Timely access to emergency hip fracture surgery is a key access and quality indicator

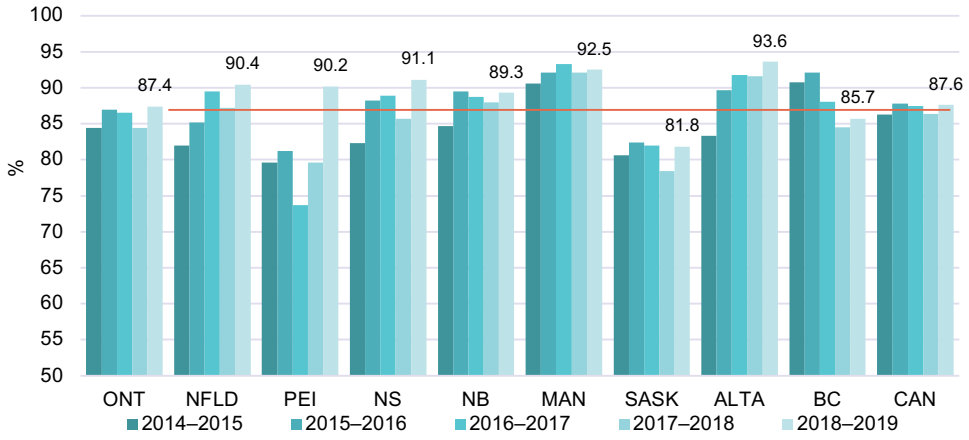
Patients waiting in the ED are not only waiting to be admitted to an inpatient bed; some are waiting for emergency surgery. One indicator of a system under stress, as well as an indicator of quality of care is the timeliness of hip fracture surgery.

According to the Canadian Medical Association, delays in hip fracture surgery increase a person's risk of death.[8] This is due to several factors including blood clots (due to being bed-bound) or fasting before surgery (worsened if surgery is canceled and rescheduled.)[9]

Ontario is performing at the national average

A 48-hour benchmark for receiving hip fracture surgery was set by a national committee of Health Ministers in 2005.[10] The percentage of Ontario hip-fracture patients getting surgery within the 48-hour benchmark was 87.4% in 2018-19, which is the same as the average rate for Canada.

Figure 16
Percentage of Hip Fracture Surgeries Performed Within 48 Hours, by Province, 2014-15 to 2018-19
(Higher is better)



Quebec data is not available.

Source: CIHI Your Health System - In Depth

Sources and Notes

[1] Ontario Ministry of Finance. 2019 Ontario Economic Outlook and Fiscal Review.

[2] Ontario Hospital Association calculation using data from Canadian Institute for Health Information (CIHI) National Health Expenditure (NHEX) Database 2019.

Note: CIHI's NHEX database release for 2019 used a revised methodology and new information in compiling health expenditure data. Major differences from past releases which impact OHA's efficiency dividend calculation relate mostly to recategorization of expenditures for Alberta and British Columbia (B.C.). In Alberta, expenditure was reclassified from *hospitals* and *other institutions* to *public health* and *other spending*. In B.C., expenditure was reclassified from *hospitals* and *public health* to *other institutions* and *other health spending*. *Total health* expenditure was not affected in these provinces. For Quebec, additional expenditures not previously included were added that impacted *total health* expenditure. In Ontario, *hospital* expenditure was not impacted; *total health* expenditure and *other health* expenditure was increased due to inclusion of *home and community care* spending not previously captured (also included for other provinces)

[3] Government of Alberta. Report and Recommendations: Blue Ribbon Panel on Alberta's Finances. August 2019. Available: https://open.alberta.ca/publications/report-and-recommendations-blue-ribbon-panel-on-alberta-s-finances. Accessed November 2019.

[4] Ontario Ministry of Finance. 1995 Fiscal and Economic Statement.

[5] Ontario Ministry of Finance. 1998 Ontario Budget.

[6] Canadian Institute for Health Information. Your Health System –In Depth. November 2019.

[7] Canadian Institute for Health Information. Your Health System – In Depth. November 2019.

[8] CMAJ August 07, 2018 190 (31) E923-E932. Available: https://www.cmaj.ca/content/190/31/E923. Accessed November 2019.

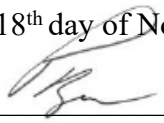
[9] Leung, W. August 6, 2018. Delayed surgery for hip fractures cause of preventable deaths, study finds. Globe and Mail. Available: https://www.theglobeandmail.com/canada/article-delayed-surgery-for-hip-fractures-cause-of-preventable-deaths-study/. Accessed November 2019.

[10] Canadian Institute for Health Information. Wait Times for Priority Procedures in Canada, 2019: Technical Notes.

200 Front Street West, Suite 2800
Toronto, Ontario M5V 3L1
www.oha.com

Ontario Hospital Association

This is **"Exhibit O"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



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A Commissioner, etc.

How COVID-19 exposed long-term health-care issues at Brampton hospital

When it comes to explaining why Brampton and its neighbouring communities have the fewest hospital beds per capita of any Ontario region, a city councillor for northeast Brampton says the reason is clear: ‘We are a racialized community and many members cannot speak English as their first language’

KELLY GRANT > HEALTH REPORTER
SIMRAN SINGH
BRAMPTON, ONT.
PUBLISHED JUNE 21, 2021

Care team members attend to a South Asian ICU patient after they were turned from a prone position, onto the supine position at Brampton Civic Hospital on May 25, 2021.

FRED LUM/THE GLOBE AND MAIL

The team of six health care workers moved with the speed and precision of a pit crew around a COVID-19 patient lying on his stomach in Brampton Civic Hospital's intensive-care unit.

A respiratory therapist secured the patient's breathing tube. Nurses checked the multiple IV lines snaking out of his body. A physiotherapist repositioned the patient's arms. Wrapping a bed sheet around his body, they counted down and flipped him onto his back.

Staff at this suburban hospital in Brampton, Ont., northwest of Toronto, have become some of the country's top experts in treating critically ill COVID-19 patients, executing this turning manoeuvre to improve lung function hundreds, if not thousands, of times over the past 16 months.

They've also become masters at prepping patients for transfer. Over the course of the pandemic, Brampton Civic transferred out at least 567 infected patients, 150 of them in critical condition, to free up space and staff. That's more transfers than any other hospital in Ontario.

But the pressure Brampton Civic faced can't be blamed on the scale of the local COVID-19 epidemic alone. As the only full-service hospital for a city of about 660,000 people, Brampton Civic was full-to-bursting long before anyone had ever heard of COVID-19. The pandemic simply drew attention to the health care funding disparity locals had been living with for years.

"It seems like we can't ever catch a break," said Vikram Kapoor, a doctor who grew up in Brampton and now serves as the division head of hospitalist medicine at Brampton Civic. "Because even before COVID, our volumes are high, our ER's so busy, our beds are underfunded. At least this kind of shines a light on it."

Many of Brampton's residents are South Asian, like the man in his 40s who was flipped from the prone to supine position on a morning in late May.

L6P

INSIDE L6P
How this Brampton community explains Canada's COVID-19 crisis like no other

EDITOR'S LETTER
Why The Globe asked this Brampton community to share its COVID-19 stories

PODCAST
Brampton: The making of a COVID-19 hotspot

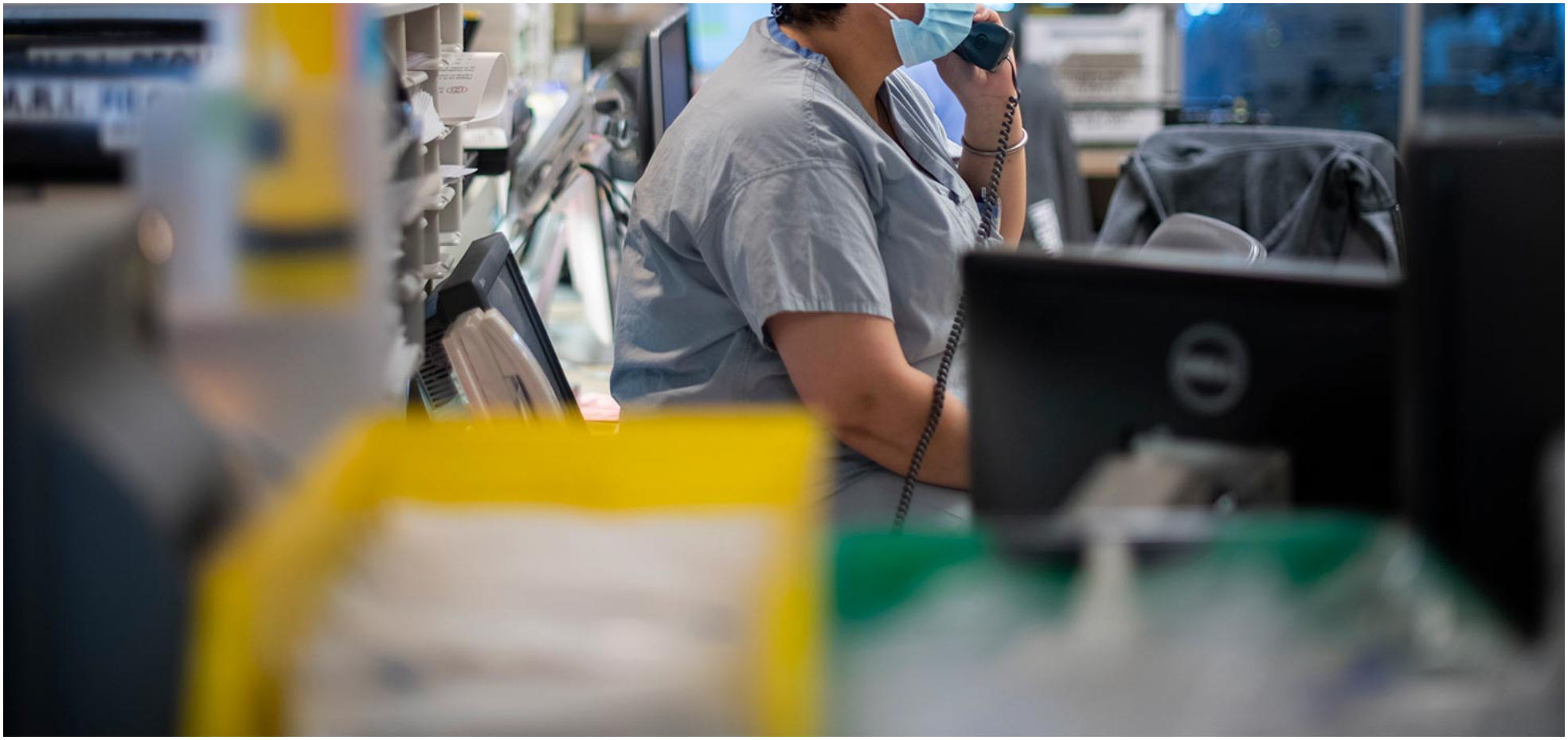
IN DEPTH
Read more stories from the series

A care team member prepares a prone ICU patient before they were turned over onto the supine position.

FRED LUM/THE GLOBE AND MAIL

Using sheets to help in the task, care team members prepare to turn a prone ICU patient over onto the supine position.

FRED LUM/THE GLOBE AND MAIL



Registered nurse Navdeep Hansra speaks to family members of a South Asian patient in the ICU.

FRED LUM/THE GLOBE AND MAIL

After the team turned him, nurse Navdeep Hansra spoke by phone, gently in Punjabi, to one of his relatives. “She was crying on the phone,” Ms. Hansra said afterward. “She was very scared.”

When it comes to explaining why Brampton and its neighbouring communities have the fewest hospital beds per capita of any Ontario region, “there’s no reason to beat around the bush,” said Harkirat Singh, a city councillor for northeast Brampton, which includes L6P, the first three characters of the postal code that has had the most per-capita cases of COVID-

19 in Ontario since the start of the pandemic. “We are a racialized community and many members cannot speak English as their first language.”

That made it difficult for residents to advocate for themselves as Brampton’s population grew, and as successive provincial governments failed to open enough new hospital beds to keep pace, Mr. Singh said.

“I would argue we were taken advantage of.”

Running out of options

On Jan. 22 of 2020, Brampton council took the extraordinary step of declaring a health care emergency in the city. The motion, moved by Mr. Singh and adopted unanimously, was primarily symbolic, but Mr. Singh felt he had run out of options.

How many more times could he forward complaints about the overcrowded hospital to the local member of provincial Parliament? How could he keep advising constituents who felt they had received subpar care to hire lawyers they could ill-afford? “I just felt like I was powerless,” Mr. Singh said in a recent interview. ”This was something that needed to be done. Obviously, it’s a capacity issue, a funding issue.”

The emergency declaration asked for two things. In the long term, Brampton wanted an additional 850 hospital beds to bring its per-capita share in line with the provincial average. In the short run, it asked for a cash injection to provide the local hospital network with “full staffing and resources in order to provide safe and quality patient care immediately.”

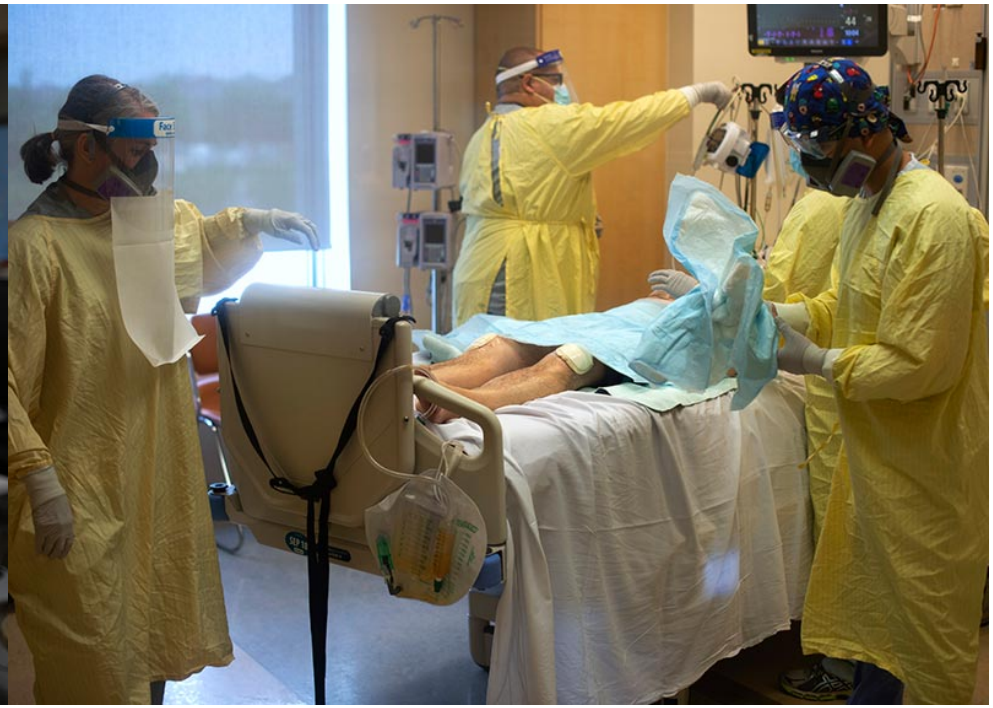
Three days after Brampton declared its health emergency, Canada reported its first case of COVID-19.

“We started the pandemic at 100-per-cent capacity, and that’s been the norm for years in Brampton,” said Mayor Patrick Brown. (Average occupancy at Brampton Civic was actually 108.7 per cent in the eight months leading up to the pandemic.

Etobicoke General was worse, with average occupancy of 130.4 per cent in the same period, according to a spokeswoman for the William Osler Health System, which includes both hospitals.)

“There’s one standard of care in older communities like Oakville or Kingston or Kitchener-Waterloo. And there’s another standard in the growing, diverse communities like Brampton, Etobicoke [and] Scarborough,” Mr. Brown said. “It’s unconscionable.”

A care team member puts on a gown before turning a prone COVID-19 patient onto the supine position.
FRED LUM/THE GLOBE AND MAIL



Care team members attend to an ICU patient after they were turned from a prone position to a supine position.
FRED LUM/THE GLOBE AND MAIL

Those divergent standards were laid bare in a 2017 briefing note that William Osler’s interim president sent to the head of the Central West Local Health Integration Network (LHIN,) one of Ontario’s old regional health authorities. The provincial

NDP obtained the note through an access-to-information request and it made headlines at the time, notably for the revelation that Brampton Civic had treated 4,352 patients in hallways in a single year.

The briefing note showed that in 2015-2016 William Osler had fewer beds and a smaller budget than hospital networks in smaller or similar-sized Ontario cities, despite coping with more emergency-department visits and admitting as many or more patients.

Residents of the old Central West LHIN – which included Brampton and a slice of northwest Etobicoke, and also extended as far north as Shelburne – had 100 hospital beds for every 100,000 residents in 2019-2020. The provincial average was 218.6, according to Ontario Health.

How did the Brampton area wind up at such a disadvantage? The provincial government, controlled by the Liberals from 2003 to 2018 and by the Progressive Conservatives thereafter, wildly underestimated the growing city's needs.

On top of that, Brampton's population exploded at a time when the Liberal governments of Dalton McGuinty and Kathleen Wynne were trying to avoid opening expensive new hospital beds, something that contributed to overcrowding in many hospitals. Their aim was to shift as much care as possible out of traditional hospitals and into the community.

Brampton Civic, which was built to accommodate 90,000 emergency department visits a year, blew past that mark less than two years after it opened in 2008. It hit 138,000 ED visits by 2016-2017, despite a third-party review that found residents visited the ED less than expected, based on provincial averages. Much of the increased traffic was comprised of patients sick enough to require admission.

At the same time, the Peel Memorial Centre for Integrated Health and Wellness, a day-surgery and urgent-care centre in Brampton that replaced the old full-service Peel Memorial Hospital, didn't syphon nearly as many less-seriously-ill patients away from Brampton Civic as forecast.

Opened in February, 2017, with funding for 10,000 visits a year, the urgent-care centre was logging 75,000 annually by 2018-2019, which explains how internal figures, also obtained by the NDP, showed traffic at the urgent-care centre topping 550 per cent of its funded capacity that year.

“When I came to Brampton, there were a lot of individuals [of] European descent,” said Ato Sekyi-Otu, an orthopedic surgeon at Brampton Civic and a member of the Black Physicians’ Association of Ontario. “That demographic has dramatically changed in the last 20 years, as has the funding. So, I mean, there’s a correlation there.”

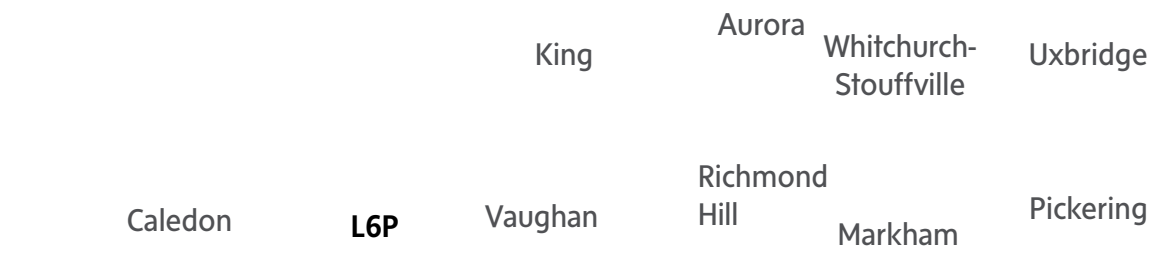
If Brampton had more hospital beds, its lone hospital would not have been forced to transfer out so many COVID-19 patients. Although Brampton’s case rate was among the highest in the province, its hospitalization and death rates weren’t, according to a Globe and Mail analysis of data from the non-profit Institute for Clinical Evaluative Sciences. (The data exclude cases in long-term care.)

L6P, for example, is first in confirmed infections per capita, but 57th in terms of hospital admissions and tied for 128th in deaths, compared with other forward sortation areas, which are defined by the first three characters of a postal code.

*Rates derived from 5 or fewer counts are suppressed.

Hospitalization rates

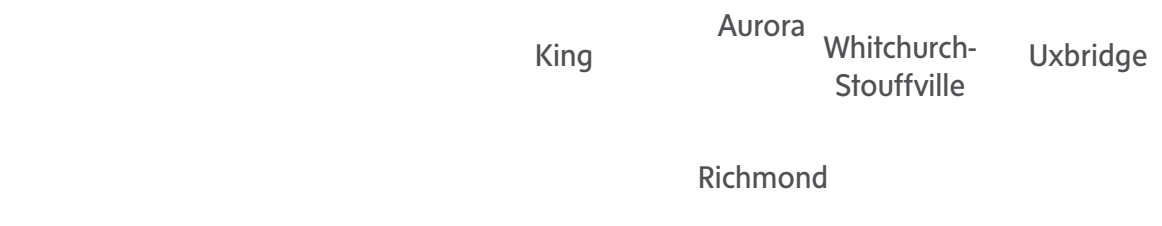
As of June 7, 2021

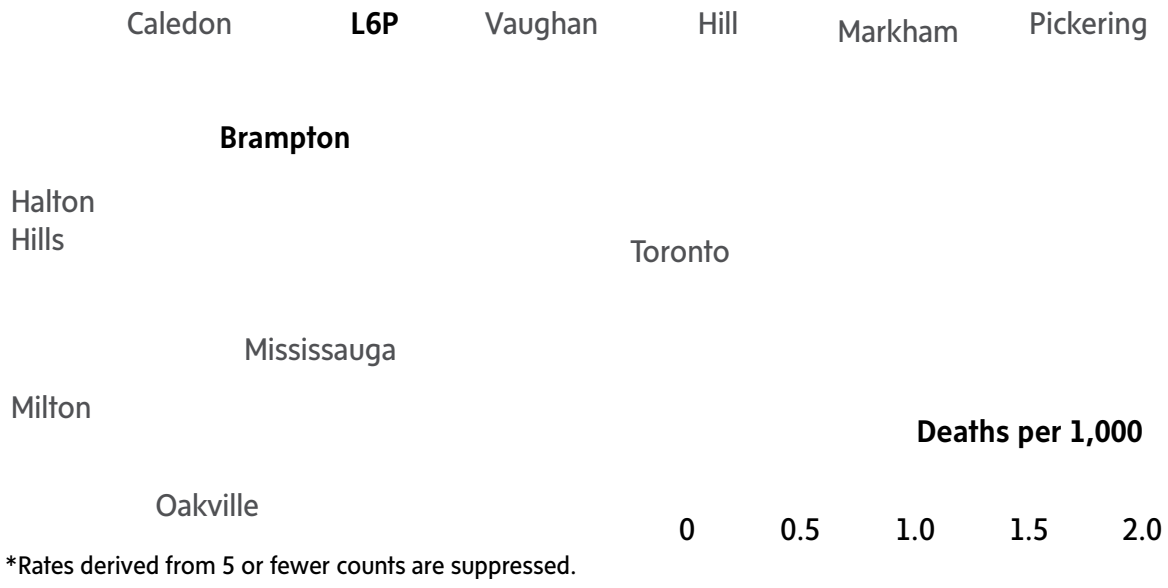


*Rates derived from 5 or fewer counts are suppressed.

Death rates

As of June 7, 2021





In late March, Ontario Premier Doug Ford announced that his government planned to expand the Peel Memorial Centre with a new building, including 250 new beds, and a 24/7 emergency department.

The Premier's announcement didn't make clear precisely what types of patients the new beds at Peel Memorial would accommodate or when the addition – which Mr. Ford described as a new hospital – would open.

Alexandra Hilkene, a spokeswoman for Ontario Health Minister Christine Elliott, said in a statement that the current plan is to reserve the new beds for "post-acute inpatient care, including complex continuing care beds and rehabilitation beds," while studying whether some acute-care beds would be needed to support a future 24/7 emergency department at Peel Memorial. In the meantime, the province has committed up to $18-million in 2021-2022 to run the urgent-care centre around the clock, Ms. Hilkene said.

William Osler spokeswoman Emma Murphy also said that the hospital network has "worked closely" with the Ministry of Health as well as Ontario Health, a provincial agency that oversees the day-to-day operations of the health care system, to address its capacity needs. "In October, 2020, Osler received additional funding to support 87 more beds to help manage

COVID-19 and an anticipated winter surge across our inpatient hospitals. These beds have supported Osler's ability to provide safe and appropriate care to patients since that time," she said by e-mail.

When Mr. Ford made his announcement at Peel Memorial on March 26, the third wave of COVID-19 was gathering speed. It would soon slam into Brampton Civic, testing the resilience of the doctors, nurses, physiotherapists and other front-line workers who had already spent more than a year caring for coronavirus patients with fewer resources than other GTA hospitals.

Claire Lee, a rehab physiotherapist, speaks to a journalist before helping turn a prone COVID-19 patient to the supine position at Brampton Civic Hospital on May 25, 2021.

FRED LUM/THE GLOBE AND MAIL

FRED LUM/ THE GLOBE AND MAIL

A well-oiled machine

Brampton Civic physiotherapist Claire Lee remembers one of the first times she saw a nursing colleague emerge after helping to flip a patient into the prone position.

It was during the first wave in the spring of 2020, and Ms. Lee, normally a rehabilitation physiotherapist, had been seconded to the ICU to help turn COVID-19 patients.

“His scrubs were soaked,” she said of the nurse. “My first thought was something exploded and got him all wet. It wasn’t. It was sweat.”

Brampton Civic recognized early on that it would have to find creative ways to respond to the sheer volume of COVID-19 patients in its care. Establishing a dedicated team of physiotherapists, including Ms. Lee, to help flip patients in the ICU, was just one of the ways the hospital pivoted to conserve critical nursing resources.

Treating critically ill COVID-19 patients in the prone position is thought to improve their lung function, but patients risk developing pressure sores if they are left on their stomachs too long. Brampton Civic’s approach is to not leave patients on their stomachs for more than 16 hours in a row.

Registered nurse Angel Flores speaking to a reporter about the current pandemic and comparing it to his experience working during SARS.

FRED LUM/THE GLOBE AND MAIL

“We became like a well-oiled machine,” said Angel Flores, a veteran ICU nurse. At the height of Ontario’s third wave, staff would perform the flipping procedure, “back to back to back to back,” he said. “The team would flip, come out, de-gown and everything, wash up, get ready and go on the next patient. … It was a lot of work and it was scary.”

As of the end of April, Osler had treated 319 COVID-19 patients in the prone position, nearly 10 per cent of the 3,054 infected patients the network admitted between April, 2020, and April, 2021.

Before the pandemic, Brampton Civic’s ICU might have treated a patient or two a month in the prone position, said Michael Miletin, chief of medicine at William Osler.

Flipping was done so rarely that when COVID-19 first hit, a physician was always at the bedside or outside the room to supervise, often reading off a safety checklist that included special attention to the patient’s breathing tube. If the tube came unhooked, even for a moment, coronavirus-filled particles could fill the air and put staff at risk.

“My confidence in our teams has soared,” Dr. Miletin said. When he identifies patients for proning on morning rounds, “they’re right on it. Everyone knows their roles. They’re confident. They have a clarity of purpose. They understand the safety portion of it as well, which is paramount for us.”

Paramedics prepare to transfer COVID-19 patient John Wylie, 76, from Brampton Civic Hospital to Halton Health Care.

FRED LUM/THE GLOBE AND MAIL

With the pandemic still ongoing, a note taped to a wall at the hospital advises people that no family or visitors are allowed to see patients.

FRED LUM/THE GLOBE AND MAIL

COVID-19 patient John Wylie is loaded into an ambulance.

FRED LUM/THE GLOBE AND MAIL

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Such expertise was essential in the punishing third wave, when Ms. Lee, who returned to her old job during the second wave, was called back to the ICU. By April of this year, Brampton's ICU had become "like a revolving door," she said. "You would see people come in on one day, the doctors would stabilize them, and then we would sometimes prone them, sometimes not," Ms. Lee said. "But then the next day you came in and they were gone."

Gone, as in transferred to other hospitals. Some were sent as far away as Windsor. In April, the torrent of severely ill COVID-19 patients coming through Brampton Civic's emergency department refused to abate. At triage, patients were met with signs warning they could be transferred to another hospital.

The transfers, co-ordinated by the GTA Hospital Incident Management System (IMS), were a lifeline for Brampton Civic and other hotspot hospitals, said Dr. Kapoor, who worked on many of the transfer cases.

As of the end of May, 3,219 GTA COVID-19 patients had been transferred since the launch of the GTA Hospital IMS in mid-November, according to Ontario Health. Nearly one-third of all transfers came from William Osler's hospitals.

COVID-19 hospital inpatients and transfers at Brampton Civic

Patients

Inpatients Transfers

THE GLOBE AND MAIL, SOURCE: WILLIAM OSLER HEALTH SYSTEM

DATA SHARE

The vast majority of families have been patient and understanding about the need to send their infected loved ones out of Brampton, Dr. Kapoor said – in part because relatives generally can't visit anyway, no matter where a COVID-19 patient is treated.

"The hardest part of this whole process, transfer or not, has been that families can't visit," he said. "Families are putting all their trust in your hands. They're not there. They're not at the bedside. So it's been very difficult."

With the third wave finally ebbing – William Osler's hospitals transferred out fewer patients in all of May than in the third week of April alone – Dr. Kapoor is hoping other GTA hospitals will continue to help Brampton Civic cope with overcrowding.

But he believes that Brampton, home to his parents and many lifelong friends, deserves better than the chronic health care underfunding that has plagued the city.

“We can’t stand for that.”

With a report from Danielle Webb

Simran Singh is Special to The Globe and Mail


AIRBORNE PRECAUTIONS
N95
Mask
Or
Equivalent
For all persons
entering room

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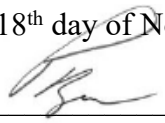
Our Morning Update and Evening Update newsletters are written by Globe editors, giving you a concise summary of the day's most important headlines. Sign up today.

This is **"Exhibit P"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Public Health Ontario | Santé publique Ontario

SYNTHESIS

(ARCHIVED) COVID-19 Transmission Through Large Respiratory Droplets and Aerosols… What We Know So Far

Published: May 2021

Archived: February 2022

Introduction

Public Health Ontario (PHO) is actively monitoring, reviewing and assessing relevant information related to Coronavirus Disease 2019 (COVID-19). "What We Know So Far" documents provide a rapid review of the evidence on a specific aspect or emerging issue related to COVID-19. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is transmitted in different ways; however, this document will focus on transmission by respiratory droplets and aerosols.

Key Findings

- The historical dichotomy of droplet versus airborne transmission, while useful in implementing infection prevention and control (IPAC) strategies, does not accurately recognize the complexity of viral respiratory transmission, including for SARS-CoV-2.
- SARS-CoV-2 is transmitted most frequently and easily at short range through exposure to respiratory particles that range in size from large droplets which fall quickly to the ground to smaller droplets, known as aerosols, which can remain suspended in the air.
- There is evidence to suggest long-range transmission can occur under the right set of favourable conditions, implicating aerosols in transmission.

- The relative role of large respiratory droplets versus smaller droplet particles in short-range transmission is challenging to quantify. Their contributions to a specific case-contact interaction vary based on contextual factors including source/receptor characteristics (e.g., forceful expulsions such as singing, coughing, sneezing; viral load) and pathway characteristics (e.g., duration of exposure; environmental conditions such as ventilation, temperature, humidity, ultraviolet light; source control; and use of personal protective equipment).

- Translation of this summary into control measures needs to take into consideration other information, such as evidence around the effectiveness of control measures to date. Several control measures applied together in a layered approach are likely to be effective irrespective of the relative contribution of droplets or aerosols, including achieving high vaccination coverage and avoiding the "3 C's" (closed spaces, crowded places and close contact).

Background

The diameter of microorganism-containing respiratory particles relevant for respiratory infections ranges from approximately 0.01 micrometres (µm) to greater than 100 µm.[1] Particles larger than about 100 µm play a role in respiratory infection transmission by impacting on mucosal surfaces, such as the nostrils, mouth and eyes. Particles smaller than 100 µm can be inhaled or impact on mucosal surfaces. Some particles are small enough that they can be suspended in the air for various periods of time (known as aerosols).[2] Environmental factors such as local air currents and humidity affect these particles, e.g., how they move, evaporate, and how long they remain in air.[3] Therefore, the mode of transmission is influenced by three key elements: the source, the pathway, and the receptor. Depending on the unique characteristics of each element, certain modes may be more likely than others.

Traditionally, respiratory particles >5 or 10 µm have been termed droplets and were thought to impact directly on mucous membranes, while smaller particles were thought to be inhaled. This dichotomy of transmission routes has been applied to infection prevention controls within health care settings worldwide. However, these transmission routes are not mutually exclusive as droplets well over 5 µm are capable of remaining suspended in air for some time and can be inhaled. At short range within about 2 metres (m), infection can occur from inhaled aerosols as well as droplets landing on mucous membranes (short-range transmission). Herein, we refer to what was traditionally called airborne transmission via inhalation of aerosols that have remained suspended over long distances and periods of time[4,5] as long-range transmission.

We describe transmission through epidemiological studies, experimental or simulation of transmission studies, and statistical or mathematical modelling. Modelling shows what is possible, experimental studies what is plausible, and epidemiologic studies observe what is actually occurring, and each type of evidence is subject to limitations. However, exact routes of SARS-CoV-2 transmission in real-life scenarios can only be inferred based on the available data.

The purpose of this rapid review is to outline the evidence for droplets and aerosols in SARS-CoV-2 transmission. We have summarized the evidence as either short-range transmission from large respiratory droplets and small droplets or aerosols, or long-range transmission from aerosols.

Methods and Scope

In considering feasibility, scope and timelines, we undertook a rapid review to update our summary of SARS-CoV-2 transmission from large respiratory droplets and aerosols. A rapid review is a knowledge synthesis where certain steps of the systematic review process are omitted in order to be timely (e.g., duplicate screening).[6]

We conducted literature searches in MEDLINE (April 22, 2021) and National Institutes of Health COVID-19 Portfolio (Preprints) (April 27, 2021), search strategies are available upon request. We searched PubMed and Google Scholar on April 28, 2021 for additional articles of interest.

English-language peer-reviewed and non-peer-reviewed records that described large respiratory droplet and aerosol routes of transmission of COVID-19 were included. We restricted the search to articles published after January 1, 2020. This rapid review concentrated on evidence from systematic reviews and meta-analyses, supplemented by primary literature where appropriate. We reviewed citations from included articles to identify additional research.

Prior to publishing, PHO subject-matter experts review all What We Know So Far documents. As the scientific evidence is expanding rapidly, the information provided in this document is only current as of the date of respective literature searches.

Out-of-scope for this document was a review of IPAC practices appropriate for individual transmission scenarios and settings. Application of a hierarchy of control measures for non-health care settings is briefly discussed in the conclusions. For additional information related to IPAC in health care settings, please see PHO's technical briefing *IPAC Recommendations for Use of Personal Protective Equipment for Care of Individuals with Suspect or Confirmed COVID-19* and *Interim Guidance for Infection Prevention and Control of SARS-CoV-2 Variants of Concern for Health Care Settings*.[7,8] Please note that the *Ministry of Health's Directive 1* is the provincial baseline standard for provision of personal protective equipment for hospitals, long-term care homes and retirement homes and that the *Ministry of Health's Directive 5* provides agency to health care workers to make professional decisions regarding the appropriate personal protective equipment when dealing with suspected, probable or confirmed COVID-19 patients or residents.[9,10] Evidence for contact/fomite transmission, and virus and host (source/receptor) factors were not reviewed in this document, but are acknowledged as contributors to short- and long-range transmission. Other routes of transmission are reviewed in PHO's synthesis *COVID-19 Routes of Transmission – What We Know So Far*.[11]

Short-range Transmission

Main Findings

SARS-CoV-2 is transmitted most frequently and easily at short range. Short-range transmission generally occurs within 2 m of an infectious individual (e.g., during a conversation with inadequate distancing, no barriers, no personal protective equipment). Theoretically, short-range transmission may occur due to droplets or aerosols, but the relative contribution of either is specific to each case-contact interaction which varies based on contextual factors including source/receptor and pathway characteristics.

Environmental Factors Affecting Short-range Droplets and Aerosols

In addition to virus and host factors, environmental factors are associated with short-range viral transmission. The distance travelled by large respiratory droplets is generally <2 m, although it can reach up to 8 m in certain circumstances. In a study by Guo et al. (2020), SARS-CoV-2 virus was detected on the floor up to 4 m away from a patient.[12] In a systematic review of studies assessing the horizontal distance travelled by respiratory droplets, Bahl et al. (2020) reported that droplets could travel up to 8 m.[13] In a mathematical model, Chen et al. (2021) reported that respiratory droplets >100 µm in diameter are only important in transmission at a distance of less than 0.2 m when the infector is talking, or within 0.5 m when the infector is coughing.[14] Modelling by Wang et al. (2021) (preprint) suggested droplets >100 µm would most often not travel past 1.75 m (most droplets >100 µm diameter settle before 1.25 m).[15]

In a review of respiratory virus transmission, Leung (2021) reported that environmental factors affecting transmission include temperature, relative humidity, ventilation, airflow and ultraviolet (UV) light.[16] Ventilation, airflow and forceful expulsion (sneezing or coughing) can make respiratory particles travel further than 2 m through momentum.[14,17] High temperature and low humidity contributes to shrinking of droplets such that they may remain suspended in air for longer periods of time.[18]

Even at short-range distances, ventilation may affect transmission. De Oliveira et al. (2021) modelled infection risk in ventilated (10 air changes per hour [ACH]) and unventilated spaces without respiratory protection during a 1-hour exposure at 2-m distance.[19] The impact of decreasing concentration of virus in the air through ventilation was notable. Estimates of infection risk were reduced by at least three times based on the parameters and assumptions of their model. The authors also commented that the direction of airflow can have a significant impact – upward air streams can maintain aerosols at face height significantly increasing infectious risk.

Indoor settings are a predominant risk factor for transmission. In a systematic review of 5 studies, Bulfone et al. (2020) reported that the odds of indoor transmission were 18.7 times (95% confidence interval [CI]: 6.0–57.9) higher than outdoor settings, and less than 10% of infections occurred outdoors.[20] Very few superspreading events have been described from exclusively outdoor exposures. The explanation for this observation is likely multifactorial which includes important differences in ventilation, UV light, humidity, as well as possible differences in behaviour.

Epidemiological and Modelling Studies Describing Short-range Transmission

The following section reviews the epidemiologic and modelling evidence supporting short-range transmission of COVID-19. It reviews the reproductive number and summarizes the epidemiological and modelling studies by setting, including transportation, health care and sports.

The reproductive number (R_0) of SARS-CoV-2 is less suggestive of long-range transmission commonly occurring, as viruses where long-range transmission commonly occurs tend to have a higher R_0.[16] For example, in a systematic review by Guerra et al. (2017), the R_0 for the measles virus in the pre-vaccine era was 6.1–27.0,[21] compared to the median range of R_0 (2.7–3.3) reported for SARS-CoV-2.[22] It is important to note that R_0 is not a direct measure or indication of transmission route, as R_0 can be setting and population-specific, and be impacted by factors such human behaviours. The R_0 for SARS-CoV-2 also displays overdispersion, where the overall R_0 is lower than pathogens that commonly transmit through aerosols at long-range, but a small proportion of cases are associated with reproductive numbers in the

range typical of viruses that commonly transmit through aerosols at long-range (i.e., superspreader events).[23] Such cases illustrate the potential variability in COVID-19 transmission, depending on differences in source/receptor characteristics and environment.

Short-range transmission was favoured in a retrospective cohort study of 18 short-to-medium haul flights (median flight time 115 minutes) to England from the beginning of the pandemic.[24] The attack rate was 0.2% (95% confidence interval [CI]: 0.1–0.5) for all aircraft-acquired cases, and was higher at 3.8% (95% CI: 1.3–10.6) if a subgroup analysis was performed only on contacts within a two-seat radius. It was assumed that no masks were worn given that it was early in the pandemic.

Family gatherings for meals are high-risk scenarios for transmission. Lo Menzo et al. (2021) reported transmission of lineage B.1.1.7 variant of concern to 8 of 9 family members during a dinner gathering.[25] The only uninfected family member was presumed to have immunity acquired from a previous infection (high antibody titres and polymerase chain reaction (PCR) negative result). Contact and fomite transmission cannot be excluded from this type of event.

In a case-control study of 154 patients 18 years and older in the United States (US), Fisher et al. (2020) reported that close contact with a person with COVID-19 was reported more often among cases (42.2%) than controls (14.5%) ($p<0.01$).[26]

Short-range transmission has been documented in school settings. Four student-to-student and one student-to-teacher transmission events were reported in Salt Lake County, Utah.[27] For four transmission events, unprotected, short-range exposures were noted. There was a lack of transmission to other students that were a median of 1 m away during class, but adhered to control measures implemented in the school. However, when household transmission associated with the secondary cases was evaluated, transmission was high for 3 of the 5 households of secondary patients. In these three households, 6 of 8 household members were also infected and may be related to challenges with physical distancing, masking, and shared surfaces in the household.

Using whole genome sequencing of SARS-CoV-2 clinical samples (n=50) in Dublin, Ireland, Lucey et al. (2020) investigated cases of hospital-acquired COVID-19 and reported that the majority of infections were among patients who required extensive and prolonged care by health care providers.[28] The authors concluded that the likely mode of transmission from health care workers to patients was through short-range transmission and close contact, rather than long-range transmission. Notably, the use of masks by health care providers was not universal and patients were not wearing masks either.

Three short-range health care-associated transmission events have been reported where large respiratory droplet transmission was less likely because masks were worn by either the source or the contact and in two of three events, the contact was also wearing eye protection.[29] In case 1, an asymptomatic, unmasked patient transmitted infection to two health care workers who wore medical masks and face shields, following multiple hours of exposure in a room with 6 ACH. A second case occurred where a presymptomatic masked health care worker transmitted infection to an unmasked patient in a room with 6 ACH. A third case involved a presymptomatic masked patient transmitting infection to a health care worker who was wearing a mask and goggles during a 45 minute face-to-face discussion at 1 m. Notably in the third case, the patient's mask was removed temporarily for oropharynx inspection. While each case was verified by whole genome sequencing, there was a lack of detail about the specific encounters (e.g., distance, duration, if direct contact occurred, if doffing errors occurred), and no airflow studies were conducted.

An analysis of SARS-CoV-2 infections in an outdoor rugby league, including video evaluation of close contact due to tackling inherent in the game, indicated that no cases among players in the league could be linked to close-contact during the outdoor rugby games.[30] Instead, transmissions were linked to other indoor short-range transmission events. While this study demonstrates examples where outdoor close-contact transmission did not occur, there were not enough close-contacts documented to provide evidence that close-contact transmission could not have occurred in the context of outdoor rugby.

In a modelling study, Zhang and Wang (2020) reported that the median infection risk via long-range aerosol transmission (10^{-6}–10^{-4}) was significantly lower than the risk via close contact (10^{-1}).[31] The model was based on a 1-hour exposure in a room with an area of 10–400 m^2, with one infected individual and a ventilation rate of 0.1–2.0 ACH. In a modelling study by Hu et al. (2020), the transmission risk from epidemiological data among train passengers as 0%–10.3% (95% CI: 5.3%–19.0%).[32] Travellers directly adjacent to the index patient had a much higher infection risk (relative risk [RR]: 18.0; 95% CI: 13.9–23.4), and the attack rate decreased with increasing distance.

Household and Non-Household Secondary Attack Rates

The consensus among systematic reviews is that household settings, where physical distancing, consistent source control mask-wearing, and disinfection of shared surfaces are potentially not feasible, are associated with a higher risk of infection compared to casual-contact settings (17%–27% compared to 0%–7%). However, the secondary household attack rates are not as high as would be expected if SARS-CoV-2 easily spread through long-range transmission (e.g., >90% in measles).[16,33]

In a systematic review and meta-analysis of 54 studies and 77,758 patients, Madewell et al. (2020) reported that the household secondary attack rate was 16.6% (95% CI: 14.0–19.3).[34] In a systematic review and meta-analysis of 45 studies, Thompson et al. (2021) estimated the household secondary attack rate as 21.1% (95% CI: 17.4–24.8; 29 studies).[35] Non-household settings had lower secondary attack rates: 1) social settings with family and friends (5.9%; 95% CI: 0.3–9.8; 7 studies); 2) travel (5.0%; 95% CI: 0.3–9.8; 5 studies); 3) health care facilities (3.6%; 95% CI: 1.0–6.9; 10 studies); workplaces (1.9%; 95% CI: 0.0–3.9; 7 studies); and casual social contacts with strangers (1.2%; 95% CI: 0.3–2.1; 7 studies). Koh et al. (2020), in a meta-analysis of 43 studies, reported that the household secondary attack rate was 18.1% (95% CI: 15.7–20.6; 43 studies), much higher than the secondary attack rate in health care settings (0.7%; 95% CI: 0.4–1.0; 18 studies).[36] In a systematic review and meta-analysis of 24 studies, Lei et al. (2020) reported that the secondary attack rate in households was 27% (95% CI: 21−32); the risk of secondary infection was 10 times higher in households compared to non-household settings (odds ratio [OR]: 10.7; 95% CI: 5.7–20.2; $p<0.001$).[37] Tian and Huo (2020), in a meta-analysis of 18 studies, reported that the household secondary attack rate was 20% (95% CI: 15–28; 15 studies; n=3,861 patients), followed by social gatherings at 6% (95% CI: 3–10; 5 studies; n=2,154 patients) and health care settings at 1% (95% CI: 1–2; 4 studies; n=1,320 patients).[38]

Long-range Transmission

Main Findings

Transmission of SARS-CoV-2 over longer distances (generally >2 m) and time occurs through inhalation of aerosols under favourable circumstances, such as prolonged exposure in an inadequately ventilated space. Current evidence supports long-range transmission of SARS-CoV-2 occurring “opportunistically”, in that long-range transmission can occur under some circumstances, but inconsistently, and is not the

predominant situation in which transmission occurs. Epidemiological and modelling studies support that long-range transmission via aerosols occurs. All of these examples include combinations of favourable source/receptor and pathway conditions such as inadequate ventilation, prolonged exposure time, high viral load, with certain activities (singing, exercising, yelling, etc.), and lack of masking for source control by the index case.

Environmental Factors Affecting Long-range Aerosols

In experimental models, researchers have demonstrated the potential for long-range transmission. In a series of experiments, simulations and modelling, Wang et al. (2021) (preprint) reported that aerosols could remain suspended for a longer period than historically predicted.[15] In general, viral copies/millilitre (ml) or concentration decreased as distance from source increased. The work showed that the evaporation time for large respiratory droplets is longer than predicted, especially at higher relative humidity (90%). In a sneeze plume, the largest respiratory droplets (>100 µm) are centrally located within the plume, with smaller respiratory droplets and aerosols at the periphery. The largest droplets contain more virus copies but are less abundant as they settle quickly to the ground, while smaller droplets carry fewer virus copies but are more abundant and remain in the air. The authors conclude that while aerosol transmission is important past 1 m from the source, aerosol transmission is likely even more important at shorter ranges.

Modelling studies have also highlighted the potential for aerosol transmission at varying distances. Xu et al. (2021) analysed the data of 197 symptomatic COVID-19 cases in the Diamond Princess cruise ship outbreak and concluded that long-range transmission did not occur between cabins based on the random distribution of symptomatic cases on all decks and the lack of spatial clusters of close contact (within cabin) infection.[39] The authors inferred that most transmission had occurred in public areas before the quarantine, possibly due to crowding and insufficient ventilation in those spaces. The authors also inferred that there was no transmission between passenger rooms during the quarantine period, and suggested that the ship's central heating, ventilation, and air conditioning (HVAC) system did not play a role in SARS-CoV-2 transmission. However, the authors noted that the lack of data on 109 of the 306 symptomatic individuals and on the 328 asymptomatic individuals may alter their estimation. In addition, their estimation did not take into consideration possible transmission between crew and passengers. Another model of the same outbreak estimated that the contribution of short-range transmission (from large droplets or aerosols) accounted for a median of 36% (mean: 35%) of transmission events, fomite (median: 21%; mean: 30%) and long-range (median: 41%; mean: 35%) contributing to the remainder.[40]

A study of aerosol particles (<5 µm diameter) by Dobramysl et al. (2021) (preprint) reported that time to infection increases approximately linearly as distance from source increases, the most important parameter for time to infection.[41] Exposure to a person breathing normally (simulating an asymptomatic individual) at a distance of 1 m led to infection after 90 minutes; however, coughing every 5 minutes led to infection in 15 minutes. Mask use and even minimal ventilation increased time to infection at a given distance. The importance of ventilation is also described in a modelling study by Jones (2020) which suggested that exposure to inhalable particles mostly (80%) occurs within close proximity to the patient.[42] In still air, aerosols will rise above head-level; however, turbulent air can change the trajectory of virus-laden aerosols, bringing aerosols closer to the head.[43-45] A modelling study by Sen (2021) found that when the ceiling-mounted elevator fan was off, about 11% of the droplets expelled by coughing fell to the ground while 89% evaporated and became smaller.[46] After travelling downward in cough-induced turbulence for approximately 6 seconds, droplets about 50 µm tended to move up and spread in the upper part of the elevator. If the cough happened at 30° to another rider, up to 40% of the droplets may

fall on the face of another elevator rider. However, when the fan is operating, up to 50% of the droplets were dragged down to the floor in less than 3 seconds.

The basement of a large wholesale market was investigated as the source of a major outbreak in Beijing, China.[47] Many factors contributed to spread across multiple possible modes of transmission including long-range transmission. A field study of the area using fluorescent powders and microspheres as tracers allowed authors to conclude that while air was circulated, the air was unfiltered and there was very little fresh air, there was high humidity, low temperature, inadequate hand sanitization supplies in washrooms, and significant contamination of surfaces possibly due in part to resuspension of droplets from wet floors.

Given that persistence of aerosols over time is a factor in long-range transmission, the viability of SARS-CoV-2 in aerosols is important to consider. The half-life of SARS-CoV-2 in aerosols is approximately 1 hour.[48,49] Humidity seems to have less of an effect on SARS-CoV-2 viability in aerosols compared to the effect of sunlight or temperature.[50,51] Increasing temperature is associated with a reduction in the half-life of SARS-CoV-2 in aerosols.[52-54] Using a rotating drum experiment similar to other studies for viability of SARS-CoV-2, simulated sunlight (UVA/UVB) was applied to aerosolized virus through a window on the drum.[51] Results indicated 90% inactivation of virus within 20 minutes.

Inadequate ventilation can contribute to spread of aerosols, where the buildup of infectious aerosols is inversely proportional to the number of air exchanges.[55-57] In a modelling study, Schijven et al. (2021) assessed the risk of aerosol transmission of SARS-CoV-2 at a distance beyond 1.5 m from continuous breathing, speaking, or singing, or from one cough or one sneeze, in an indoor environment of 100 m^3.[58] Where there was no ventilation, the mean risk of transmission (derived from dose-response data for human coronavirus 229E) after 20 minutes of exposure to a person with 10^7 RNA copies/ml of mucous was estimated at 0.1%, except for sneezing with high aerosol volume (40,000 picolitres/sneeze). The mean risk of transmission increased to above 30% for sneezing with high aerosol volume and above 10% for singing after an exposure of 2 hours to a person with mucous RNA concentration above 10^8 copies/ml. Ventilation at 1 ACH reduced the risk by approximately half and at 6 ACH, the risk of transmission was reduced by a factor of 8–13 for sneezing and coughing, and by a factor of 4–9 for singing, speaking and breathing.

Estimates for minimum infectious dose, amount of viable virus in aerosols and quantified exposure rates are lacking. One preprint study assessed superspreading events related to long-range transmission in order to determine a minimum infectious dose for transmission.[59] The model used rate of aerosolized virion shedding based on data from other coronaviruses and a destabilization rate measured for SARS-CoV-2. They reported a critical exposure threshold for aerosol transmission of 50 virions. A computational characterization of inhaled droplets by Basu (2021) reported an estimated inhaled infectious dose around 300 virions, which was similar to estimates of 500 virions for ferrets.[60] The author acknowledged that this estimate could vary widely depending on environmental and individual biological factors.

Epidemiological and Modelling Studies Describing Long-range Transmission

Epidemiological case studies have reported long-range transmission of SARS-CoV-2, exclusively in indoor settings (e.g., bus, church, restaurant, concert halls, apartment building, office building).[61-67] In most of these case studies, long-range transmission was inferred as the dominant route of transmission, given

that infectees were usually further than 2 m away from index cases. In addition, in these case studies, susceptible people were exposed to index cases for prolonged periods (>50 minutes) in indoor environments with inadequate ventilation and, in some instances, with increased respirations (e.g., singing, yelling, or exercising) and/or no face mask use (by case and/or contact). As with most epidemiological studies on transmission events, it was difficult to exclude other contributing routes of transmission. We summarize a few of these case studies, highlighting settings and contributing contextual factors to long-range transmission.

Stagnant indoor conditions can contribute to aerosol transmission. One example is a series of transmissions linked to an individual who developed symptoms around the time they were playing squash in an unventilated squash court.[68] Players who arrived hours after the index case and played in the same squash court were later identified as positive cases, though the role of other potential routes (e.g. unidentified staff contacts, shared surfaces) may have contributed as well and the source of transmission could not be confirmed. In contrast, a post-operative analysis of susceptible patients (no previous SARS-CoV-2 infection or vaccination) in a surgical suite within 48 hours following the use of the suite by SARS-CoV-2 positive patients indicated that there were no transmission events. The event rate was lower than the number of events in a control group (0% vs. 1.9%).[69] Ventilation was likely a significant factor that prevented transmission in the surgical suite.

In a study of six indoor singing events (five with transmission) in the Netherlands, Shah et al. (2021) (preprint) reported that long-range transmission was the likely route of transmission (short-range transmission possibly contributing to transmission at three of these events and indirect contact transmission possibly contributing to transmission at one of the events).[62] The authors assigned transmission likelihood as either less likely or possible; however, the authors do not state how these were defined. Attack rates at these events ranged from 25%–74% (9–21 people aged 20–79 years attended the events) and authors hypothesize that singing led to transmission. The authors note that they cannot quantify the contribution of each route of transmission. Genomic sequencing was not performed to help rule out other sources of SARS-CoV-2.

In a choir group (Washington, US), 53 of 60 individuals (excluding the index patient) were confirmed or strongly suspected to have been infected during a 2.5 hour rehearsal in a main hall.[64] Individuals who moved to another area of the building from the index case to practice for 45 minutes were less likely to become infected than those who remained in the main hall for the full duration of the rehearsal.

Twelve secondary cases of SARS-CoV-2 were linked to an index case, an 18-year-old chorister with high viral load who sang at four 1-hour services.[70] The index case was seated at a piano raised approximately 3 m from the ground floor and facing away from the secondary cases. Secondary cases sat between 1–15 m (horizontal distance) from the index case. Use of masks was not in place and there was minimal ventilation during the service (ventilation system was off, fans were off and doors and windows were largely closed). Interestingly, no new cases were linked to exposure that occurred the day of respiratory symptom-onset, and no explanation could be provided for why only a certain section near the chorister was affected and other sections (including those directly in front of the index case) were not.

In a case study by Shen et al. (2020), passengers who were not wearing masks were exposed to a presymptomatic index patient for 100 minutes while on a bus in eastern China.[61] Twenty-four of 67 passengers became infected, including several passengers seated beyond 2 m distance. The bus containing the index patient was heated and air was recirculated without filtration. Infections occurred in individuals at either end of the bus and the index case was located roughly in the middle. Risk of infection was only moderately higher for individuals sitting closer to the index patient. In contrast, seven

of 172 other people attending the same religious event were positive for SARS-CoV-2. Some of the cases became positive after 14 days from exposure; thus, transmission likely did not occur on the bus for these case. The authors of this study postulate that the poor ventilation in the bus supports aerosol transmission in this cluster; however, other routes of transmission such as close contact from movement within the bus or fomites could not be excluded.

Vehicles are also potential environments for short-range and long-range transmission. A patient transport van was implicated in long-range aerosol transmission despite physical distancing observed by the infected drivers in two distinct transmission events.[71] One driver did not wear a mask, but all passengers wore a single-layer mask. The passengers were exposed for 2 hours during both events. Transmission was confirmed by whole genome sequencing. Fans were on medium speed and windows were closed. Airflow experiments were conducted with different size aerosols demonstrating plausibility of spread from the driver.

An epidemiological investigation of a chain of transmissions was reported beginning with a flight from India to New Zealand, a bus ride to a quarantine facility, a stay at a quarantine facility, a bus ride to the airport, and subsequent household transmissions.[72] Based on positivity test dates, genome sequencing, flight positions and hotel room placement the transmission events were ascribed to both short-range and long-range transmission on flights, within the quarantine facility, and within households. Masks were required on flights and bus rides. One of the transmission events occurred between two adjacent hotel rooms in the quarantine facility. The authors used recorded video and observed >20 hours between any shared items and no direct contact. The authors concluded that fomite transmission was unlikely and attributed transmission to aerosols in the corridor outside of the hotel rooms wherein the space was enclosed and unventilated. Notably, the hotel rooms themselves, based on a review of the ventilation system, exerted positive pressure relative to the corridor.

An investigation by Lin et al. (2021) into an outbreak of nine COVID-19 cases from three families living in vertically-aligned units of an apartment building in Wuhan, China supported the possibility of long-range transmission.[66] Phylogenetic analysis of respiratory samples showed that all cases were infected by the same strain of SARS-CoV-2. Epidemiological investigation revealed that 4/5 cases of the index family in apartment 15-b had a travelling history to Wuhan, while the other four cases in apartments 25-b and 27-b had neither a travelling history to Wuhan nor close contact with any COVID-19 cases prior to their infection. Transmission through close contact in the elevators was considered unlikely as video records in the elevator did not show any close contact between the index family and the cases from units 25-b and 27-b. However, there was an incident where one unmasked occupant of unit 27-b took the elevator 8 minutes after two unmasked occupants from the index family had left the elevator. Epidemiologically, the infection rate for residents in units b was significantly higher ($p<0.05$) than that in units a and c. Testing of wind speed at the bathtub drain and floor drain found that the airflow produced by toilet flushing on one storey can influence the entire building as the drain pipes for toilets and the sewage pipes connected with floor drains were connected with the exhaust pipe. An experiment with a tracer gas indicated that gas could spread from one storey to another via the drainage and vent systems, especially as the seals in U-shaped traps in the floor drains were dried out in some units and the use of exhaust fans could create a negative pressure in the pipeline system. A similar situation was reported involving air ducts in a naturally ventilated apartment complex in Seoul, South Korea.[67] There were no valves blocking air from entering the bathrooms from the shared natural ventilation shafts (not for building or apartment unit ventilation). Limitations of this outbreak investigation included no genome sequencing or air sampling. Direct applicability to Canadian contexts may be limited by different building construction standards and practices.

Independent of ventilation, movement of air from an infected individual to others nearby can be an important factor in long-range transmission. Direct airflow was deemed responsible for a long-range transmission event in a restaurant in Korea.[73] The suspected index case sat 4.8 m and 6.5 m away and directly upwind of the airflow from two secondary cases at different tables. Nine other visitors in the restaurant did not test positive for SARS-CoV-2 even though at least two were closer to the index case for longer but not in the direct path of airflow originating from the index case. Notably the transmission in one case was suspected to have occurred from an exposure as short as five minutes, and three patrons sitting with the secondary cases but facing away from the index cases were not infected.

An investigation by Lu et al. (2020) into a COVID-19 outbreak in a restaurant in Guangzhou, China involving three families sitting at three tables in close proximity for about 1 hour concluded that the air conditioning (AC) system likely contributed to transmission.[63] In this scenario, a presymptomatic index case and secondary cases were present in the same area for 53–73 minutes. The location of a consistently running AC unit was in the airflow path of the secondary cases and was in an enclosed environment. No secondary cases occurred in staff or at adjacent tables that were outside of the likely "air column". The furthest distance between index and secondary cases was approximately 3 m. Additional investigation indicated that the exhaust fans had been closed due to cold outside temperatures.[74] The airflow assessment indicated that air was recirculating in a defined area, which exposed the three families.

A report involving group exercise at three facilities in Hawaii, US calculated attack rates of 25%–100%.[75] There was no fresh air ventilation and exposure occurred over a duration of 1 hour. Extended close contact and lack of masks in some cases were concluded as contributing to the transmission.

An outbreak in a multi-bed hospital room occurred wherein three patients and six health care workers became infected despite the use of masks and presence of ventilation of 3–4 ACH.[76] The presymptomatic index case was a parent located in a chair beside their child's bed who constantly wore a surgical mask, near the entrance to the room. Notably the air conditioning unit appeared to be located on the ceiling and no details were given about how it operated (e.g., constant versus timed/triggered) and what amount of fresh air circulation it provided. There were no exhaust vents indicated on the room diagram. Exposures for health care workers were in the range of 10–15 minutes, most at distances further than 2 m from the index patient. The report noted that masks were worn as personal protective equipment by health care workers. Transmission was based on the epidemiology of the outbreak without corroboration by genomic analysis of infections.

Detection of SARS-CoV-2 in Air Samples

Air sampling for virus refers to the process of collecting volumes of air by a device to determine if aerosols may contain virus. Collection can vary by aerodynamic size captured, duration of collection, volume per second collected, and media on which samples deposit. Air samples can then be tested by molecular methods such as reverse transcription PCR (RT-PCR) to amplify viral nucleic acids and/or viral culture. RT-PCR cannot determine whether the microorganisms detected are viable. Viral culture is used to determine whether a sample containing the virus is capable of replication. While there are several factors that contribute to the probability of infection, replication is a surrogate measure for inducing infection. To detect viability, researchers apply a sample to a susceptible cell culture and incubate up to a few weeks to detect morphological changes.

Detection of SARS-CoV-2 RNA in air samples has been inconsistent.[77] Multiple air sampling studies performed in proximity to confirmed COVID-19 cases were unable to detect any virus by RT-PCR.[78-86]

Kenarkoohi et al. detected SARS-CoV-2 RNA by RT-PCR in 1/5 samples from a ward containing intubated, severely ill patients, but did not find any positive air samples in other areas of the hospital such as wards with suspected, confirmed and mild patients (culturing of virus was not attempted in this study).[87] Chia et al. (2020), in an extended study of Ong et al. (2020), detected SARS-CoV-2 RNA by RT-PCR in air samples collected within 1 m of patients in two of three airborne infection isolation rooms (AIIRs) (no culture of virus attempted).[88] Lei et al. (2020) reported limited detection of SARS-CoV-2 RNA virus by air sampling in open wards, private isolation rooms and bathrooms.[85] One PCR-positive air sample was obtained during an endotracheal intubation within 10 cm of the patient's head in a naturally ventilated room (window open with fan attached), eleven other air samples near patients and 17 samples outside patient rooms and at nursing stations were PCR-negative.[89] The stage of infection and level of infectiousness of the patient populations sampled were not reported.

In a study of SARS-CoV-2 RNA in air samples collected from a variety of settings, Liu et al. (2020) reported that the highest concentration of viral RNA was reported from patient and staff areas of hospitals, compared to public areas.[90] Gharehchahi et al. (2021) (preprint) found SARS-CoV-2 RNA in 7/17 (41.2%) of air samples in a hospital for COVID-19 patients, including a mechanically-ventilated temporary waste storage area, two naturally-ventilated offices (one in the admission and discharge area, the other in an administrative department), and within 2 m of patients' beds in two intensive care units (ICUs), a negative pressure room, and an accident and emergency ward that are mechanically-ventilated with or without natural ventilation.[91] SARS-CoV-2 RNA was not detected from the four samples at nursing stations 2–5 m from patients' beds. The authors speculated that the detection of RNA in non-clinical areas could be due to inadequate ventilation and the occasional presence of infected health care workers.

Stern et al. (2021) sampled air in locations outside of patient care areas in an acute care hospital and found 8/90 (9%) of the samples positive for SARS-CoV-2 RNA, with concentrations ranging from 5–51 copies/m^3.[92] The size of the RNA-positive samples ranged from ≤2.5 to ≥10 μm. Locations adjacent to negative-pressured wards designated for COVID-19 patients did not appear to increase the likelihood of detecting viral RNA, having higher viral concentration, or finding particles of specific sizes in air samples. However, a significant positive association was observed between the average number of COVID-19 patients staying in the hospital during each sampling period, and the likelihood of an air sample testing positive for SARS-CoV-2 RNA. Furthermore, areas where staff congregated during times of high community rates of COVID-19 were associated with positive air samples. Of note, one RNA-positive air sample was taken when the unit was closed for cleaning and not under negative pressure, and the unit doors were left open for cleaning staff who had to pass by the air sampler to access the area for cleaning.

When air samples were RT-PCR-positive, culturing attempts were infrequently successful. In a systematic review and meta-analysis of 24 studies, Birgand et al. (2020) reported that 17.4% (82/471) of air samples from patient environments were RNA-positive (there was no difference in positivity at ≤1 m [2.5%] or 1–5 m [5.5%]; p=0.22), while culturing produced viable virus in 8.6% (7/81; 2 out of 5 studies) of samples.[93] A study by Guo et al. (2020) detected SARS-CoV-2 by RT-PCR in 35% (14/40) of air samples in an ICU and 12.5% (2/16) of air samples in the general ward that managed patients with COVID-19. Fifteen of 16 RT-PCR-positive air samples were from within 2 m of patients, with 1/8 samples positive at 4 m away.[12] Ben-Shmuel et al. (2020) conducted limited sampling (generally one air sample per area) in rooms with ventilated and non-ventilated patients, at a nursing station, and in private and public areas of a quarantine hotel.[94] RT-PCR-positive air samples were detected in a room with a ventilated patient (distance from patient was not reported) (n=1/1), at a nursing station (n=1/1), and in a quarantine hotel

room (n=1/1). However, there were no positive air samples in rooms of non-ventilated patients (n=0/3), a doffing area (n=0/1), and a public area of a quarantine hotel (n=0/1). The authors attempted viral culturing; however, no samples were positive.

At this time, only three studies, two from the same research group and one preprint from July 2020, have successfully cultured viable virus from the air. The preprint and one published study were already referred to above in the summary of Birgand et al. (2020). Sampling techniques and equipment may have caused the lack of culture viability despite RT-PCR detection in other studies. Future studies should aim to replicate the use of equipment and culture methods as these studies.

Lednicky et al. (2021) used a prototype and commercial version of an air sampler and custom RT-PCR probes for detection of SARS-CoV-2 in a patient room with two patients. One patient was discharged soon after sampling periods began and after receiving a negative RT-PCR test.[95] The remaining patient began experiencing respiratory illness two days prior to admission to the room. The study detected RT-PCR-positive air samples following 3 hours of sampling as well as positive viral cultures. Researchers positioned samplers 2–4.8 m from the recently symptomatic patient's head. The ventilation unit provided 6 ACH, filtering air and treating air with UV irradiation before recycling the air. Estimates of virus per volume of air ranged from 6–74 tissue culture infective dose $(TCID)_{50}$ units/L of air. Recently, a second study by Lednicky et al. was performed to detect viable SARS-CoV-2 virus from the front passenger seat area of a car driven by a SARS-CoV-2-positive patient without cough symptoms.[96] This study involved a sampler affixed to the sun visor in the passenger seat collecting particles sizes in ranges of <0.25 µm, 0.25–0.50 µm, 0.50–1.0 µm, 1.0–2.5 µm and >2.5 µm. The patient drove for 15 minutes with the windows up and air conditioner on. The sampler was turned off 2 hour after the patient completed the 15 minute drive. Viable virus was cultured only from the 0.25–0.5 µm fraction, which also had the highest quantity of detectable copies of viral RNA.

Further research is needed to reconcile differences in viral RNA detection and virus viability in air samples, despite RT-PCR-positive samples found on the surfaces of ventilation units.[97] Differences may be due to several factors, including: 1) air sampling devices are potentially not capable of maintaining viability of captured virus; 2) timing of air sampling varies by time since onset of symptoms, severity of disease or viral load; and 3) the conditions of ventilation (engineering controls) reducing concentrations of viral aerosols to undetectable levels. Even in rooms with high air exchanges, Tang et al.'s review of SARS-CoV-2 aerosols indicates that viral RNA copies can still be detected in air samples from patient rooms (1.8–3.4 viral RNA copies/m^3), toilet rooms (19 copies/m^3), and personal protective equipment doffing rooms (18–42 copies/m^3).[98] In a series of distinct room types (two AIIR with 15+ ACH, an isolation room without negative pressure and a shared cohort room) for patients admitted within 7 days of symptom-onset, Kim et al. reported that 32 air samples were negative and 20 air samples from anterooms were also negative.[86] Culturing viruses is technically challenging; therefore, the lack of positive cultures does not necessarily indicate an absence of infectious virus. On the other hand, the detection of SARS-CoV-2 viral RNA on surfaces that are rarely touched suggests that the virus may be transported through the air to those no-touch surfaces.[99]

Conclusions

Respiratory virus transmission occurs on a spectrum, from larger droplets that spread at short range, to aerosols that are present at short ranges but may also contribute to long-range transmission. As a result, categorizing SARS-CoV-2 transmission as either droplet or airborne does not accurately reflect this spectrum. Other respiratory viruses, like influenza, have similarly been described to demonstrate a spectrum of droplet sizes contributing to transmission.[100,101]

The highest risk of SARS-CoV-2 transmission likely occurs via close (<2 m), unprotected exposure (lacking multiple prevention measures) to an infectious individual. While there is a lower risk of transmission at longer distances with unprotected exposure, this kind of transmission has only been documented to occur under certain conditions, usually involving inadequate ventilation or with recirculation of unfiltered or untreated air in combination with activities involving increased exhalation/expulsion (e.g., shouting, singing, exercising), and often with a lack of source control masking.[102] Defining measures or cutoffs for inadequate ventilation was not possible based on the available descriptions of the contexts in which inadequate ventilation was reported to contribute to transmission. However, they included situations where air is circulated without filtration or exchange with fresh air, where there is no ventilation (e.g., windowless rooms without a ventilation system), and where the size of the room and ventilation rate relative to the quantity of infectious aerosols generated exceeds an unknown threshold of risk for infection. VOCs may be more effectively transmitted across all modes of transmission; however, there is no evidence that any VOCs transmit by fundamentally different routes.[103-105]

The delineation of relative contributions of short-range large respiratory droplets and aerosols and long-range aerosols to overall transmission patterns is complicated by the variable confluence of dynamic source/receptor factors and pathway factors. For example, each infector/infectee interaction is affected by source activities and amount of source viral load (e.g., forceful expulsion of droplets during coughing or singing, and timing in the course of illness), source/receptor adherence to preventative measures in place (e.g., hand hygiene, physical distancing, surface disinfection, mask-wearing and ventilation), and pathway factors that include airflow, UV, temperature, and humidity in indoor or outdoor environments.[16] It is likely that the relative contribution of respiratory particle size to transmission will depend on these combination of factors.

A large body of evidence is emerging related to SARS-CoV-2. Studies related to identification of a specific mode of transmission are generally low quality. Moreover, data from different fields (e.g., epidemiology versus modelling) can be at odds with respect to conclusions drawn about the role of different sized droplets in short-range transmission and relative importance of long-range transmission events. Ongoing study is needed for further evidence regarding the quantity of viral particles required to cause infection. Additional assessment of SARS-CoV-2 viability in aerosols is needed. Lastly, elucidation of setting-specific risk factors for transmission (e.g., differences between source/receptor and pathway factors in health care settings, residential buildings, schools, warehouses, transportation) may provide further insight into mechanisms for transmission.

The COVID-19 pandemic has identified the importance of interdisciplinary collaboration towards understanding and having a common lexicon for describing virus transmission. When the analysis and interpretation of data is challenged by variable terminology used between and within public health, clinicians, aerosol scientists and the public, this can limit progress towards identification and application of appropriate mitigation measures.[106]

Implications for Practice

This document summarizes the evolving evidence on transmission through respiratory particles and acknowledges the role for both larger droplets and aerosols in transmission. While our understanding of how transmission occurs has evolved and the relative contribution of droplets and aerosols continues to be studied, this may not necessitate a change in infection control measures, but highlights the importance of incorporating multiple infection control layers to mitigate transmission. Translation of this information into recommendations for control measures also needs to take into consideration evidence not reviewed in this document on the overall effectiveness of control measures to date: 1) effectiveness

of measures in isolation and in combination as layered mitigation; 2) effectiveness in the community vs. health care settings; and 3) effectiveness and the impact of implementation fidelity.

A detailed assessment of the evidence for infection prevention and control measures was out of scope for this document and thus limits discussion of recommendations for specific measures in different contexts. Of note, vaccination against SARS-CoV-2 is a relatively recent measure that is very effective at reducing transmission regardless of the mode of transmission and should be the priority control measure both in health care and community settings.[107]

In health care settings, recommendations for IPAC measures are described in *IPAC Recommendations for Use of Personal Protective Equipment for Care of Individuals with Suspect or Confirmed COVID-19* and *Interim Guidance for Infection Prevention and Control of SARS-CoV-2 Variants of Concern for Health Care Settings*.[7,8] These documents integrate the existing evidence around droplet, aerosol and contact transmission with jurisdictional experience with control measures and outbreak management to date, and recommends the use of the hierarchy of hazard controls to reduce the risk of transmission.

The bulk of disease transmission occurs in the community and in workplaces, not in health care settings. As SARS-CoV-2 transmits early in the course of infection, most commonly in the asymptomatic or presymptomatic period[108-111] and within the first two days of symptom-onset, cases may not seek health care during their most transmissible phase. In all settings it is necessary to utilize multiple control measures to mitigate the dynamic transmission factors and address potential routes of transmission. Infection prevention controls should also be context-dependent and take into account vaccination status/coverage, the ability to physically distance and avoid crowding, the feasibility of proper wearing of appropriate personal protective and source control equipment, training and education on the appropriate use of personal protective equipment, hand hygiene, surface disinfection, indoor ventilation, and early identification and isolation of infectious persons. Finally, application of measures should also be in the context of overall rates of community transmission and risk of exposure.

Several resources exist for community guidance (e.g., non-health care workplaces, public and private spaces) on how to reduce the risk of SARS-CoV-2 transmission through a layered approach of multiple public health measures designed to mitigate short-range and long-range transmission.[112-114] In general these involve avoiding the "3 C's": closed spaces, crowded places, and close contact. The degree to which various mitigation layers are necessary or possible will depend on the setting and risk context. Transmission can be mitigated through:

- Getting vaccinated[115,116] (higher vaccine coverage in the population can reduce risk for individuals unable to receive a vaccine)
- Staying home when sick[117,118] (e.g., active and passive screening prior to entry into public settings)
- Limiting the number and duration of contacts with individuals outside your household
- Physical distancing[114] and avoiding crowded spaces
- Consistently and appropriately using a well-fitted, well-constructed (2-3-layer) mask for source control and personal protective equipment.[119-122]
- Ensuring that ventilation systems[123] are well-maintained and optimized with the support of professionals according to relevant recommendations (e.g., from American Society of Heating,

Refrigerating and Air-Conditioning Engineers) and/or using outdoor environments whenever possible.

- Performing hand hygiene, respiratory etiquette, and environmental cleaning[124]

The above measures are effective means of reducing risk of transmission irrespective of the relative contribution of larger droplets or aerosols to transmission. Some controls will be more effective than others and it is the combination and consistent application of these controls that is most effective for reducing disease spread.

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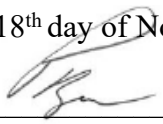
Ontario

This is **"Exhibit Q"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

World Health Organization

< Go back to all Coronavirus disease 2019 Q&As

Coronavirus disease (COVID-19): How is it transmitted?

13 December 2020 | Q&A

The English version was updated on 30 April 2021.

How does COVID-19 spread between people?

We know that the disease is caused by the SARS-CoV-2 virus, which spreads between people in several different ways.

The virus can spread from an infected person's mouth or nose in small liquid particles when they cough, sneeze, speak, sing or breathe. These particles range from larger respiratory droplets to smaller aerosols.

- **Current evidence suggests that the virus spreads mainly between people who are in close contact with each other, typically within 1 metre (short-range). A person can be infected when aerosols or droplets containing the virus are inhaled or come directly into contact with the eyes, nose, or mouth.**
- **The virus can also spread in poorly ventilated and/or crowded indoor settings, where people tend to spend longer periods of time. This is because aerosols remain suspended in the air or travel farther than 1 metre (long-range).**

People may also become infected by touching surfaces that have been contaminated by the virus when touching their eyes, nose or mouth without cleaning their hands.

Further research is ongoing to better understand the spread of the virus and which settings are most risky and why. Research is also under way to study virus variants that are emerging and why some are more transmissible. For updated information on SARS-CoV-2 variants, please read the weekly epidemiologic updates.

When do infected people transmit the virus?

What is the difference between people who are asymptomatic or pre-symptomatic? Don't they both mean someone without symptoms?

Are there certain settings where COVID-19 can spread more easily?

How can I reduce my risk of getting COVID-19?

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Related

Transmission of SARS-CoV-2: implications for infection prevention precautions

World Health Organization

< Go back to all Coronavirus disease 2019 Q&As

Coronavirus disease (COVID-19): How is it transmitted?

13 December 2020 | Q&A

The English version was updated on 30 April 2021.

How does COVID-19 spread between people?

When do infected people transmit the virus?

Whether or not they have symptoms, infected people can be contagious and the virus can spread from them to other people.

Laboratory data suggests that infected people appear to be most infectious just before they develop symptoms (namely 2 days before they develop symptoms) and early in their illness. People who develop severe disease can be infectious for longer.

While someone who never develops symptoms can pass the virus to others, it is still not clear how frequently this occurs and more research is needed in this area.

What is the difference between people who are asymptomatic or pre-symptomatic? Don't they both

What is the difference between people who are asymptomatic or pre-symptomatic? Don't they both mean someone without symptoms?

Are there certain settings where COVID-19 can spread more easily?

How can I reduce my risk of getting COVID-19?

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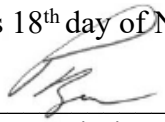
Related

Transmission of SARS-CoV-2: implications for infection prevention precautions

Access the publication

This is **"Exhibit R"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Avoid the Three Cs

World Health Organization
Western Pacific Region

Be aware of different levels of risk in different settings.

There are certain places where COVID-19 spreads more easily:

1

Crowded places

with many people nearby

2

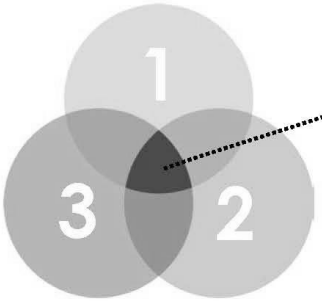
Close-contact settings

Especially where people have close-range conversations

3

Confined and enclosed spaces

with poor ventilation

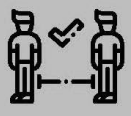


The risk is higher in places where these factors overlap.

Even as restrictions are lifted, consider where you are going and #StaySafe by avoiding the Three Cs.

WHAT SHOULD YOU DO?

Avoid crowded places and limit time in enclosed spaces



Maintain at least 1m distance from others

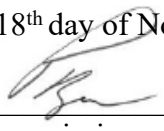
When possible, open windows and doors for ventilation

Keep hands clean and cover coughs and sneezes

Wear a mask if requested or if physical distancing is not possible

If you are unwell, stay home unless to seek urgent medical care.

This is **"Exhibit S"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

The airborne lifetime of small speech droplets and their potential importance in SARS-CoV-2 transmission

Valentyn Stadnytskyi[a], Christina E. Bax[b], Adriaan Bax[a,1], and Philip Anfinrud[a,1]

[a]Laboratory of Chemical Physics, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD 20892-0520; and [b]Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104

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Speech droplets generated by asymptomatic carriers of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) are increasingly considered to be a likely mode of disease transmission. Highly sensitive laser light scattering observations have revealed that loud speech can emit thousands of oral fluid droplets per second. In a closed, stagnant air environment, they disappear from the window of view with time constants in the range of 8 to 14 min, which corresponds to droplet nuclei of *ca.* 4 μm diameter, or 12- to 21-μm droplets prior to dehydration. These observations confirm that there is a substantial probability that normal speaking causes airborne virus transmission in confined environments.

COVID-19 | speech droplet | independent action hypothesis | respiratory disease | disease transmission

It has long been recognized that respiratory viruses can be transmitted via droplets that are generated by coughing or sneezing. It is less widely known that normal speaking also produces thousands of oral fluid droplets with a broad size distribution (*ca.* 1 μm to 500 μm) (1, 2). Droplets can harbor a variety of respiratory pathogens, including measles (3) and influenza virus (4) as well as *Mycobacterium tuberculosis* (5). High viral loads of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have been detected in oral fluids of coronavirus disease 2019 (COVID-19)–positive patients (6), including asymptomatic ones (7). However, the possible role of small speech droplet nuclei with diameters of less than 30 μm, which potentially could remain airborne for extended periods of time (1, 2, 8, 9), has not been widely appreciated.

In a recent report (10), we used an intense sheet of laser light to visualize bursts of speech droplets produced during repeated spoken phrases. This method revealed average droplet emission rates of *ca.* 1,000 s^{-1} with peak emission rates as high as 10,000 s^{-1}, with a total integrated volume far higher than in previous reports (1, 2, 8, 9). The high sensitivity of the light scattering method in observing medium-sized (10 μm to 100 μm) droplets, a fraction of which remain airborne for at least 30 s, likely accounts for the large increase in the number of observed droplets. Here, we derive quantitative estimates for both the number and size of the droplets that remain airborne. Larger droplets, which are also abundant but associated with close-proximity direct virus transfer or fomite transmission (11), or which can become resuspended in air at a later point in time (12), are not considered here.

According to Stokes' law, the terminal velocity of a falling droplet scales as the square of its diameter. Once airborne, speech-generated droplets rapidly dehydrate due to evaporation, thereby decreasing in size (13) and slowing their fall. The probability that a droplet contains one or more virions scales with its initial hydrated volume, that is, as the cube of its diameter, d. Therefore, the probability that speech droplets pass on an infection when emitted by a virus carrier must take into account how long droplet nuclei remain airborne (proportional to d^{-2}) and the probability that droplets encapsulate at least one virion (proportional to d^3), the product of which is proportional to d.

The amount by which a droplet shrinks upon dehydration depends on the fraction of nonvolatile matter in the oral fluid, which includes electrolytes, sugars, enzymes, DNA, and remnants of dehydrated epithelial and white blood cells. Whereas pure saliva contains 99.5% water when exiting the salivary glands, the weight fraction of nonvolatile matter in oral fluid falls in the 1 to 5% range. Presumably, this wide range results from differential degrees of dehydration of the oral cavity during normal breathing and speaking and from decreased salivary gland activity with age. Given a nonvolatile weight fraction in the 1 to 5% range and an assumed density of 1.3 $g{\cdot}mL^{-1}$ for that fraction, dehydration causes the diameter of an emitted droplet to shrink to about 20 to 34% of its original size, thereby slowing down the speed at which it falls (1, 13). For example, if a droplet with an initial diameter of 50 μm shrinks to 10 μm, the speed at which it falls decreases from 6.8 $cm{\cdot}s^{-1}$ to about 0.35 $cm{\cdot}s^{-1}$. The distance over which droplets travel laterally from the speaker's mouth during their downward trajectory is dominated by the total volume and flow velocity of exhaled air (8). The flow velocity varies with phonation (14), while the total volume and droplet count increase with loudness (9). Therefore, in an environment of stagnant air, droplet nuclei generated by speaking will persist as a slowly descending cloud emanating from the speaker's mouth, with the rate of descent determined by the diameter of the dehydrated speech droplet nuclei.

The independent action hypothesis (IAH) states that each virion has an equal, nonzero probability of causing an infection. Validity of IAH was demonstrated for infection of insect larvae by baculovirus (15), and of plants by Tobacco etch virus variants that carried green fluorescent protein markers (16). IAH applies to systems where the host is highly susceptible, but the extent to which IAH is valid for humans and SARS-CoV-2 has not yet been firmly established. For COVID-19, with an oral fluid average virus RNA load of 7×10^6 copies per milliliter (maximum of 2.35×10^9 copies per milliliter) (7), the probability that a 50-μm-diameter droplet, prior to dehydration, contains at least one virion is ∼37%. For a 10-μm droplet, this probability drops to 0.37%, and the probability that it contains more than one virion, if generated from a homogeneous distribution of oral fluid, is negligible. Therefore, airborne droplets pose a significant risk only if IAH applies to human virus transmission. Considering that frequent person-to-person transmission has been reported in community and health care settings, it appears likely that IAH

Author contributions: C.E.B., A.B., and P.A. designed research; V.S., A.B., and P.A. performed research; V.S. analyzed data; and C.E.B., A.B., and P.A. wrote the paper.

The authors declare no competing interest.

Data deposition: Movies that show the experimental setup and the full 85-minute observation of speech droplet nuclei have been deposited at Zenodo and can be accessed at https://doi.org/10.5281/zenodo.3770559.

[1]To whom correspondence may be addressed. Email: bax@nih.gov or philip.anfinrud@nih.gov.

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applies to COVID-19 and other highly contagious airborne respiratory diseases, such as influenza and measles.

Results and Discussion

The output from a green (532 nm) Coherent Verdi laser operating at 4-W optical power was transformed with spherical and cylindrical optics into a light sheet that is ∼1 mm thick and 150 mm tall. This light sheet passed through slits centered on opposite sides of a cubic 226-L enclosure. When activated, a 40-mm, 12-V muffin fan inside the enclosure spatially homogenizes the distribution of particles in the enclosure. A movie showing the arrangement is available (17). Movie clips of speech droplet nuclei were recorded at a frame rate of 24 Hz with high-definition resolution (1,920 × 1,080 pixels). The camera lens provided a horizontal field of view of ∼20 cm. Therefore, the volume intercepted by the light sheet and viewed by the camera is ∼30 cm^3. The total number of particles in the enclosure can be approximated by multiplying the average number of particles detected in a single movie frame by the volume ratio of the enclosure to the visualized sheet, which is ∼7,300. Slow convection currents, at speeds of a few centimeters per second, remained for the duration of the recording. These convection currents are attributed to a 0.5 °C temperature gradient in the enclosure (bottom to top) that presumably is due to heat dissipated by the iPhone11 camera, which was attached to the front side of the enclosure. Since the net air flux across any horizontal plane of the enclosure is zero, this convection does not impact the average rate at which droplet nuclei fall to the bottom of the enclosure.

With the internal circulation fan turned on, the enclosure was purged with HEPA-filtered air for several minutes. Then, the purge shutter was closed, the movie clip was started, the speaker port was opened, and the enclosure was "filled" with speech droplets by someone repeating the phrase "stay healthy" for 25 s. This phrase was chosen because the "th" phonation in the word "healthy" was found to be an efficient generator of oral fluid speech droplets. The internal fan was turned off 10 s after speech was terminated, and the camera continued recording for 80 min. The movie clip was analyzed frame by frame to determine the number of spots/streaks whose maximum single-pixel intensity exceeded a threshold value of 30. Fig. 1 charts the time-dependent decrease in the number of scattering particles detected. We are not yet able to quantitatively link the observed scattered light intensity to the size of the scattering particle because the light intensity varies across the sheet. However, the brightest 25% were found to decay more quickly than the dimmer fraction, with the two curves reasonably well described by exponential decay times of 8 and 14 min, respectively (Fig. 1*A*). These fits indicate that, near time 0, there were, on average, approximately nine droplet nuclei in the 30-cm^3 observation window, with the larger and brighter nuclei (on average) falling to the bottom of the enclosure at faster speeds than the smaller and dimmer ones.

With the assumption that the contents of the box are homogenized by the muffin fan at time 0, the average number of droplets found in a single frame near time 0 corresponds to *ca.* 66,000 small droplets emitted into the 226-L enclosure, or *ca.* 2,600 small droplet nuclei per second of speaking. If the particle size distribution were a delta function and the particles were uniformly distributed in the enclosure, the particle count would be expected to remain constant until particles from the top of the enclosure descend to the top of the light sheet, after which the particle count would decay linearly to background level. The observation that the decay profiles are approximately exponential points to a substantial heterogeneity in particle sizes, even after binning them into two separate groups.

The weighted average decay rate (0.085 min^{-1}) of the bright and dim fractions of particles (Fig. 1*A*) translates into a half-life in the enclosure of *ca.* 8 min. Assuming this half-life corresponds to the time required for a particle to fall 30 cm (half the height of the box), its terminal velocity is only 0.06 $cm{\cdot}s^{-1}$, which corresponds to a droplet nucleus diameter of ∼4 μm. At the relative humidity (27%) and temperature (23 °C) of our experiment, we expect the droplets to dehydrate within a few seconds. A dehydrated particle of 4 μm corresponds to a hydrated droplet of *ca.* 12- to 21-μm diameter, or a total hydrated volume of ∼60 nL to 320 nL for 25 s of loud speaking. At an average viral load of 7×10^6 per milliliter (7), we estimate that 1 min of loud speaking generates at least 1,000 virion-containing droplet nuclei that remain airborne for more than 8 min. These therefore could be inhaled by others and, according to IAH, trigger a new SARS-CoV-2 infection.

The longest decay constant observed by us corresponds to droplets with a hydrated diameter of ≥12 μm when exiting the mouth. The existence of even smaller droplets has been

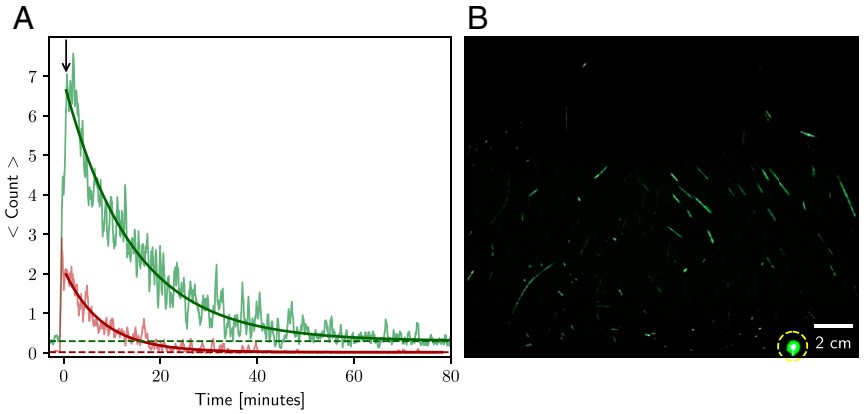

Fig. 1. Light scattering observation of airborne speech droplet nuclei, generated by a 25-s burst of repeatedly speaking the phrase "stay healthy" in a loud voice (maximum 85 dB_B at a distance of 30 cm; average 59 dB_B). (*A*) Chart of particle count per frame versus time (smoothed with a 24-s moving average), with the red curve representing the top 25% in scattering brightness and the green curve representing the rest. The bright fraction (red) decays with a time constant of 8 min, and the dimmer fraction (green) decays with a time constant of 14 min. Both exponential decay curves return to their respective background level of *ca.* 0 (red horizontal dashed line) and 0.4 (green dashed line) counts per frame. Time "0" corresponds to the time the stirring fan was turned off. The 25-s burst of speaking started 36 s before time 0. The black arrow (at 0.5 min) marks the start of the exponential fits. (*B*) Image of the sum of 144 consecutive frames (spanning 6 s) extracted shortly after the end of the 25-s burst of speaking. The dashed circle marks the needle tip used for focusing the camera. The full movie recording is available in ref. 17, with time "0" in the graph at time point 3:38 in the movie.

established by aerodynamic particle sizer (APS) measurements (2). APS is widely used for detecting aerosol particulates and is best suited for particles in the 0.5- to 5-μm range. Morawska et al. (2) detected as many as 330 particles per second in the 0.8- to 5.5-μm range upon sustained "aah" vocalization. Considering the short travel time (0.7 s) between exiting the mouth and the APS detector, and the high relative humidity (59%) used in that study, droplet dehydration may have been incomplete. If it were 75% dehydrated at the detector, an observed 5.5-μm particle would have started as an 8.7-μm droplet when exiting the mouth, well outside the 12- to 21-μm range observed above by light scattering. This result suggests that APS and light scattering measurements form a perfect complement. However, we also note that, even while the smallest droplet nuclei effectively remain airborne indefinitely and have half-lives that are dominated by the ventilation rate, at a saliva viral load of 7×10^6 copies per milliliter, the probability that a 1-μm droplet nucleus (scaled back to its originally hydrated 3-μm size) contains a virion is only 0.01%.

Our current setup does not detect every small particle in each frame of the movie, and our reported values are therefore conservative lower limit estimates. We also note that the saliva viral load shows large patient-to-patient variation. Some patients have viral titers that exceed the average titer of Wölfel et al. by more than two orders of magnitude (7, 18), thereby increasing the number of virions in the emitted droplets to well over 100,000 per minute of speaking. The droplet nuclei observed in our present study and previously by APS (2, 9) are sufficiently small to reach the lower respiratory tract, which is associated with an increased adverse disease outcome (19, 20).

Our laser light scattering method not only provides real-time visual evidence for speech droplet emission, but also assesses their airborne lifetime. This direct visualization demonstrates how normal speech generates airborne droplets that can remain suspended for tens of minutes or longer and are eminently capable of transmitting disease in confined spaces.

Data Availability Statement. All raw data used for analysis are available in ref. 17.

ACKNOWLEDGMENTS. We thank Bernhard Howder for technical support, Clemens Wendtner, William A. Eaton, Roland Netz, and Steven Chu for insightful comments. This work was supported by the Intramural Research Program of the National Institute of Diabetes and Digestive and Kidney Diseases.

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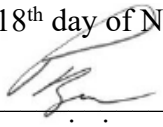
This is **"Exhibit T"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Title: Characteristics associated with household transmission of SARS-CoV-2 in Ontario, Canada

Authors:

Lauren A. Paul, MSc[a]	lauren.paul@oahpp.ca
Nick Daneman, MD[a-f]	nick.daneman@sunnybrook.ca
Kevin A. Brown, PhD[a,c,g]	kevin.brown@oahpp.ca
James Johnson, MPH[h]	james.johnson@oahpp.ca
Trevor van Ingen, MPH[f,i]	trevor.vaningen@oahpp.ca
Eugene Joh, MPH[a]	eugene.joh@oahpp.ca
Sarah E. Wilson, MD[a,c,g]	sarah.wilson@oahpp.ca
Sarah A. Buchan, PhD[a,c,g]	sarah.buchan@oahpp.ca

Affiliations:
[a]Health Protection, Public Health Ontario, 661 University Ave., Floor 17, Toronto, ON, M5G 1M1, Canada
[b]Sunnybrook Research Institute, Sunnybrook Health Sciences Centre, 2075 Bayview Ave., Toronto, ON, M4N 3M5, Canada
[c]ICES, 2075 Bayview Ave., Room G1 06, Toronto, ON, M4N 3M5, Canada
[d]Division of Infectious Diseases, Sunnybrook Health Sciences Centre, 2075 Bayview Ave., Room B1 03, Toronto, ON, M4N 3M5, Canada
[e]Department of Medicine, University of Toronto, 6 Queen's Park Cres. W, Floor 3, Toronto, ON, M5S 3H2, Canada
[f]Institute of Health Policy, Management and Evaluation, University of Toronto, 155 College St., Suite 425, Toronto, ON, M5T 3M6, Canada
[g]Dalla Lana School of Public Health, University of Toronto, 155 College St., Room 500, Toronto, ON, M5T 3M7, Canada
[h]Environmental and Occupational Health, Public Health Ontario, 480 University Ave., Suite 300, Toronto, ON, M5G 1V2, Canada
[i]Knowledge Services, Public Health Ontario, 480 University Ave., Suite 300, Toronto, ON, M5G 1V2, Canada

Corresponding Author:
Sarah Buchan, PhD
Public Health Ontario
661 University Avenue, Floor 17
Toronto, Ontario, M5G 1M1
Tel: 647-260-7274
Email: sarah.buchan@oahpp.ca

Abstract

BACKGROUND: Within-household transmission of SARS-CoV-2 infection has been identified as one of the main sources of spread of COVID-19 after lockdown restrictions and self-isolation guidelines are implemented. Secondary attack rates among household contacts are estimated to be five to ten 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 laboratory-confirmed cases of 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 neighbourhood characteristics associated with transmission.

FINDINGS: Between January and July, 2020, there were 26,152 cases of COVID-19 residing in 21,226 households. Longer testing delays (≥5 days versus 0 days OR=3·02, 95% CI: 2·53 - 3·60) and male sex (OR=1·28, 95% CI: 1·18 - 1·38) were associated with greater odds of household secondary transmission, while being a healthcare worker (OR=0·56, 95% CI: 0·50 - 0·62) was associated with lower odds of transmission. Neighbourhoods with larger average economic family size and a higher proportion of households with multiple persons per room were also associated with greater odds of transmission.

INTERPRETATION: 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 neighbourhoods with large family sizes and/or crowded households.

FUNDING: This study was supported by Public Health Ontario.

KEYWORDS: COVID-19; SARS-CoV-2; household; transmission

Research in Context

EVIDENCE BEFORE THIS STUDY: We searched PubMed and Google Scholar up to September 3, 2020 to identify individual-level cohort studies or meta-analyses on household transmission of COVID-19. We used the search terms ("COVID" OR "SARS-CoV-2") AND ("household" [Title]), and also reviewed the reference lists of any studies found during the search to identify additional studies. We considered studies that reported secondary attack rates and/or other measures of association (i.e., relative risk, odds ratio, or hazard ratio) for household transmission. We did not consider any modelling studies, studies that focused specifically on children, or small case studies that included less than three households. The search returned 53 studies, of which 51 were included in three meta-analyses. Pooled household secondary attack rates from the three meta-analyses were 19%, 27%, and 30%; secondary attack rates in households were estimated to be five to ten times as high as in non-household settings. Most studies were conducted in Asia and identified households from contact tracing, with individual studies reporting on fewer than 6000 households. Most studies did not consider households with no secondary transmission, and focused on a limited set of secondary case characteristics.

ADDED VALUE OF THIS STUDY: We applied an address matching algorithm, which identified 21,226 private households of laboratory-confirmed cases of COVID-19 in Ontario, Canada. Ontario has the advantage of a universal healthcare system and population-wide data for the entire province. To our knowledge, this study contains the largest number of private households with at least one confirmed case of COVID-19. We compared a variety of individual- and neighbourhood-level characteristics of households with and without secondary transmission. We also applied logistic regression models to determine index case characteristics associated with transmission, which gave important insights into factors that may help reduce secondary transmission in households.

IMPLICATIONS OF ALL THE AVAILABLE EVIDENCE: Findings from this study and existing evidence suggest that testing delays and household crowding play important roles in whether household secondary transmission occurs. Odds of household transmission may be reduced by cases seeking testing as soon as symptoms appear, and self-isolating outside the home or in a room alone if possible. These strategies may be considered by public health officials to reduce household transmission and mitigate local spread of COVID-19. Future research should further investigate the role of children and youth in household transmission.

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Contributors
LP performed the analysis and drafted the manuscript. SB, ND, and KB conceptualized the study. SB, ND, KB, and LP developed the methodology. SB, KB, and LP verified the underlying data. JJ and TvI contributed to the analysis. SB, ND, KB, JJ, TvI, EJ, and SW reviewed the manuscript.

Declaration of interests
The authors have no conflicts of interest to declare.

Data sharing
Data sharing requests should be directed to Public Health Ontario.

Introduction

Transmission and acquisition of SARS-CoV-2 infection has become an active area of COVID-19 research since person-to-person transmission was confirmed at the beginning of 2020.[1,2] In many countries, the primary source of acquisition of SARS-CoV-2 infection has transitioned from travel-related transmission early in the pandemic, to local transmission as countries implemented travel restrictions to reduce imported infections. Within-household transmission in particular has been highlighted as an important source of COVID-19 transmission for communities.[3–7] The shift to household transmission has arisen due to the fact that many public health measures, ranging from teleworking to full lockdowns, encourage individuals to spend more time at home where there is increased duration and intensity of contact among household members.[4,5] However, it is unclear which individuals are more likely to transmit infection within their households.

Existing individual-level observational studies of household transmission typically included household contacts identified through contact tracing.[4–6,8–10] These studies have estimated secondary attack rates among household contacts to be five to ten times as high as in non-household settings.[4,6] Most of these studies were conducted in Asia, included smaller numbers of households, and/or did not compare to households where no secondary 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) in the household.

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 characteristics of cases in households that experienced secondary transmission (i.e., additional laboratory-confirmed cases following the index case) versus those that did not, and also sought to determine individual- and neighbourhood-level characteristics of index cases associated with transmission. This work may help inform future public health strategies to reduce within-household transmission during the ongoing pandemic.

Methods

Study population

We assembled a cohort of all confirmed cases of COVID-19[11] reported in Ontario, Canada's most populous province (14 million residents), among residents of private households from January 1, 2020 to July 28, 2020. We identified confirmed cases of COVID-19 using data from provincial reportable disease systems 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 multi-unit dwellings (e.g., apartment buildings) were considered private households. For address matching, we applied a natural language processing algorithm using Python's sklearn library to identify unique households that contained at least one COVID-19 case.[13] Briefly, we broke down cases' whole address fields (including street address, city, and postal code) and found a closest match in a master list of addresses, containing congregate facilities and previously identified households. This match was then validated by checking for exact matches in the numerical portion of the address field. For unmatched addresses, we again used a natural language processing algorithm to identify duplicates, and added unique addresses to the master list for future comparisons. We excluded any cases whose address matched a known congregate facility or who had a risk factor flag for residing in a congregate setting in provincial reportable disease systems. We also examined addresses that were matched with apartment buildings in the master list for suite information, and excluded cases missing suite information as we were unable to determine conclusively whether these individuals resided in the same suite as others in the building. We excluded any cases with missing or incomplete address information.

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.[8,10,14] 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 cases on the index date ("index clusters") from the cohort as they would present challenges for estimating the predictive value of individual-level characteristics. We also considered two secondary outcomes of interest: household transmission to older adults (≥60 years), and household transmission to severe cases (ICU admission or death).

Individual-level characteristics

We considered a variety of individual-level and neighbourhood-level covariates in our analyses that were hypothesized to influence household transmission. At the individual level, we obtained information on each case's age, sex, and health region of residence (Supplementary Table S1). 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 known COVID-19 outbreak outside the home (e.g., association with a workplace outbreak or long-term care home outbreak).[11]

We also considered three delay metrics for each case: (1) the delay between the case's symptom onset and when their 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 begins 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 that 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 neighbourhood level.

Neighbourhood-level characteristics

At the neighbourhood level, we had information available from 2016 Canadian census records (98·4% response rate[15]). 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.[15] We linked neighbourhood characteristics at the aggregate dissemination area level, which divides the country into areas with populations between 5,000 and 15,000 persons, on average. These included characteristics such as the average economic family size, proportion of households with multiple persons per room, proportion of multi-family households, and urban/rural status (see Supplementary Definitions). A full list of the neighbourhood characteristics is found in Table 3.

Statistical analysis

We applied logistic regression models to obtain both unadjusted and adjusted odds ratios (OR) and 95% confidence intervals (CI) for the associations between covariates and the odds of secondary transmission within a household. We also carried out several descriptive analyses to compare the characteristics of index cases, secondary cases, and cases that were not involved in any household transmission. We explored the breakdown of these groups by outcome severity (i.e., hospital admission, ICU admission, death, or no serious or severe outcome) and examined the direction of transmission by age group and high risk status. We 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 May 29; testing approaches expanded as of May 29, which may have improved the ability to identify secondary transmission in households.[16]

Role of the funding source

This study was supported by Public Health Ontario. The authors had full access to all data in the study and accept responsibility for the decision to submit for publication.

Results

As of July 28, 2020, there were 38,984 confirmed cases of COVID-19 reported in Ontario. After removing cases based on our inclusion criteria, we were left with 26,152 cases residing in private households, of which 18,159 cases were from households with no secondary transmission and 7,993 cases were from households with secondary transmission (Figure 1). Of the 3,067 index cases from households with secondary transmission, the median number of secondary cases in the same household was one (25^{th} percentile=one case, 75^{th}=two cases, 90^{th}=three cases). The average age of the cohort was approximately 44 years and 53% were female.

Timing and direction of transmission

The median serial interval from index case to secondary case was four days (25^{th} percentile=two days, 75^{th}=seven days, 90^{th}=ten days) (Supplementary Figure S1). For the direction of transmission from index cases to secondary cases, individuals in the 20-59 year age group and low risk individuals were both the most frequent transmitters and most frequent acquirers of SARS-CoV-2 infections within households (Figure 2). Transmissions to secondary cases in different age or risk groups than the index case were less frequent.

Comparison of individual-level characteristics

Compared to index cases with no household transmission, index cases with household transmission were less likely to be healthcare workers or associated with a known COVID-19 outbreak (Table 1). However, they were more likely to be male and had median testing delays that were twice as long as index cases without household transmission (four days versus two days). There was no difference in median reporting delay or data entry delay for the two 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 S2). They were also less likely to have serious or severe outcomes (Supplementary Table S3).

Associations with delay metrics

From adjusted logistic models, we observed increased odds of any household transmission with longer testing delays for the index case compared to 0-day (i.e., the individual was tested on the same day as their 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 3, Supplementary Table S4). Individuals with no symptoms flagged in provincial reportable diseases systems had lower odds of any household transmission (0·48, 95% CI: 0·38 - 0·61). This trend was similar in our models for household transmission to older adults and to cases with severe outcomes. Conversely, there were no notable trends for increased odds of household transmission with reporting delays or data entry delays.

Associations with other individual-level characteristics

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 to female index cases, and older (≥60 years) and younger (20-49 years) index cases had lower odds of any household transmission compared to the 50-59 year reference group (Table 2). We observed increased odds of household transmission if the index case was high risk (1·14, 95% CI: 0·97 - 1·34), and decreased odds if the index case was a healthcare worker (0·56, 95% CI: 0·50 - 0·62) or was associated with a known outbreak (0·61, 95% CI: 0·55 - 0·68). There were also some trends for decreased odds of transmission from May to July.

Associations with neighbourhood-level characteristics

The strongest associations observed for household transmission were in neighbourhoods with larger average economic family size (1·88 per person increase, 95% CI: 1·70 - 2·09 per person increase) or neighbourhoods with a higher proportion of households with multiple persons per room (1·25 per 10% increase, 95% CI: 1·13 - 1·38). We also observed increased odds for neighbourhoods with a higher proportion of multi-family 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 neighbourhoods with a higher proportion of individuals in the ≥65 year age group; individuals below the low income cut off; individuals with less than high school education; unsuitable housing; recent immigrants; non-White, non-Indigenous groups; and apartments with five or more floors

(Table 2). Odds were lower for neighbourhoods with a higher proportion of individuals participating in the labour force, as well as more remote areas compared to large urban areas.

Sensitivity analysis

We compared the estimates from our primary outcome model with those produced in our three sensitivity analyses (i.e., household transmission 2-14 days after index cases and 1-28 days after index cases, and index case dates on or after May 29), and found that our associations were robust (Supplementary Table S5). Notably, longer testing delays continued to display strong trends towards increased odds of household transmission. Larger average economic family size and a higher proportion of households with multiple persons per room also continued to exhibit the strongest associations at the neighbourhood level.

Results from unadjusted models are not presented, but overall displayed similar associations to the adjusted models.

Discussion

In this retrospective study of 26,152 confirmed cases of COVID-19 residing in 21,226 private households, we found that longer testing delays and male sex were associated with greater odds of household secondary transmission, while being a healthcare worker or linked to a known outbreak was associated with lower odds of household transmission. Additionally, neighbourhoods with larger average economic 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 (SARs), defined as the proportion of household members of confirmed cases that acquire infection. The majority of these studies were conducted in Asia, and 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 SARs of 19% (95% CI: 15% - 23%), 27% (21% - 32%), and 30% (18% - 43%), respectively. Some of the included studies compared SARs in household settings verses non-household settings, and pooled estimates found that household SARs were five[4] to ten[6] times as high as non-household SARs, which highlights the role of household transmission in the spread of COVID-19.

We identified only two other studies that considered the impact of testing delays on household transmission; Xin et al.[17] and Wang et al.[14] examined the time from illness onset to laboratory confirmation. They reported hazard ratios for household transmission of 2·32 (95% CI 0·89 - 6·10) (<7-day delays versus ≥7-day delays) calculated from 106 households, and 2·35 (95% CI 0·63 - 8·77) (<3-day delays versus ≥3-day delays) calculated from 124 households, respectively. It has been estimated that infectivity peaks 3-5 days after symptom onset[18,19], 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 SARs among asymptomatic or mildly symptomatic individuals[4,20], although it may be that SARs are underestimated in these groups due to lower testing rates.[20] 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, two studies found similar positive associations with male sex and immunodeficiency[8], and an inverse association with healthcare employment.[21] In addition to healthcare employment, we also found lower odds of household transmission among individuals linked to a known outbreak. This may reflect testing practices, where outbreak-linked cases are identified and isolated faster than non-outbreak-linked cases. 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 access to or use of personal protective equipment as compared to non-healthcare workers.

Madewell et al.[4] and Lopez Bernal et al.[10] further reported inverse relationships between household size and SAR. These findings are contrasted to our result of higher odds of household transmission among neighbourhoods with larger average economic 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 >2 persons per bedroom compared to 1-2 persons per bedroom. Our findings of

higher odds of household transmission among neighbourhoods with a higher proportion of multiple persons per room and multi-family households may support this hypothesis, and our association with economic family size may be capturing aspects of household crowding at the neighbourhood-level (e.g., neighbourhoods with larger average economic family size tended to be neighbourhoods with a higher proportion of multiple persons per room). One approach that has been implemented in some jurisdictions to mitigate this issue is voluntary self-isolation facilities for those who are unable to self-isolate in their home. 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 included households experienced secondary transmission. As we did not have information on total household size, it may be that we included 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 or the characteristics of uninfected household members, thus we were unable to calculate the proportion of household contacts infected to generate SARs. However, we were able to control for some neighbourhood-level characteristics of household composition including economic family size and proportion of households with multiple persons per room or multi-family households. 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 (e.g., asymptomatic or symptomatic but did not seek testing), and we may have misclassified some secondary cases if their infection was acquired outside the household. We may also have missed secondary cases within a household that were untested. Third, we only considered one index case per household, and considered all subsequent cases within a 14-day period to be secondary cases (i.e., did not account for tertiary transmission). Fourth, as this study encompasses a period before schools were re-opened in the fall, there were few index cases among children (N=190) and as such, we were not able to determine the extent to which children played a role in household 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 one 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 fewer than 6000 households) compared to the 21,226 households we were able to identify through address matching of all confirmed cases of 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 one study from Israel that used a municipal database of residents to identify household members of cases.[22] Additionally, we considered a large set of individual- and neighbourhood-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.

Conclusion

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. These strategies may be considered by public health officials to reduce household transmission and help mitigate the ongoing spread of COVID-19. Future research should focus on 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.

Figure 1. Flow diagram of study cohort

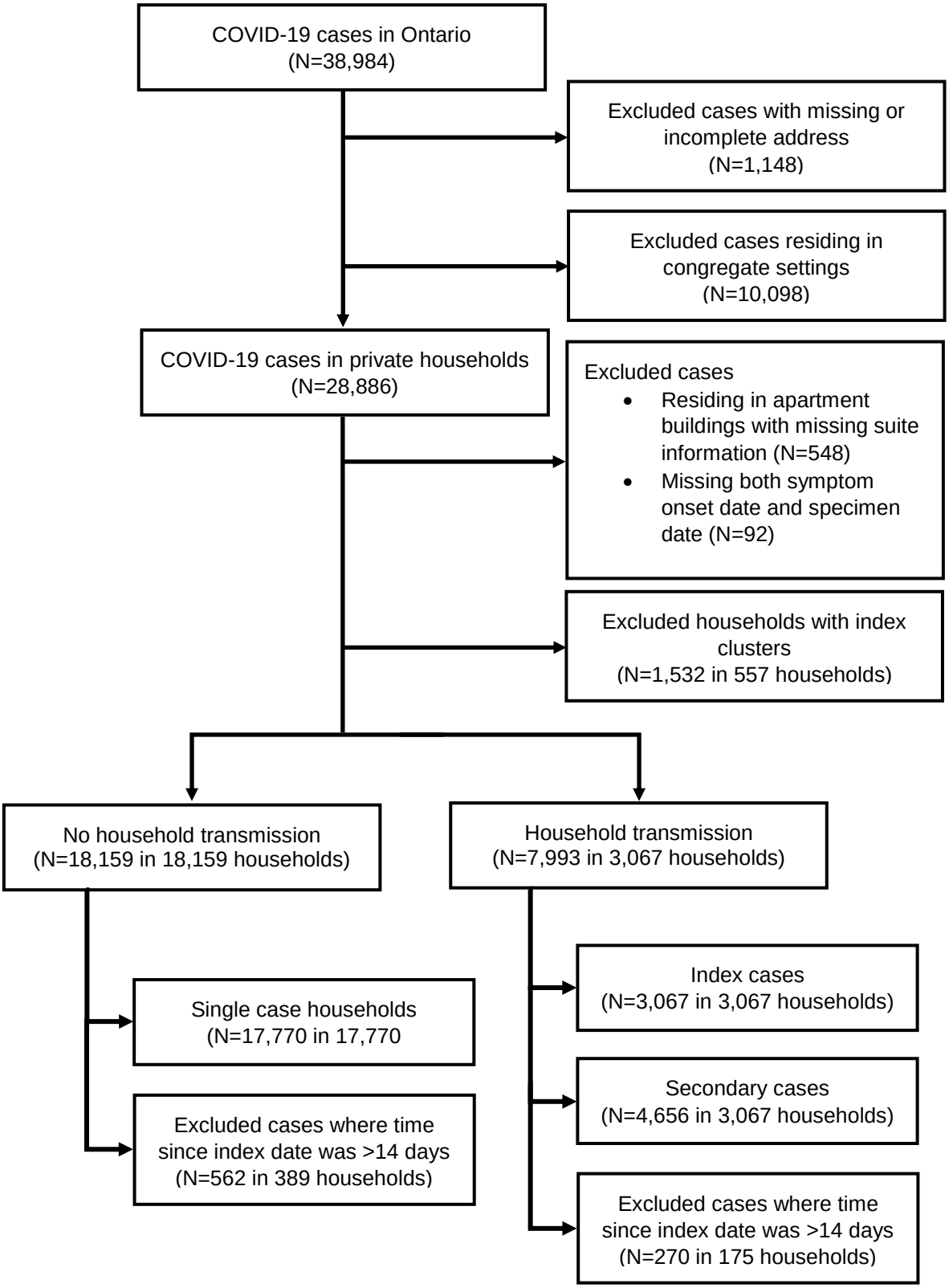
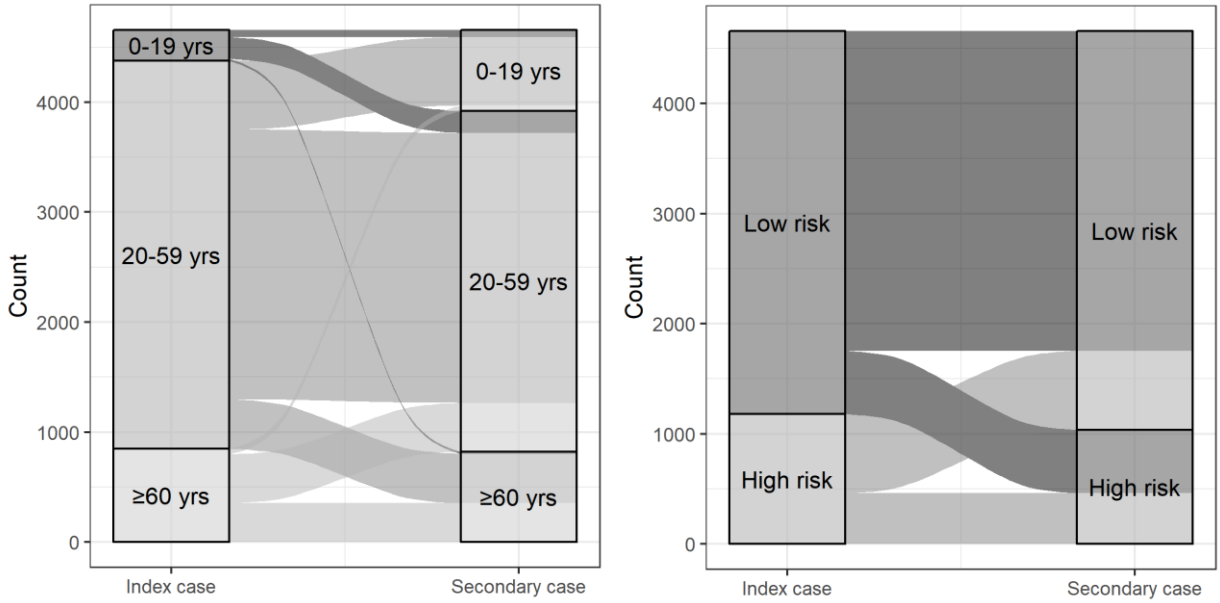


Figure 2. Direction of transmission from index case to secondary case by (A) age group and (B) high risk status



The line represents the direction of transmission from index case to secondary case. The shade of the line represents the age group or risk group of the index case. The width of the line is proportional to the frequency of transmission between index and secondary cases in their respective age or risk groups.
Yrs=years.

Table 1. Characteristics of index cases in households with no household transmission compared to index cases of households with household transmission

	Index cases with no household transmission (N=18,159)	**Index cases with household transmission (N=3,067)**
Sex (N, %)		
Female	9,890 (54·5)	1,464 (47·7)
Male	8,214 (45·2)	1,595 (52·0)
Age, years (median, IQR)	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	3,387 (18·7)	523 (17·1)
30-39 years	3,169 (17·5)	481 (15·7)
40-49 years	3,256 (17·9)	571 (18·6)
50-59 years	3,711 (20·4)	726 (23·7)
60-69 years	2,271 (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, %)	5,066 (27·9)	844 (27·5)
Outbreak-associated* (N, %)	4,901 (27·0)	540 (17·6)
Healthcare worker (N, %)	4,916 (27·1)	517 (16·9)
Month reported (N, %)		
January	1 (0·0)	1 (0·0)
February	8 (0·0)	3 (0·1)

March	2,009 (11·1)	312 (10·2)
April	6,374 (35·1)	945 (30·8)
May	4,978 (27·4)	989 (32·2)
June	2,931 (16·1)	528 (17·2)
July	1,858 (10·2)	289 (9·4)
Region (N, %)		
Toronto	6,292 (34·6)	1,025 (33·4)
Central East	5,891 (32·4)	1,236 (40·3)
Central West	2,445 (13·5)	343 (11·2)
Eastern	1,569 (8·6)	231 (7·5)
Northern	199 (1·1)	32 (1·0)
South West	1,763 (9·7)	200 (6·5)
Testing delay†, days (median, IQR)	2 [0, 6]	4 [2, 8]
Testing delay distribution† (N, %)		
No symptoms‡	2,883 (16·2)	131 (4·3)
<0 days§	963 (5·4)	60 (2·0)
0 days	1,745 (9·8)	164 (5·4)
1 day	1,955 (11·0)	349 (11·5)
2 days	1,958 (11·0)	341 (11·2)
3 days	1,560 (8·8)	327 (10·8)
4 days	1,230 (6·9)	276 (9·1)
≥5 days	5,529 (31·0)	1,390 (45·8)
Reporting delay, days (median, IQR)	2 [1, 3]	2 [1, 3]
Reporting delay distribution (N, %)		
<0 days	312 (1·7)	43 (1·4)
0 days	1,165 (6·4)	200 (6·5)
1 day	5,931 (32·8)	1,038 (34·0)
2 days	5,276 (29·2)	926 (30·3)
3 days	2,414 (13·4)	390 (12·8)
4 days	1,010 (5·6)	188 (6·2)
≥5 days	1,966 (10·9)	271 (8·9)
Data entry delay, days (median, IQR)	0 [0, 1]	0 [0, 1]
Data entry delay distribution (N, %)		
<0 days	1,065 (5·9)	173 (5·6)
0 days	11,050 (60·9)	1,852 (60·4)
1 day	3,699 (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)

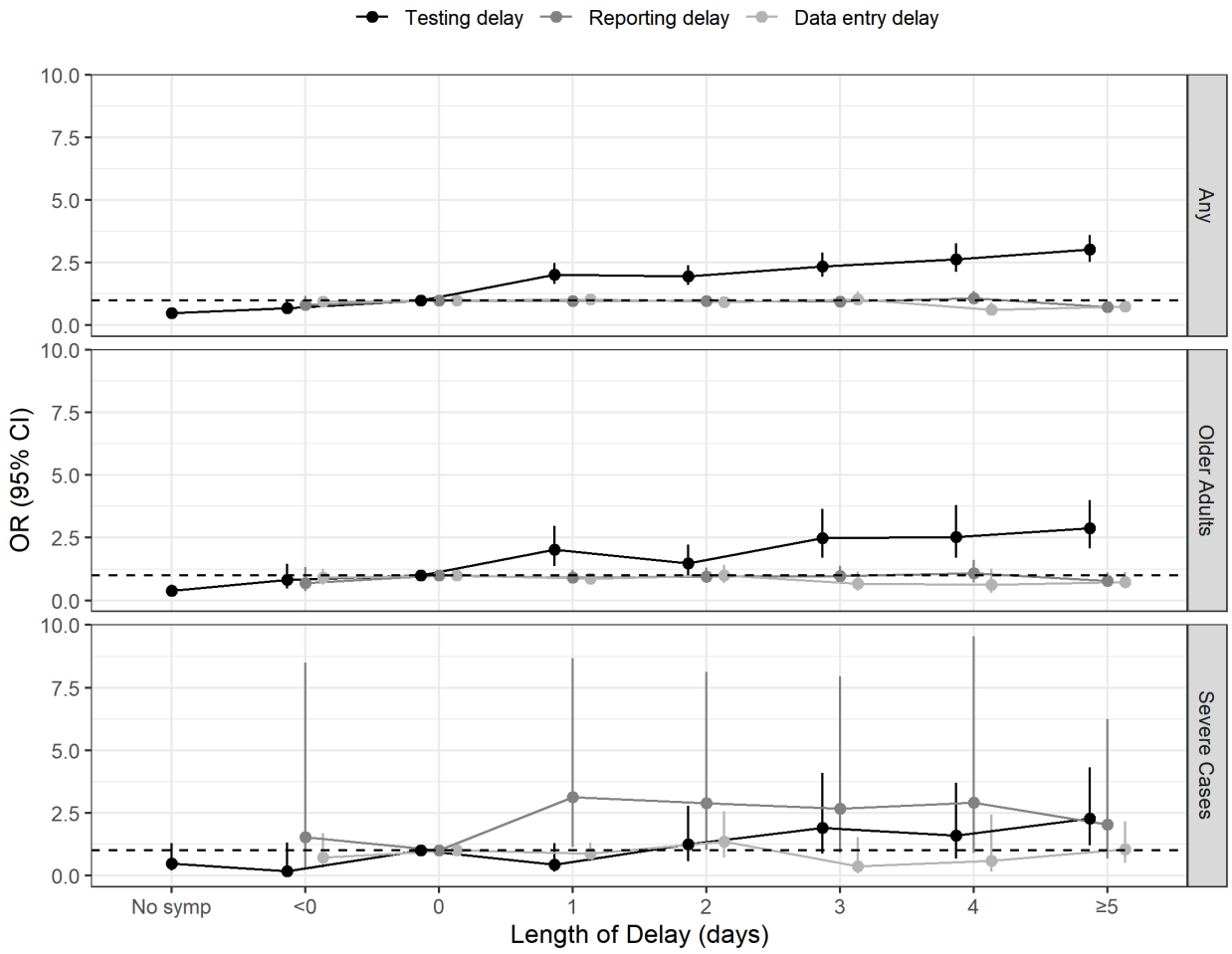
*Cases associated with a public health declared outbreak outside the home.

†269 cases were excluded 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 that 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.

Figure 3. Adjusted odds ratios and 95% confidence intervals for the associations between index case delay metrics and odds of household transmission



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 that 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 line at OR=1 indicating no association.
No symp=no symptoms.

Table 2. Adjusted odds ratios and 95% confidence intervals for the associations between index case characteristics and odds of household transmission

	OR (95% CI)*		
	Any household transmission	**Household transmission to older adults (aged ≥60 years)**	**Household transmission to severe cases (ICU or death)**
Individual-level characteristics			
Sex			
Female	Ref	Ref	Ref
Male	1·28 (1·18 - 1·38)	1·19 (1·02 - 1·38)	0·94 (0·68 - 1·32)
Age group			
<10 years	0·87 (0·57 - 1·34)	0·18 (0·02 - 1·27)	Insufficient data
10-19 years	1·20 (0·97 - 1·49)	0·65 (0·37 - 1·17)	0·83 (0·25 - 2·74)
20-29 years	0·78 (0·69 - 0·89)	0·60 (0·45 - 0·80)	0·54 (0·30 - 1·00)
30-39 years	0·80 (0·71 - 0·91)	0·72 (0·55 - 0·94)	0·50 (0·27 - 0·93)
40-49 years	0·90 (0·80 - 1·02)	0·66 (0·50 - 0·86)	0·92 (0·56 - 1·51)
50-59 years	Ref	Ref	Ref
60-69 years	0·93 (0·81 - 1·06)	2·15 (1·72 - 2·69)	0·90 (0·52 - 1·56)
70-79 years	0·78 (0·64 - 0·95)	2·67 (2·04 - 3·49)	1·66 (0·90 - 3·05)
≥80 years	0·58 (0·45 - 0·76)	2·07 (1·49 - 2·88)	1·97 (1·04 - 3·76)
High risk (≥60 years, immunocompromised, cardiovascular, COPD)			
No	Ref	Ref	Ref
Yes	1·14 (0·97 - 1·34)	1·17 (0·84 - 1·64)	1·08 (0·55 - 2·12)
Outbreak-associated†			
No	Ref	Ref	Ref
Yes	0·61 (0·55 - 0·68)	0·49 (0·39 - 0·61)	0·41 (0·26 - 0·66)
Healthcare worker			
No	Ref	Ref	Ref
Yes	0·56 (0·50 - 0·62)	0·47 (0·37 - 0·59)	0·40 (0·25 - 0·66)
Month reported			
January	7·91 (0·46 - 136·45)	Insufficient data	Insufficient data
February	2·55 (0·67 - 9·77)	4·25 (0·86 - 20·95)	Insufficient data
March	1·09 (0·95 - 1·26)	1·48 (1·18 - 1·86)	1·14 (0·70 - 1·84)
April	Ref	Ref	Ref
May	1·25 (1·13 - 1·38)	1·12 (0·93 - 1·36)	0·78 (0·53 - 1·16)
June	1·14 (1·01 - 1·28)	0·90 (0·70 - 1·14)	0·31 (0·15 - 0·62)
July	1·04 (0·90 - 1·21)	0·85 (0·62 - 1·16)	0·19 (0·06 - 0·62)
Region			
Toronto	Ref	Ref	Ref
Central East	1·04 (0·94 - 1·15)	1·22 (1·01 - 1·47)	1·04 (0·70 - 1·54)
Central West	0·91 (0·79 - 1·04)	0·87 (0·66 - 1·15)	0·62 (0·33 - 1·17)
Eastern	1·08 (0·92 - 1·26)	1·02 (0·75 - 1·39)	0·80 (0·40 - 1·59)
Northern	1·28 (0·87 - 1·89)	1·30 (0·65 - 2·61)	1·80 (0·55 - 5·89)
South West	0·84 (0·71 - 0·99)	0·77 (0·55 - 1·08)	0·41 (0·16 - 1·03)
Neighbourhood-level characteristics‡			
% Age group			
0-14 years	0·89 (0·78 - 1·02)	0·69 (0·53 - 0·89)	0·63 (0·35 - 1·12)
15-64 years	0·93 (0·84 - 1·02)	0·84 (0·70 - 1·01)	0·80 (0·53 - 1·18)
≥65 years	1·12 (1·02 - 1·22)	1·34 (1·14 - 1·58)	1·44 (1·01 - 2·05)
% Male	0·89 (0·68 - 1·16)	0·95 (0·58 - 1·56)	1·25 (0·45 - 3·46)
% Recent immigrants	1·35 (1·21 - 1·51)	1·13 (0·92 - 1·41)	1·68 (1·09 - 2·59)
% Non-White, non-Indigenous	1·05 (1·03 - 1·08)	1·04 (0·99 - 1·09)	1·12 (1·01 - 1·23)
Non-White, non-Indigenous groups			

% Black	1·05 (1·00 - 1·11)	0·93 (0·83 - 1·04)	0·85 (0·66 - 1·10)
% East/Southeast Asian	1·02 (0·98 - 1·06)	1·04 (0·98 - 1·10)	1·13 (1·00 - 1·28)
% Latin American	1·41 (1·19 - 1·66)	1·18 (0·84 - 1·65)	0·64 (0·28 - 1·45)
% Middle Eastern	1·06 (0·96 - 1·17)	0·83 (0·67 - 1·02)	1·43 (0·97 - 2·12)
% South Asian	1·04 (1·00 - 1·08)	1·09 (1·02 - 1·16)	1·14 (0·98 - 1·32)
% Below low income cut-off	1·06 (1·00 - 1·13)	0·94 (0·83 - 1·06)	1·23 (0·97 - 1·57)
% Labour force participation	0·89 (0·83 - 0·95)	0·87 (0·77 - 0·99)	0·67 (0·50 - 0·89)
% Less than high school education	1·08 (1·02 - 1·15)	1·02 (0·91 - 1·15)	1·04 (0·81 - 1·35)
% Unsuitable housing§	1·19 (1·11 - 1·27)	1·02 (0·89 - 1·17)	1·27 (0·98 - 1·65)
% Households with multiple persons per room§	1·25 (1·13 - 1·38)	1·10 (0·90 - 1·34)	1·62 (1·15 - 2·29)
% Multi-family households§	1·10 (0·92 - 1·31)	1·63 (1·17 - 2·26)	1·16 (0·55 - 2·44)
Economic family size§	1·88 (1·70 - 2·09)	1·82 (1·50 - 2·21)	1·58 (1·02 - 2·44)
% Households living in apartments with ≥5 floors	1·02 (1·00 - 1·04)	1·00 (0·97 - 1·04)	1·06 (0·98 - 1·15)
% Households living in apartments with <5 floors	1·00 (0·96 - 1·04)	0·93 (0·86 - 1·01)	0·85 (0·70 - 1·03)
Community type§			
Large urban	Ref	Ref	Ref
Medium/small	0·93 (0·78 - 1·10)	0·90 (0·65 - 1·25)	0·83 (0·39 - 1·80)
Rural	0·97 (0·79 - 1·18)	1·05 (0·72 - 1·53)	1·03 (0·43 - 2·45)
Remote	0·73 (0·53 - 1·01)	1·07 (0·64 - 1·79)	0·57 (0·13 - 2·49)

*Estimates were adjusted for age group, sex, month reported, health region, and economic family size.

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

‡Odds ratios for neighbourhood-level characteristics are reported per 10% increase, except for economic family size and community type.

§Defined in Supplementary Definitions.

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This is **"Exhibit U"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

A Commissioner, etc.

COVID-19 Outbreak Associated with a 10-Day Motorcycle Rally in a Neighboring State — Minnesota, August–September 2020

Melanie J. Firestone, PhD[1,2]; Haley Wienkes, MPH[1]; Jacob Garfin[1]; Xiong Wang, DVM, PhD[1]; Kelley Vilen, MPH[1]; Kirk E. Smith, DVM, PhD[1]; Stacy Holzbauer, DVM[1,3]; Matthew Plumb, MS[1]; Kelly Pung[1]; Carlota Medus, PhD[1]; Joseph D. Yao, MD[4]; Matthew J. Binnicker, PhD[4]; Andrew C. Nelson, MD, PhD[5]; Sophia Yohe, MD[5]; Kathryn Como-Sabetti, MPH[1]; Kris Ehresmann, MPH[1]; Ruth Lynfield, MD[1]; Richard Danila, PhD[1]

On November 20, 2020, this report was posted as an MMWR *Early Release on the* MMWR *website (https://www.cdc.gov/mmwr).*

During August 7–16, 2020, a motorcycle rally was held in western South Dakota that attracted approximately 460,000 persons from across the United States to numerous indoor and outdoor events over a 10-day period. During August–September 2020, the Minnesota Department of Health (MDH) investigated a coronavirus disease 2019 (COVID-19) outbreak associated with the rally in Minnesota residents. Fifty-one primary event-associated cases were identified, and 35 secondary or tertiary cases occurred among household, social, and workplace contacts, for a total of 86 cases; four patients were hospitalized, and one died. Approximately one third (34%) of 87 counties in Minnesota had at least one primary, secondary, or tertiary case associated with this rally. Genomic sequencing supported the associations with the motorcycle rally. These findings support current recommendations for mask use, physical distancing, reducing the number of attendees at gatherings, isolation for patients with COVID-19, and quarantine for close contacts to slow the spread of SARS-CoV-2 (*1*). Furthermore, although these findings did not capture the impact of the motorcycle rally on residents of other states, they demonstrate the rationale for consistent mitigation measures across states.

Investigation and Findings

On August 21, 2020, MDH identified confirmed COVID-19 cases in persons who reported attending the motorcycle rally in the neighboring state of South Dakota. A primary, event-associated case was defined as an illness in a person who reported attending the rally or who traveled to western South Dakota by motorcycle during August 7–16 and who had symptom onset or specimen collection before August 30 (within 14 days after the end of the rally). Reverse transcription–polymerase chain reaction testing for SARS-CoV-2, the virus that causes COVID-19, was used to confirm cases. All confirmed cases among Minnesota residents were reported to MDH. MDH or local public health department staff members interviewed patients with confirmed SARS-CoV-2 infection to identify exposures and persons who might have been in contact with patients during their infectious period (2 days before through 10 days after symptom onset).* To assess exposures, interviews included questions about travel and being in specific settings, such as bars or restaurants, schools, health care facilities, or events or social gatherings in the 14 days before symptom onset. During August–September 2020, MDH and local health department staff members interviewed >80% of patients with a confirmed SARS-CoV-2 infection.

Secondary and tertiary cases were identified from case interview data. Confirmed secondary cases were defined as laboratory-confirmed infections in persons who did not attend the rally but who received SARS-CoV-2–positive test results after having contact with a person who had a primary case during their infectious period. Tertiary cases were laboratory-confirmed cases in persons who had contact with a person who had a secondary case during their infectious period. Likely event-associated secondary cases were confirmed infections in patients who had contact with a person who had symptoms of COVID-19 and had attended the motorcycle rally but who were not tested. Likely event-associated tertiary cases were confirmed infections in patients who had contact with persons who had a likely event-associated secondary case during their infectious period.

To investigate genomic similarity among COVID-19 cases, available SARS-CoV-2 RNA-positive clinical specimens were obtained from clinical laboratories, and whole genome sequencing was conducted at the MDH Public Health Laboratory on 38 specimens using previously described methods (*2*). Phylogenetic relationships, including distinct clustering of viral whole genome sequences, were inferred based on nucleotide differences via IQ-TREE† using general time reversible substitution models (*3*) as a part of the Nextstrain§ workflow (*4*). This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy.¶

* The infectious period was estimated to begin 2 days before symptom onset and end 10 days after symptom onset, according to CDC guidance. https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/investigating-covid-19-case.html.

† http://www.iqtree.org/.

§ https://nextstrain.org/.

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Summary

What is already known about this topic?

Gatherings present an opportunity for rapid spread of COVID-19.

What is added by this report?

Following a 10-day motorcycle rally in South Dakota attended by approximately 460,000 persons, 51 confirmed primary event-associated cases, 21 secondary cases, and five tertiary cases were identified in Minnesota residents. An additional nine likely rally-associated secondary or tertiary cases occurred. Four patients were hospitalized, and one died. Genomic sequencing supported the associations with the motorcycle rally.

What are the implications for public health practice?

The impact of gatherings as a source of virus transmission underscores the importance of reducing the number of attendees at gatherings, using face masks, and encouraging physical distancing to prevent ongoing transmission of SARS-CoV-2. Furthermore, these findings demonstrate the rationale for consistent mitigation measures across states.

This investigation identified 86 cases, including 51 (59%) primary event-associated cases,** 26 (30%) confirmed secondary and tertiary cases, and nine (10%) likely event-associated secondary or tertiary cases. Four patients were hospitalized, and one died (Table). The median interval between specimen collection and interview was 3 days (range = 1–13 days). Overall, 64 (74%) patients were symptomatic, including 39 (76%) of 51 patients with a primary case and 25 (71%) of 35 patients with secondary and tertiary cases. Among patients with primary cases and symptom onset after the start of the rally, onset dates ranged from August 8 to August 26 (Figure 1). Two patients reported symptom onset before the event and attended the rally during their infectious period. Among primary patients, the median age was 44 years (range = 26–76 years), and 31 (61%) were male. Sixteen (33%) of 48 interviewed patients reported working while infectious, including five who worked at the rally and four who worked in health care after returning from the rally.

Forty-one (80%) interviewed patients with primary event-associated COVID-19 reported having close contact†† with others during their infectious period, with an average of 2.5 close contacts per patient (range = 1–8). Overall, 36 (75%) of 48 interviewed patients with primary event-associated cases reported having close contact with persons in their household while infectious, and 17 (35%) reported having other (social/workplace) close contacts while infectious. Patients reported a total of 59 household contacts (range = 0–4 per patient) and 43 social/workplace contacts (range = 0–6 per patient).

Among the 35 patients with confirmed or likely event-associated secondary/tertiary COVID-19, 25 (71%) were symptomatic, with symptom onset dates during August 12–29 (Table). The median age was 32 years (range = 1–83 years), and 13 (37%) were male. Fifteen (43%) persons with secondary or tertiary COVID-19 were household contacts of a person with a primary or secondary infection, 12 (34%) were social contacts, and eight (23%) were workplace contacts. Secondary transmission from this rally occurred via two workplace outbreaks, one wedding outbreak, and one funeral outbreak. Approximately one third (34%) of Minnesota's 87 counties had at least one primary, secondary, or tertiary case associated with this rally.

Whole Genome Sequencing

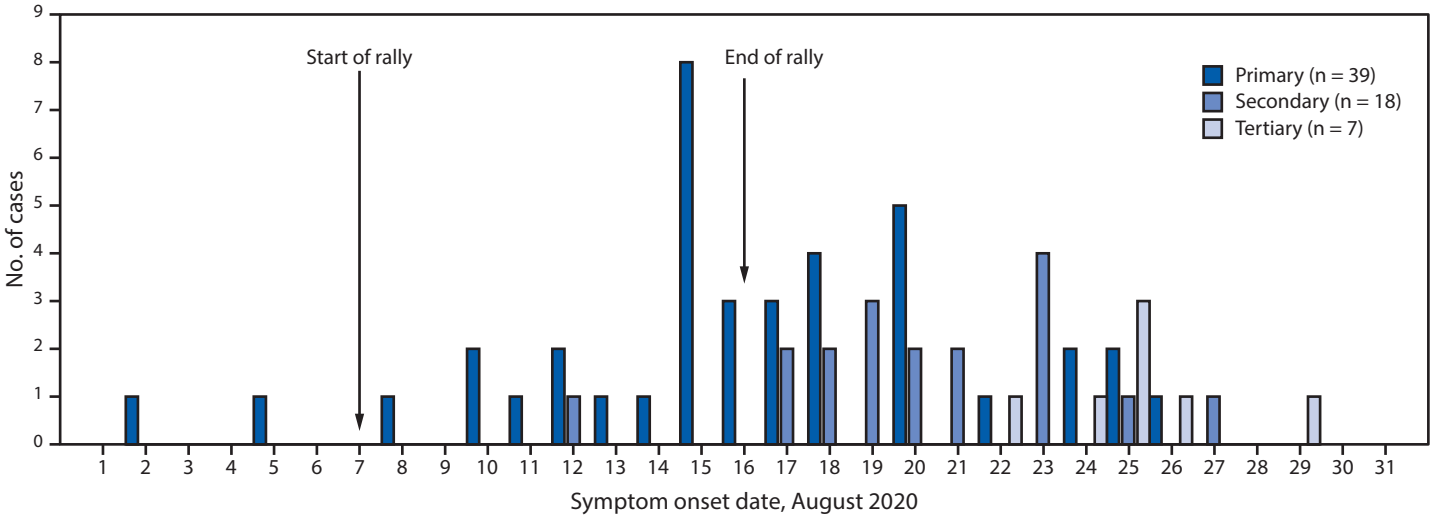
Specimens were obtained from 52 (60%) patients. Among these, 38 (73%) specimens (23 [61%] from primary and 15 [39%] from secondary and tertiary cases) were successfully sequenced, covering at least 98% of the SARS-CoV-2 genome. Six genetically similar clusters with known epidemiologic links were identified (i.e., cases in patients who were close contacts or who had common exposures at the rally), five of which demonstrated secondary or secondary and tertiary transmission. Cluster A (Figure 2) included genetically similar specimens for seven primary cases and one secondary case (specimen MN-MDH-1710). Among primary cases, specimens were collected from two patients who reported working at the rally, including one who worked at a restaurant. Two other patients in this cluster reported visiting that restaurant. Another patient who attended the rally also reported visiting the same restaurant; this patient was a household contact of the patient with specimen MN-MDH-1710. Cluster B represented a chain of transmission in a workplace setting that included five cases. The secondary case in this cluster (with specimen MN-MDH-STU0004) occurred in a workplace contact of a motorcycle rally attendee (specimen MN-MDH-STU0001) and a social contact of one of the persons with a tertiary case (specimen MN-MDH-STU0008). Another secondary case§§ in this cluster was in a workplace contact of the rally attendee and was a household contact of two of the three patients with tertiary cases in this cluster (specimens MN-MDH-1708 and MN-MDH-1709). Cluster C represented secondary transmission from a rally attendee (specimen MN-MDH-1651) to a household contact (specimen MN-MD-1705). Cluster D

** One patient reported attending the rally but refused interview. Two additional patients who refused to be interviewed were identified as having attended the rally through secondary case interviews in which other patients reported them as primary event-associated contacts.

†† Close contact was defined as being within 6 feet of a patient with laboratory-confirmed COVID-19 infection for ≥15 minutes. https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/contact-tracing.html.

§§ Although the specimen from this patient was obtained, sequencing was incomplete.

FIGURE 1. Date of symptom onset among symptomatic patients with primary,* secondary,† and tertiary§ COVID-19 (N = 64) associated with a motorcycle rally in a neighboring state — Minnesota, August 2020



Abbreviation: COVID-19 = coronavirus disease 2019.

* Laboratory-confirmed SARS-CoV-2 infection in a person who attended the motorcycle rally or traveled to western South Dakota by motorcycle during August 7–16 and had symptom onset or specimen collection within 14 days of the end of the rally.

† Laboratory-confirmed infection in a person who had contact with a laboratory-confirmed primary case during the infectious period or with a symptomatic rally attendee who was not tested.

§ Laboratory-confirmed infection in a person who had contact with a secondary case or likely event-associated secondary case.

represented likely event-associated cases of secondary transmission (specimens MN-MDH-STU0002, MN-MDH-1706, and MD-MDH-1712) and tertiary transmission (specimens MN-MDH-STU-0005 and MN-MDH-1711) related to a wedding. The index patient at this wedding reportedly had COVID-19–like symptoms at the wedding after attending the rally but did not receive testing. Cluster E comprised two cases (specimens MN-MDH-1567 and MN-MH-1714) in persons who were household contacts, both of whom attended the rally. Cluster F represents workplace and household contacts (specimens MN-MDH-1715, MN-MDH-1716, MN-MDH-1713, and MN-MDH-STU0007) of the primary patient with specimen MN-MDH-1569. Specimen MN-MDH-1569 was from a musician who performed at the rally and later at another concert with a different band whose members did not attend the rally. Primary event-associated cases with specimens MN-MDH-1571 and MN-MDH-1572 had no known connection to each other or identified common exposure at the rally; however, the reported symptom onset dates and travel dates for these cases were identical. Similarly, primary event-associated cases with specimens MN-MDH-1568 and MN-MDH-1707 had no known epidemiologic link but had identical symptom onset dates. This might indicate a common exposure that was not identified through epidemiologic evidence.

Public Health Response

On August 5, MDH recommended through media events that motorcycle rally attendees quarantine for 14 days upon return and be tested 5–7 days later even if they were asymptomatic. Attendees and their close contacts with confirmed COVID-19 were instructed to self-isolate. Contacts of patients with confirmed COVID-19 were instructed to quarantine.

Discussion

Eighty-six Minnesota COVID-19 cases were associated with the South Dakota motorcycle rally; approximately one third of counties in Minnesota reported at least one case epidemiologically linked to this event. These findings highlight the far-reaching effects that gatherings in one area might have on another area. The motorcycle rally was held in a neighboring state that did not have policies regarding event size and mask use, underscoring the implications of policies within and across jurisdictions. The findings suggest that this rally not only had a direct impact on the health of attendees, but also led to subsequent SARS-CoV-2 transmission among household, social, and workplace contacts of rally attendees upon their return to Minnesota. Whole genome sequencing results supported the finding of secondary and tertiary transmission associated with this rally.

TABLE. Demographic and clinical characteristics of confirmed* and likely event-associated COVID-19 cases (N = 86) associated with a 10-day motorcycle rally in a neighboring state — Minnesota, August–September 2020

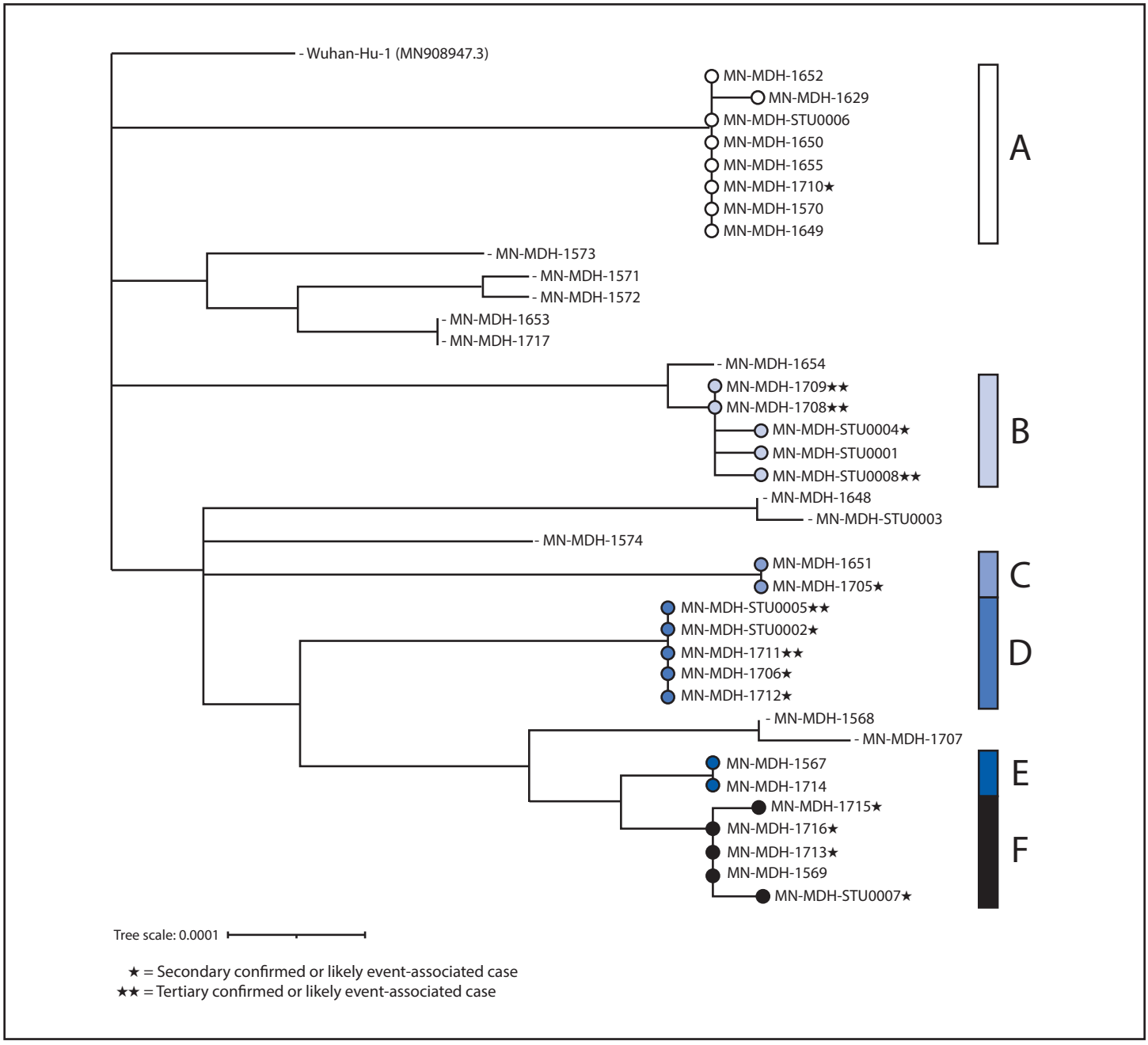
Characteristic	No. of cases (%)		
	Primary event–associated† (n = 51)	Confirmed secondary§/tertiary¶ (n = 26)	Likely event-associated secondary**/tertiary†† (n = 9)
Demographic			
Sex			
Female	20 (39.2)	16 (61.5)	6 (66.7)
Male	31 (60.8)	10 (38.5)	3 (33.3)
Age, yrs, median (range)	44 (26–76)	43 (12–83)	22 (1–51)
Age group, yrs			
<18	0 (—)	3 (11.5)	3 (33.3)
18–24	0 (—)	2 (7.7)	2 (22.2)
25–44	26 (51.0)	8 (30.8)	3 (33.3)
45–64	21 (41.2)	10 (38.5)	1 (11.1)
≥65	4 (7.8)	3 (11.5)	0 (—)
Race/Ethnicity			
White, NH	43 (84.3)	22 (84.6)	8 (88.9)
More than one race/Other, NH	1 (2.0)	0 (—)	1 (11.1)
Unknown	7 (13.7)	4 (15.4)	0 (—)
Clinical			
Symptomatic§§	39 (76.5)	19 (73.1)	6 (66.7)
Hospitalized	3 (5.9)	1 (3.8)	0 (—)
ICU admission	1 (2.0)	0 (—)	0 (—)
Died	1 (2.0)	0 (—)	0 (—)
Close contacts			
Household	NA	12	3
Social	NA	6	6
Workplace	NA	8	0

Abbreviations: COVID-19 = coronavirus disease 2019; ICU = intensive care unit; NA = not applicable; NH = non-Hispanic.
* Receipt of a positive SARS-CoV-2 reverse transcription–polymerase chain reaction test result.
† Laboratory-confirmed SARS-CoV-2 infection in a person who attended the motorcycle rally or traveled to western South Dakota by motorcycle during August 7–16 and had symptom onset or specimen collection within 14 days of the end of the rally.
§ Laboratory-confirmed infection in a person who had contact with a primary case during that person's infectious period.
¶ Laboratory-confirmed infection in a person who had contact with a secondary case during that person's infectious period.
** Laboratory-confirmed infection in a person who had contact with a symptomatic person who attended the rally but was not tested.
†† Laboratory-confirmed infection in a person who had contact with a likely secondary case.
§§ Symptom status was unknown for three patients with a primary case, three with a secondary/tertiary case, and one with a likely event-associated secondary/tertiary case.

The findings in this report are subject to at least three limitations. First, despite in-depth epidemiologic investigation, the findings represent an underestimate of the motorcycle rally's impact in Minnesota and did not capture the impact within South Dakota or other states. Case interviews were voluntary, and patients could choose not to respond to certain questions. Ten patients reported having close contacts but refused to disclose additional details regarding these contacts. Therefore, it was not possible to identify all contacts of patients who attended the rally. Second, attendees and their contacts might not have been tested for SARS-CoV-2. Two rally attendees indicated that their contacts had COVID-19–like symptoms but did not plan to be tested. As such, the findings underrepresent the number of cases, close contacts, and secondary and tertiary cases. Finally, only 52 specimens were received at the MDH Public Health Laboratory because many testing laboratories do not retain or store specimens long-term. Among these specimens, only 38 were successfully sequenced. The lack of whole genome sequencing data from all cases hindered establishment of complete genetic relatedness for epidemiologic investigation.

A large event in a neighboring state triggered chains of SARS-CoV-2 transmission within Minnesota. Other studies have shown that chains of transmission associated with gatherings are not uncommon within the United States (*5*,*6*). Despite underascertainment of the rally's full impact in Minnesota and other states, these findings highlight the importance of reducing the number of attendees at gatherings and emphasizing mask use, physical distancing, isolation for patients with COVID-19, and quarantine for close contacts as strategies for reducing the spread of COVID-19. Furthermore, these findings demonstrate the rationale for consistent mitigation measures across states.

FIGURE 2. Phylogenetic tree* showing genetic distance between available† SARS-CoV-2 virus specimens collected from South Dakota motorcycle rally attendees and their contacts (N = 38) — Minnesota, August 2020



* This figure was created using Interactive Tree of Life (version 5.7; European Molecular Biology Laboratory). https://itol.embl.de/.
† Genetic divergence based on nucleotide difference is indicated by length of branches in substitutions per site. Available specimens include specimens from clinical labs where specimens could be retrieved and RNA could be extracted.

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Corresponding author: Melanie J. Firestone, mfirestone@cdc.gov.

[1]Minnesota Department of Health; [2]Epidemic Intelligence Service, CDC; [3]Division of State and Local Readiness, Center for Preparedness and Response, CDC [4]Mayo Clinic, Rochester, Minnesota; [5]Department of Laboratory Medicine and Pathology, University of Minnesota.

All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. Matthew J. Binnicker reports personal fees from DiaSorin Molecular for an educational webinar on COVID-19 diagnostics and as a member of the advisory board. No other potential conflicts of interest were disclosed.

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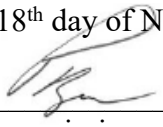
This is **"Exhibit V"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

BACKGROUNDER

Roadmap to Reopen

May 20, 2021

Office of the Premier

Health

Roadmap to Reopen is a cautious three-step plan that will guide a safe and gradual reopening of the province and the lifting of public health measures based on the provincewide vaccination rate and improvements in key public health and health system indicators.

The province will remain in each of the steps for at least 21 days to evaluate any impacts on key public health indicators. If at the end of the 21 days, the vaccination thresholds have been met, alongside positive trends of other key public health and health system indicators, then the province will move forward.

Public health and workplace safety measures would continue to apply across all steps, including maintaining physical distance, capacity limits and wearing face coverings in indoor spaces and whenever physical distancing is a challenge.

The three steps of the Roadmap, which will be applied provincially, are the following :

Step One

Step One of the roadmap may begin after 60 per cent of Ontario's adults receive at least one dose of a COVID-19 vaccine and if public health indicators, such as hospitalizations, ICU occupancy and new admissions and case rates indicate the province can safely move to this step of the roadmap. Based on current trends in key health indicators, including the provincial vaccination rate, the government expects to enter Step One of the Roadmap the week of June 14, 2021. The province will confirm closer to the expected start of Step One.

Step One will permit the resumption of more outdoor activities with smaller, well-managed crowds where risk of transmission is minimized and will permit retail, all with restrictions in place, including but not limited to :

- Outdoor gatherings up to 10 people;

- Outdoor dining up to 4 people per table;
- Outdoor fitness classes, personal training and sports training up to 10 people;
- Essential retail at 25 per cent capacity and can sell all goods (including discount and big box);
- Non-essential retail at 15 per cent capacity;
- Retail stores in malls closed unless the stores have a street facing entrance;
- Outdoor religious services, rites and ceremonies with capacity limited to permit 2 metres' physical distancing;
- Horse racing and motor speedways without spectators;
- Outdoor horse riding;
- Outdoor pools and wading pools with capacity limited to permit 2 metres' physical distancing;
- Outdoor zoos, landmarks, historic sites, and botanical gardens with capacity limits;
- Campsites, campgrounds and short-term rentals; and
- Overnight camping at Ontario Parks.

Step Two

Ontario will remain in Step One for at least 21 days. If at the end of those 21 days the province has vaccinated 70 per cent of adults with one dose and 20 per cent of adults with two doses and there are positive trends in public health and health system indicators, Ontario will move to Step Two.

Step Two will further expand outdoor activities and will resume limited indoor services with small numbers of people where face coverings are worn, with other restrictions in place, including but not limited to :

- Outdoor gatherings up to 25 people;
- Indoor gatherings up to 5 people and other restrictions;
- Outdoor dining up to 6 people per table;
- Outdoor sports and leagues;
- Overnight camps;
- Outdoor meeting and event spaces with capacity limits;
- Non-essential retail at 25 per cent capacity; essential retail at 50 per cent capacity;
- Personal care services where face coverings can be worn at all times with capacity limits;
- Outdoor cinemas and performing arts with capacity limits;
- Horse racing and motor speedways for spectators with capacity limits;
- Outdoor tour and guide services with capacity limits;

- Indoor religious services, rites or ceremony gatherings at 15 per cent capacity;
- Public libraries with capacity limits;
- Outdoor waterparks and amusement parks with capacity limits; and
- Fairs and rural exhibitions with capacity limits.

Step Three

Ontario will remain in Step Two for at least 21 days. If at the end of those 21 days the province has vaccinated 70 to 80 per cent of adults with one dose and 25 per cent of adults with two and positive trends in public health and health system indicators continue, Ontario will move to Step Three.

Step Three will permit the resumption of indoor services with larger numbers of people, with restrictions in place, including but not limited to :

- Outdoor gatherings with larger capacity limits;
- Indoor gatherings with larger capacity limits and other restrictions;
- Indoor dining with capacity limits;
- Indoor sports and recreational fitness facilities with capacity limits;
- Indoor meeting and event spaces with capacity limits;
- Essential and non-essential retail capacity expanded;
- Personal care services with capacity expanded and other restrictions;
- Indoor cinemas and performing arts facilities with capacity limits;
- Indoor and outdoor religious services, rites or ceremony gatherings with capacity limited to permit 2 metres' physical distancing;
- Indoor museums and art galleries with capacity limits;
- Indoor zoos, aquariums, waterparks and amusement parks with capacity limits;
- Casinos and bingo halls with capacity limits; and
- Other outdoor activities from Step Two permitted to operate indoors.

This list is not exhaustive. The government will continue to work with sectors on reopening plans, to ensure that they have full awareness of when they can begin to safely reopen and how.

Roadmap to Reopen at a glance :

Subject / Sector	Before Step One	Step One	Step Two	Step Three

Retail	Essential retail at 25% capacity; Other restrictions apply to some essential retailers (e.g. restricted hours, appointments required, etc.) In-store shopping at discount and big box retailers limited to essential goods Curbside pick-up or delivery for non-essential retail Restrictions on shopping malls	Essential retail at 25% capacity and and can sell all goods (including discount and big box) Non-essential retail at 15% capacity Retail stores in malls closed unless the stores have a street facing entrance.	Essential retail at 50% capacity Non-essential retail at 25% capacity	Essential and non-essential retail open with capacity limited to permit 2m physical distancing
Liquor stores	Open at 25% capacity, with restricted hours	Open at 25% capacity	Open at 50% capacity	Open with capacity limited to permit 2m physical distancing

Restaurants and bars	Open for take-out, drive-through and delivery service	Outdoor dining with 4 people per table and other restrictions	Outdoor dining with 6 people per table and other restrictions Karaoke permitted with restrictions (outdoor)	Indoor dining with capacity and some other restrictions Outdoor dining with capacity limited to permit 2m physical distancing Buffets permitted Karaoke permitted with restrictions
Personal care services	Closed	Closed Sensory deprivation pods permitted when prescribed by a regulated health professional	Open at 25% capacity to maximum of 5 people Appointment required Services that require the removal of a face covering not permitted Only patrons being served can be in the setting	Open with capacity limited to permit 2m physical distancing and other restrictions

Sports and recreational fitness facilities	Closed for indoor use except for high-performance athletes, child care, mental health and addiction support services, social services, and physical therapy (subject to conditions)	Outdoor team sports – training only, 10 people max, 3m distance Closed for indoor use except for high-performance athletes, social services, and physical therapy	Outdoor sports leagues open Training for professional or amateur athletes and/or competitions	Indoor open, with some restrictions Outdoor open, with some restrictions
Personal fitness and training	Closed – no indoor or outdoor sports or recreational classes at any indoor or outdoor sport and recreational facilities	Outdoor fitness classes – 10 people max, 3m distance Outdoor personal training – 10 people max, 3m distance Outdoor sports training only – 10 people max, 3m distance	Outdoor fitness classes – 25 people max, 3m distance Outdoor personal training – 25 people max, 3m distance	Indoor open, with some restrictions Outdoor open, with some restrictions

Outdoor recreational amenities	Open, including golf courses, tennis courts, skateboarding parks, sports fields, BMX and skate parks, shooting ranges and archery ranges, and others, with restrictions. Horse riding permitted, with restrictions No outdoor sports or recreational classes are permitted.	Open	Open	Open

Water features	Splash pads, spray pads	Outdoor pools, splash pads, spray pads, whirlpools, wading pools and water slides open with capacity limited to permit 2m physical distancing	Outdoor pools, splash pads, spray pads, whirlpools, wading pools and water slides open with capacity limited to permit 2m physical distancing	Indoor and outdoor pools, splash pads, spray pads, whirlpools, wading pools and water slides open with capacity limited to permit 2m physical distancing
Meeting and event spaces	Closed with exceptions for certain purposes including social services, government operations, court services, in-person examinations for select professions (subject to conditions)	Closed with exceptions for certain purposes including social services, government operations, court services, in-person examinations for select professions (subject to conditions)	Outdoor spaces open at 25% capacity and other restrictions Indoor meeting and event spaces closed, with exceptions for certain purposes, and except for viewing for potential booking of a future event	Indoor spaces open with capacity and other restrictions, including for tradeshows, conferences and exhibitions
Day camps	Closed	Open based on guidance from the Chief Medical Officer of Health	Open based on guidance from the Chief Medical Officer of Health	Open based on guidance from the Chief Medical Officer of Health

Overnight camps	Closed	Closed	Open based on guidance from the Chief Medical Officer of Health, including epidemiological context and other specific conditions	Open based on guidance from the Chief Medical Officer of Health, including epidemiological context and other specific conditions
Commercial film/TV production	Open with no audience No more than 50 performers on set Distance or equipment requirements for crew, hair and makeup services, and musicians Must comply with industry guidance Post-production, visual effects, animation studios open	Open with no audience No more than 50 performers on set Distance or equipment requirements for crew, hair and makeup services, and musicians Must comply with industry guidance Post-production, visual effects, animation studios open	Open with no audience Distance or equipment requirements for crew, hair and makeup services, and musicians Must comply with industry guidance Post-production, visual effects, animation studios open	Open with capacity restrictions for studio audiences. Distance or equipment requirements for crew, hair and makeup services, and musicians Must comply with industry guidance Post-production, visual effects, animation studios open

Performing arts	Closed	Closed	Indoor closed, permitted only for the purpose of rehearsing or performing a recorded or broadcasted event Outdoor open, including live music, with capacity and other restrictions	Indoor open, including live music, with capacity and other restrictions Outdoor open, including live music, with capacity restrictions
Cinemas	Closed	Drive-in open	Indoor closed Outdoor open with capacity and other restrictions	Indoor open with capacity and other restrictions Outdoor open with capacity and other restrictions
Casino, bingo halls and gaming establishments	Closed	Closed	Closed	Open with capacity and other restrictions
Horse Racing	Training only No members of the public permitted at the facility	Outdoor with capacity and crew restrictions No spectators	Open with spectator capacity and other restrictions	Open with spectator capacity and other restrictions

Motorsports and speedways	Closed	Outdoor with capacity and crew restrictions No spectators	Open with spectator capacity and other restrictions	Open with spectator capacity and other restrictions
Weddings, funerals and religious services, rites and ceremonies (Does not apply to receptions)	Max 10 persons indoors Max 10 people permitted outdoors	10 indoors Outdoor permitted with capacity limited to permit 2m physical distancing	Indoor permitted at 15% capacity Outdoor permitted with capacity limited to permit 2m physical distancing	Larger indoor services, rites, and ceremonies Outdoor permitted with capacity limited to permit 2m physical distancing
Gatherings	Max 5 people for outdoor gatherings	Max 10 people for outdoor gatherings and organized public events Indoor not permitted	Max 25 people for outdoor gatherings and organized public events Max 5 people for indoor gatherings and organized public events with other restrictions	Larger indoor and outdoor gatherings and organized public events with size limits

Short-term rentals (does not include hotels, motels, lodges, resorts, etc but does apply to cabins and cottages)	Only for people in need of housing	Open	Open	Open
Public libraries	Curbside pickups for materials Access to computers, photocopiers, and similar services permitted	Curbside pickups for materials Access to computers, photocopiers, and similar services permitted	Open with 25% capacity and other restrictions	Open, with capacity limited to permit 2m physical distancing and other restrictions
Museums, Attractions, etc.	Closed Zoos and aquariums open to care for animals	Outdoor zoos, landmarks, historic sites, botanical gardens, and similar attractions open with reduced capacity and other restrictions (excludes public events)	Outdoor waterparks open with reduced capacity and other restrictions Outdoor amusement parks open with reduced capacity and other restrictions, including on rides	Museums and art galleries open with capacity limited to permit 2m physical distancing and other restrictions Indoor zoos and aquariums, waterparks, and amusement parks open with capacity restrictions

Fairs and Rural Exhibitions	Closed	Closed	Outdoor open at reduced capacity and other restrictions	Indoor and outdoor open at reduced capacity and other restrictions
Tour and Guide Services (e.g., boat tours)	Closed	Closed	Outdoor open with capacity and other restrictions	Indoor open with capacity and other restrictions
Construction	Open with some limitations to commercial projects	All construction open	All construction open	All construction open
Driving Instruction and Testing	Not permitted, except for drivers of commercial vehicles	Driving testing permitted with restrictions	Driving testing permitted with restrictions Driving instruction permitted with restrictions	Driving testing permitted with restrictions Driving instruction permitted with restrictions
Veterinary services	Open	Open	Open	Open
Pet grooming, animal shelters, stables, pet sitters, pet walkers, pet trainers	Open	Open	Open	Open

Lawn care and landscaping services	Open	Open	Open	Open
Ontario Parks and Campgrounds	Ontario Parks open for day use Overnight only open for individuals in need of housing or with full seasonal contracts; only sites with electricity, water and sewage facilities may be provided for use All recreational facilities in the campground and all other shared facilities in the campground, other than washrooms and showers, must be closed	Open	Open	Open

Marinas / Boating Clubs	Open with limited services including, repairs or servicing of boats, placing boats in water, and enabling individuals' access to their residence or property Recreational boating permitted but only members of a household can gather on a boat Clubhouse, rec facilities closed; restaurants open for take-out only	Permitted with clubhouses, and other indoor amenities closed	Permitted with clubhouses, and other indoor amenities closed	Open with restrictions.
Strip clubs	Permitted to operate as a restaurant in alignment with restaurant restrictions	Permitted to operate as a restaurant in alignment with restaurant restrictions	Permitted to operate as a restaurant in alignment with restaurant restrictions	Permitted to operate as a strip club in alignment with restaurant and performance restrictions

Note : Bolded measures indicate new measures coming into effect as of May 22, 2021 at 12 :01 a.m.

Additional Resources

- Ontario Releases Three-Step Roadmap to Safely Reopen the Province

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Related Topics

Health and Wellness

Get help navigating Ontario's health care system and connecting with the programs or services you're looking for. Learn more

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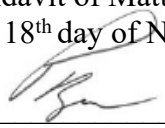
Media Contacts

Ivana Yelich
Premier's Office
ivana.yelich@ontario.ca

Alexandra Hilken
Minister Elliott's Office
alexandra.hilkene@ontario.ca

This is **"Exhibit W"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

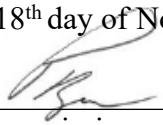
Number of individuals who have received at least 1 dose of a COVID-19 vaccine and vaccination coverage estimates as a percentage of the total population of Ontario

April 1, 2021 to April 30, 2021

Vaccine data are updated biweekly. Data are shown using the date of vaccine administration. The bars show the cumulative number of individuals vaccinated over time, while the line shows the proportion of the population vaccinated over time. Coverage estimates reflect total vaccinations among the total population of Ontario, or the selected public health unit, since the start of Ontario's vaccine program.

View the trends in your area by selecting your public health unit. View the **vaccinations map** for more vaccine data, including coverage estimates among the vaccine-eligible population of Ontario.

This is **"Exhibit X"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



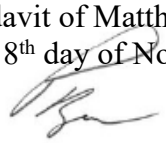
A Commissioner, etc.

Vaccine data are updated biweekly. Data are shown using the date of vaccine administration. The bars show the cumulative number of individuals vaccinated over time, while the line shows the proportion of the population vaccinated over time. Coverage estimates reflect total vaccinations among the total population of Ontario, or the selected public health unit, since the start of Ontario's vaccine program.

View the trends in your area by selecting your public health unit. View the **vaccinations map** for more vaccine data, including coverage estimates among the vaccine-eligible population of Ontario.

See metric descriptions in Glossary

This is **"Exhibit Y"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Ontario

Français

ONTARIO REGULATION 265/21

made under the

EMERGENCY MANAGEMENT AND CIVIL PROTECTION ACT

Made: April 7, 2021 (1:02 p.m.) Filed: April 7, 2021
Published on e-Laws: April 7, 2021
Printed in The Ontario Gazette: April 24, 2021

STAY-AT-HOME ORDER

Terms of Order
1. The terms of this Order are set out in Schedule 1.

Application
2. This Order applies as of 12:01 a.m. on April 8, 2021.

SCHEDULE 1

Requirement to remain in residence
1. (1) Every individual shall remain at the residence at which they are currently residing at all times unless leaving their residence is necessary for one or more of the following purposes:

Work, school and child care

1. Working or volunteering where the nature of the work or volunteering requires the individual to leave their residence, including when the individual's employer has determined that the nature of the individual's work requires attendance at the workplace.
2. Attending school or a post-secondary institution.
3. Attending, obtaining or providing child care.
4. Receiving or providing training or educational services.

Obtaining goods and services

5. Obtaining food, beverages and personal care items.
6. Obtaining goods or services that are necessary for the health or safety of an individual, including vaccinations, other health care services and medications.
7. Obtaining goods, obtaining services, or performing such activities as are necessary for landscaping, gardening and the safe operation, maintenance and sanitation of households, businesses, means of transportation or other places.
8. Purchasing or picking up goods through an alternative method of sale, such as curbside pickup, from a business or place that is permitted to provide the alternative method of sale.
9. Attending an appointment at a business or place that is permitted to be open by appointment only.
10. Obtaining services from a financial institution or cheque cashing service.

11. Obtaining government services, social services and supports, mental health support services or addictions support services.

Assisting others

12. Delivering goods or providing care or other support or assistance to an individual who requires support or assistance, or receiving such support or assistance, including,

    i. providing care for an individual in a congregate care setting, and

    ii. accompanying an individual who requires assistance leaving their residence for any purpose permitted under this Order.

13. Taking a child to the child's parent or guardian or to the parent or guardian's residence.
14. Taking a member of the individual's household to any place the member of the household is permitted to go under this Order.

Health, safety and legal purposes

15. Doing anything that is necessary to respond to or avoid an imminent risk to the health or safety of an individual, including,

    i. protecting oneself or others from domestic violence,

    ii. leaving or assisting someone in leaving unsafe living conditions, and

    iii. seeking emergency assistance.

16. Exercising, including,

    i. walking or moving around outdoors using an assistive mobility device, or

    ii. using an outdoor recreational amenity that is permitted to be open.

17. Attending a place as required by law or in relation to the administration of justice.
18. Exercising an Aboriginal or treaty right as recognized and affirmed by section 35 of the *Constitution Act, 1982*.

Multiple residences and moving

19. Travelling to another residence of the individual if,

    i. the individual intends to be at the residence for less than 24 hours and is attending for one of the purposes set out in this Order, or

    ii. the individual intends to reside at the residence for at least 14 days.

20. Travelling between the homes of parents, guardians or caregivers, if the individual is under their care.
21. Making arrangements to purchase or sell a residence or to begin or end a residential lease.
22. Moving residences.

Travel

23. Travelling to an airport, bus station or train station for the purpose of travelling to a destination that is outside of the Province.

Gatherings

24. Attending a gathering for the purpose of a wedding, a funeral or a religious service, rite or ceremony that is permitted by law or making necessary arrangements for the purpose of such a gathering.
25. If the individual lives alone, gathering with the members of a single household.

Animals

26. Obtaining goods or services that are necessary for the health or safety of an animal, including obtaining veterinary services.
27. Obtaining animal food or supplies.

28. Doing anything that is necessary to respond to or avoid an imminent risk to the health or safety of an animal, including protecting an animal from suffering abuse.
29. Walking or otherwise exercising an animal.

(2) Despite subsection (1), no person shall attend a business or place that is required by law to be closed, except to the extent that temporary access to the closed business or place is permitted by law.

(3) This Order does not apply to individuals who are homeless.

(4) If this Order allows an individual to leave their residence to go to a place, it also authorizes them to return to their residence from that place.

(5) The requirement in subsection (1) to remain at an individual's residence does not prevent the individual from accessing outdoor parts of their residence, such as a backyard, or accessing indoor or outdoor common areas of the communal residences in which they reside that are open, including lobbies.

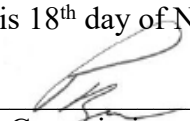
(6) For greater certainty, nothing in this Order permits a business or place to be open if it is required by law to be closed.

(7) For greater certainty, nothing in this Order permits an individual to gather with other individuals if the gathering is not permitted by law.

(8) For greater certainty, individuals may only attend an outdoor organized public event or social gathering for a purpose set out in subsection (1) if the event or gathering is permitted by law.

Français

This is **"Exhibit Z"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



A Commissioner, etc.

Ontario

Français

ONTARIO REGULATION 441/21

made under the

REOPENING ONTARIO (A FLEXIBLE RESPONSE TO COVID-19) ACT, 2020

Made: June 7, 2021
Filed: June 7, 2021
Published on e-Laws: June 7, 2021
Printed in The Ontario Gazette: June 26, 2021

AMENDING O. REG. 363/20

(STAGES OF REOPENING)

1. The English version of the title to Ontario Regulation 363/20 is revoked and the following substituted:

STEPS OF REOPENING

2. Section 1 of the Regulation is revoked and the following substituted:

Steps
1. The areas listed in Schedule 1 are at Step 1 of reopening.

3. Schedule 1 to the Regulation is revoked and the following substituted:

SCHEDULE 1
AREAS IN THE SHUTDOWN ZONE, AREAS AT STEP 1

Shutdown Zone
1. No areas are in the Shutdown Zone.

Step 1
2. The following areas are at Step 1:

1. Brant County Health Unit.
2. Chatham-Kent Health Unit.
3. City of Hamilton Health Unit.
4. City of Ottawa Health Unit.
5. City of Toronto Health Unit.
6. The District of Algoma Health Unit.

7. Durham Regional Health Unit.
8. The Eastern Ontario Health Unit.
9. Grey Bruce Health Unit.
10. Haldimand-Norfolk Health Unit.
11. Haliburton, Kawartha, Pine Ridge District Health Unit.
12. Halton Regional Health Unit.
13. Hastings and Prince Edward Counties Health Unit.
14. Huron Perth Health Unit.
15. Kingston, Frontenac and Lennox and Addington Health Unit.
16. Lambton Health Unit.
17. Leeds, Grenville and Lanark District Health Unit.
18. Middlesex-London Health Unit.
19. Niagara Regional Area Health Unit.
20. North Bay Parry Sound District Health Unit.
21. Northwestern Health Unit.
22. Oxford Elgin St. Thomas Health Unit.
23. Peel Regional Health Unit.
24. Peterborough County — City Health Unit.
25. Porcupine Health Unit.
26. Renfrew County and District Health Unit.
27. Simcoe Muskoka District Health Unit.
28. Sudbury and District Health Unit.
29. Thunder Bay District Health Unit.
30. Timiskaming Health Unit.
31. Waterloo Health Unit.
32. Wellington-Dufferin-Guelph Health Unit.
33. Windsor-Essex County Health Unit.
34. York Regional Health Unit.

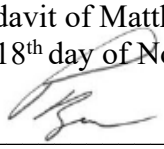
4. Schedules 2 and 3 to the Regulation are revoked.

Commencement

5. This Regulation comes into force on the later of June 11, 2021 and the day this Regulation is filed.

Français

This is **"Exhibit AA"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



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A Commissioner, etc.

Outdoor Transmission of SARS-CoV-2 and Other Respiratory Viruses, a Systematic Review

Tommaso Celeste Bulfone, MS,[a] Mohsen Malekinejad, MD, DrPh,[b] George W. Rutherford, MD, AM, [b,c] Nooshin Razani MD, MPH[b,c,*]

a. Joint Medical Program, University of California, Berkeley - University of California, San Francisco. 2121 Berkeley Way, Room 5302 Berkeley, CA 94720-7360, USA.

b. Department of Epidemiology and Biostatistics, University of California, San Francisco. 550 16th St 2nd floor, San Francisco, CA 94158, USA

c. Department of Pediatrics, University of California, San Francisco

Corresponding author: Nooshin Razani, MD 550 16th St 2nd floor, San Francisco, CA 94158, nooshin.razani@ucsf.edu, 415-722-1915

Summary:

This systematic review found that while outdoor environments do seem at lower risk for transmission of SARS-CoV-2 and other respiratory viruses than indoor environments, there are data showing that infection transmission is possible outdoors, thus warranting further rigorous investigation.

Abstract

Background

While risk of outdoor transmission of respiratory viral infections is hypothesized to be low, there is limited data of SARS-CoV-2 transmission in outdoor compared to indoor settings.

Methods

We conducted a systematic review of peer-reviewed papers indexed in PubMed, EMBASE and Web of Science and pre-prints in Europe PMC through August 12th, 2020 that described cases of human transmission of SARS-CoV-2. Reports of other respiratory virus transmission were included for reference.

Results

Five identified studies found that a low proportion of reported global SARS-CoV-2 infections have occurred outdoors (<10%) and the odds of indoor transmission was very high compared to outdoors (18.7 times; 95% CI 6.0, 57.9). Five studies described influenza transmission outdoors and two described adenovirus transmission outdoors. There was high heterogeneity in study quality and individual definitions of outdoor settings which limited our ability to draw conclusions about outdoor transmission risks. In general, factors such as duration and frequency of personal contact, lack of personal protective equipment and occasional indoor gathering during a largely outdoor experience were associated with outdoor reports of infection.

Conclusion

Existing evidence supports the wide-held belief that the the risk of SARS-CoV-2 transmission is lower outdoors but there are significant gaps in our understanding of specific pathways.

Keywords: coronaviruses, SARS-CoV-2, COVID-19, transmission, outdoor

Background

Recommendations about methods to curb transmission of the severe acute respiratory syndrome coronavirus type 2 (SARS-CoV-2) beyond wearing masks and maintaining social distance have varied, especially regarding outdoor transmission.[1] This variability reflects a general lack of information on how SARS-CoV-2 is transmitted outdoors.

Outdoor spaces generally allow for more physical distancing, which mitigates the risk of virus transmission through larger respiratory droplets [2]. Outdoor spaces allow for airflow, ventilation, and lack of recycled air, which all minimize the theoretical risk of aerosol transmission through smaller respiratory droplets. While aerosol spread in community settings is controversial, emerging data suggest that indoor recycled air can spread SARS-CoV-2 — with examples of spreading events in a restaurant in Guangzhou [3], at an indoor choir practice in Skagit, Washington, USA [4], at a South Korean call center [5], at meat-packing plants in the USA [6] and in a nursing home in the Netherlands [7]. In areas with low ventilation, aerosolized droplets have the capacity to linger for longer before being inhaled or falling to a surface, which could result in fomite transmission [8]. In enclosed environments, low humidity, air conditioning, and low UV light may all contribute to longer survival of viral particles [9]. Outdoor environments also generally have fewer high touch surfaces that may harbor the virus. UV light, present outdoors from sunlight, results in a ten-fold decrease in virus survival on surfaces [10]. Finally, indoor environments may increase host susceptibility; the low indoor humidity has been associated with slower host ciliary clearance and complications such as pneumonia, and lack of sunlight has been associated with lower vitamin D levels [11]. For these reasons, the risk of virus transmission in outdoor locations has been hypothesized to be lower than in indoor spaces.

We sought to quantify the risk of SAR-CoV-2 transmission in outdoor settings. We conducted a systematic review of the literature on transmission of SARS-CoV-2 to better understand the risks of outdoor transmission. Where data was available, we estimated the risk of outdoor compared to indoor transmission**.** Anticipating a paucity of data on SARS-CoV-2, we chose a broad search strategy that included other human beta coronaviruses and respiratory viruses.

Methods

Search strategy and selection criteria

Data for this review were identified by searches of PubMed, EMBASE, Web of Science, as well as preprints available in Europe PMC [12]. Details of our search strategies and eligibility criteria can be found in our protocol published on August 3rd, 2020 on PROSPERO (ID: 183826). The search was conducted on June 17th, 2020, and because of the rapidly expanding data on SARS-CoV-2, the search was repeated to include most recent literature on August 12th, 2020.

Exposures and outcomes

The exposure of interest - outdoor gatherings - was defined as persons congregating outdoors for work, social or recreational activities (Supplementary Material 1 for our full search strategy). The outcome of interest included cases of transmission of SARS-CoV-2 or other respiratory viruses identified by a case report, illness, or mortality. We also included secondary outcomes of clusters or outbreaks of cases. Our search included any viral infection that can be spread by respiratory droplets and, in addition to SARS-CoV-2, included the other

two recognized human beta-human coronaviruses viruses (SARS-CoV-1 and Middle East Respiratory Syndrome), human influenza viruses, adenoviruses, rhinoviruses, human metapneumoviruses, and respiratory syncytial virus.

We included studies (experimental or observational with empirical data collection) that described human-to-human transmission of respiratory viruses between humans in an outdoor setting, any review of these studies, and any study (experimental or observational) that compared respiratory viral transmission among humans in an outdoor versus indoor settings.

We excluded reviews of previously published data, studies of exclusively indoor outbreaks, outdoor outbreaks within animal populations or between animals and humans, and outbreaks where the site of transmission was not listed or was unclear. We also excluded studies limited to built environments (homes, apartment buildings, military barracks), hospitals, or forms of transportation (airplanes, trains, buses, cars, ships).

Data Selection and Extraction

After removing duplicate records, one author (TCB) reviewed all downloaded citations based on their titles and pre-specified inclusion criteria. A second co-author (MM) reviewed a 5% random sample of the excluded titles (rejected from initial search results) for quality control. Two authors (TCB and NR) then independently screened the titles, abstracts and descriptor terms and compared and discussed discrepancies until consensus was reached; a third author (MM) served as an arbiter when needed. Two authors (TCB and NR) then independently inspected the full texts of the remaining studies for relevance based on exposure, design and outcome measures to select the included papers, and discussed discrepancies until consensus was reached with a third author (MM) serving as arbiter. We used Endnote X9.3.2 (Clarivate

Analytics, Philadelphia, Pennsylvania, USA) and Rayyan (Qatar Computing Research Institute, Doha, Qatar) web-based software to manage search results [13].

Two authors (TCB and NR) extracted the following data from each paper into a pre-piloted data extraction form in Excel spread sheets : complete citation, study location, study design, details of participants (risk group or groups, sample size), exposure details (type of gathering, characteristics of gathering place, number of people, duration, proportion of time spent outdoors, amount if any of indoor transmission, how the non-exposure state (indoors) was defined, outcomes (numerators and denominators associated with each outcome, definitions and descriptions of outcomes provided in papers, details of how outcomes were assessed, individual cases of infection and/or large spreading events, mortality), methodological details (sample characteristics, how the information was gathered, how the outbreak was investigated), and details related to bias assessment.

Results

The combined searches yielded 10,912 unique citations, of which 12 studies met our inclusion criteria. Nine studies were identified from the June 17th search, two from the August 12th, and one from a targeted search. Out of the 12 that met our inclusion criteria, five were pertaining to SARS-CoV-2 **(Table 1 and 2)**, five reported on influenza or influenza-like viruses **(Table 3)**, and two reported on adenovirus transmission. Of note, 33 studies were excluded because they did not specify the location of transmission (Supplementary Material 2). The PRISMA diagram is shown in **Figure 1**.

Five studies related to SARS-CoV-2 transmission found that less than 10 percent of reported transmission occurred in outdoor settings, less than 5% of cases were related to outdoor

occupations, and the odds of transmission or super spreading are much lower outdoors **(Table 1)** [14–17].

Of 318 identified outbreaks involving three or more cases in China reported to local Municipal Health Commissions from January 4 to February 11, 2020, Qian et al. found that all occurred in indoor environments [14]. They reported a single transmission that occurred outdoors (one case of outdoor transmission out of 7,324 total reported cases). This report, however, might be affected by strict interventions prohibiting mass gatherings outdoors, which may have contributed to the low number of cases contracted outdoors. Additionally, relying on local health department reports may have led to underestimates of the total number of transmissions, especially those which were asymptomatic [14].

Nishiura et al. [15] analyzed the transmission pattern of COVID-19 reported through February 28, 2020 (11 clusters and sporadic cases) in Japan. They concluded that the odds of a primary case transmitting COVID-19 in a closed environment were 18.7 times greater compared to outdoor setting (defined as an open-air environment) (95% confidence interval [CI]: 6.0, 57.9). The odds of a single case spreading to 3 or more individuals, which they defined as a super spreader event, in closed environments compared to open air were as 32.6 (95% CI: 3.7, 289.5). This report, however, included no description of the context or location of the outdoor transmission nor were any raw data provided. It is unclear whether this report is relying on proportions, which again, may be subject to the fact that fewer people would have been outdoors during winter months in Japan .

Leclerc et al. [16] reviewed 201 transmission clusters of COVID-19 world-wide that had been reported up to March 30, 2020. The vast majority of these transmissions were associated

with “indoor” or “indoor/outdoor” settings (197/201 clusters or 21/22 locations). The one “outdoor” setting was at multiple construction sites in Singapore, where four outbreaks occurred.

Lan et al. [17] investigated 103 possible work-related cases of COVID-19 among a total of 690 local cases in six Asian countries or regions, including Hong Kong, Japan, Singapore, Taiwan, Thailand, and Vietnam. In this paper, construction workers in Singapore constituted only 5% of the total work-related transmissions. While this paper did not explicitly state whether the location of work-related transmission was outdoor or indoors, it was included based on Leclerc’s classification of the same construction workers as an “outdoor” setting. This does not rule out that that transmission may have occurred in indoor locations at construction sites.

Szablewski et al. [18] report SARS-CoV-2 transmission at an overnight camp in Georgia, USA, where attack rates increased with increasing length of time at the camp, and with co-housing. Staff members, who stayed the longest at camp, had the highest attack rate (56%). The outbreak was clustered by cabin assignments, which suggests a high likelihood of transmission in indoor spaces during overnight cabin stays rather than during outdoor activities during the day. The authors state that non-pharmaceutical interventions such as cohorting and adults wearing masks during the day, were not protective, although no further information is given about this claim.

While there is high heterogeneity in the studies describing outdoor transmission of SARS-CoV-2, the studies we found highlight the conditions of outdoor exposure and transmission. The location and context of SARS-CoV-2 transmissions reported in this review are summarized in **Table 4**. Among these are examples of transmissions at a gathering in a park,

but over multiple days with the same people, and at a camp, which lasted for several days and had indoor housing components.

Five other studies included in **Table 3** describe outdoor transmission of influenza or influenza-like viruses. Summers et al. [19] conducted a historical analysis of a large outbreak of the 1918 influenza virus on a military troop ship in July 1918. The outbreak involved over 1000 of the 1,217 crew members and caused 68 deaths. Analysis of factors that might have contributed to mortality revealed a significant association between individuals who slept indoors, in cabins with bunks (mortality of 146.1/1,000 population), versus individuals who slept in hammocks in open-air areas (mortality of 34.1/1,000 population). This study is of particular interest because the duration of exposure and distance between individuals was held constant. This was one of the few studies which investigated potential confounders such as age and social class – mortality changed with age, but not with social class or rurality. Age did not change the discrepancy in deaths seen outdoors compared to indoors.

Pestre et al. [20] conducted a retrospective analysis of a 2009 H1N1 influenza outbreak at a summer camp in France. Investigations revealed that all febrile individuals had travelled together in the same train wagon to reach camp, suggesting that the enclosed space facilitated transmission. The three individuals out of 32 that had not travelled in the same train wagon as all the other participants never developed symptoms, even though they were still present at camp for two days with all other infected individuals - presumably mostly in outdoor spaces.

Finally, three manuscripts about respiratory illnesses at mass open-air gatherings emphasized that while influenza outbreaks were uncommon, the duration of the event (multi-day over single day) and communal housing were risk factors for outbreaks (**Table 3**). [21–23] Rainey

et al. concluded that all reported outbreaks in summer camps had social contact and communal housing, none were reported without a shared housing component.[21] Of note, no single-day mass gathering related outbreaks were detected in the 72 outbreaks they detail. Figueroa et al. also did not identify any single day event-related outbreaks.[22] Botelho et al. found four outbreaks of Influenza A (H1N1) and one of Influenza A and B; all events with an outbreak were multi-day sport events while single-day events had none.[23]

Two articles discussed adenovirus outbreaks associated with lakes [24] and outdoor swimming pools [25]. In both studies respiratory viral infection occurred in swimmers and in others who did not swim, such as fellow camp attendees and family members, suggesting human-to-human transmission prevalently occurring outdoors.

Discussion

While the studies included in this review were highly heterogeneous, ranging in methodology, definition of "outdoor" transmission, and virus studied, several common factors were identified. The studies with direct comparison of SARS-CoV-2 location of transmission reported dramatically lower proportions occurring outdoors. The exact determinants of outdoor transmission that can be gleaned from this review are limited, the cases of outdoor transmission of SARS-CoV-2 we identified were affected by the duration of exposure, frequency of exposure, density of gathering, whether maks were used, and were confounded by the possibility of indoor transmission.

Historical evidence gleaned from influenza outbreaks further support the lower risk of transmission outdoors. Summers et al. showed that influenza mortality on a ship was significantly lower outdoors (sleeping in hammocks) compared to indoors (sleeping in cabins). While mortality does not provide direct information about transmission, it serves as a

useful proxy. Outcomes from several investigations of influenza outbreaks during mass outdoor gatherings suggest that outdoor, single day events without communal sleeping arrangements have lower risks of influenza transmission than multi-day events with indoor components [21–23].

These findings, as well as reports of influenza outbereaks and adenovirus outbreaks in outdoor bodies of water, suggest that while outdoor transmission is less common than indoor, it is not impossible. Case reports identified after our review was completed provide further evidence that high density outdoor gatherings, particularly with low mask use, may lead to higher transmission rates. Miron et. al noted that incidence of COVID-19 cases was significantly higher in 14 out of 20 counties that had a large outdoor gathering 15 days prior.[26] Dave et al. estimates that in the three weeks following the start of the Sturgis motorcycle rally started on August 7th 2020, South Dakota, USA, an multi-day event with 500,000 participants, cases grew more in counties with weak mitigation policies than those with strong mitigation policies (such as closure of restaurants and bars, or mask-wearing mandates) as participants returned to their homes [27]. In contrast, although COVID-19 rates increased in the three weeks following the mass protests in the United States [28], the uptick in cases due to these events was less than expected because social distancing and masking measures were more widespread [29]. The importance of protective measures is further exemplified by the outdoor outbreak that occurred at the White House Rose Garden event on September 26th 2020, where few of the 200 attendees were wearing masks or maintaining social distancing measures.[30]

Of note, our search did not find any studies on the transmission of COVID-19 in settings of outdoor agricultural work. In California prevalence of COVID-19 for agricultural workers is

two to three times higher than the rate for workers in all other industries [31]. The experience of agricultural workers suggests that crowded working or sleeping conditions may be a substantive risk factor for transmission, but the contribution of work in outdoor spaces to transmission risk has not been assessed. We found that outdoor, single day events without communal sleeping arrangements have lower risks of transmission compared to multi-day, mass outdoor gatherings in the spread of influenza [21–23].

In order to better characterize the risks of outdoor SARS-CoV-2 exposure, future studies should fill the research gaps we have identified in this review. First, many research studies we identified did not report the location of transmission at all. This may be because understanding relationships between cases is more important than the location of interaction, or may be related to practical challenges in contact tracing outdoors. Second, it is difficult to isolate an outdoor exposure to a virus. While outdoor gatherings could be largely safe, if they are accompanied by time in indoor locations such as cabins or trains, it might be challenging to identify exact location of transmission. Szablewski et al., which was included in our review, while the summer camp may have been largely outdoors, it does not preclude from exposure in the dining halls or cabins. As for construction sites, once a building is framed and enclosed, it may be considered indoor work, which may in fact be the majority of the work. Third, in many reports published early in the SARS-CoV-2 pandemic, the measured outcome was "illness or death" due to viral infection, not SARS-CoV-2 infection itself, which was rarely assessed. If asymptomatic infections are more likely to occur outdoors, this could represent a systematic bias. Fourth, the definition of being “outdoors” is ambiguous, and the effect of exposure is likely modified by variable proximity to and contact with others. Fifth, in order to test the hypothesis that the risk of infection is lower outdoors, future research should collect data about time spent indoors versus outdoors. Given that 90% of time is spent

indoors in high-and-middle income countries [32], then it would be expected that 90% of transmission to occur indoors, all else being equal. Lastly, there are few data that examine how respiratory droplets spread outdoors, such as how far they travel during running, biking, or during windy conditions. A study examined these variables but was calculated with no account of ventilation, sunlight, or humidity. [33]

Finally, most of the transmission events we identified in the literature did not report the socioeconic status of those impacted. Spreading events often occur in settings where marginalized and disempowered populations live or work such as lower-income, higher density urban settings, work settings such as meat packing plants, or even prisons [34]. While there are multiple reasons for the disproportionate impacts of COVID-19 in these populations, we postulate that lack of opportunity to move high-risk activities outdoors may be one of them. [35,36] While it was our intention to further explore this hypothesis by analyzing sub-group socio-economic and ethnicity data in the studies included in this review, the studies did not include these metrics.

Future studies could compare SARS-CoV-2 case rates at outdoor gatherings to known rates for indoor gatherings. There are several examples of studies that estimate the risk of indoor transmissison [37–39] which have ranged from 10.3% (95% confidence interval [CI] 5.3% – 19.0%) in a study of trains in China to 78% in a church in Arkansas [38]. Accurate estimation of the risk of outdoor transmission will require determining person-time at risk for infection, incidence rate ratios, and more nuanced information about the exposure environment; these data are still lacking.

Better understanding of how SARS-CoV-2 is transmitted outdoors is needed to inform sound policies that reconcile shelter-in-place orders with the many health benefits associated with time spent outdoors [40]. This is particularly relevant to outdoor parks and recreation agencies, which seek clear guidance on how being outdoors has a low risk of transmission. Other policy implications are to encourage moving essential activities outdoors, with appropriate masking and social distancing measures, given that transmission can still occur outdoors. The long term and potentially deleterious social and emotional effects of school closures can be potentially mitigated if, for example, it is known that outdoor schooling is a viable alternative. Finally, encouraging outdoor time may serve as a harm reduction model in allowing people to congregate, and therefore better tolerate long-term shelter in place mandates.

This systematic review has several limitations. The few and heterogenous studies on outdoor transmission of respiratory viruses had used various metrics, exposures and outcomes, making it challenging to compare findings quantitatively. The low proportion of outdoor COVID-19 cases may reflect the general decrease in outdoor activities since strict lockdowns were enacted in the countries surveyed. Relying on reports of symptomatic infections may under-represent asymptomatic cases that occur outdoors. If the viral inoculum affects the severity of respiratory viral infection, an outdoor exposure may reduce the viral inoculum to which the individual is exposed and therefore the subsequent clinical impact of the disease. If this theory were true for SARS-CoV-2, it may increase the proportion of infections that are asymptomatic.[41] The studies in this review did not contain much information about potential confounders such as the age of infected individuals, activities in which they participated, ethnicity, or social class. There was minimal information on mitigation efforts such as masks and social distancing and how that may have impacted/influenced viral

transmission. This review did not explicitly include gray literature (such as case reports from health departments, lay newspaper sources) in its search strategy, as other comprehensive reviews of transmissions have done.[16] Including preprints may have decreased our risk of information bias.

Conclusion

While it has been acknowledged that spending time outside has general health benefits, our review posits that there are also benefits in reducing transmission of SARS-CoV-2 by reducing exposure time (substituting time indoors with time outdoors). These results suggest that moving activities to outdoor settings may reduce infections and ultimately save lives. However, it is important to note that infections are possible outdoors and the advantage may be overtaken by relaxed mitigation efforts.

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Table 1. Comparison of respiratory virus transmission outdoors compared to indoors ordered by virus studied.

Outcome	Virus Studied	Estimate of effect		Relative estimate of effect	Number of participants in the study
		Outdoor	Indoor		
Number of cases [14]	SARS-CoV-2	2/7,324 cases	7,322/7,324 cases	<1% of transmissions happened outdoors	7,324 cases, totaling 318 outbreaks.
Number of cases [17]	SARS-CoV-2	4/103 cases	99/103 cases	5% of work-related cases occurred outdoors	103 possible work-related cases among a total of 690 local transmissions.
Odds of transmission [15]	SARS-CoV-2	*(Raw data not available)*	*(Raw data not available)*	Odds of transmission in closed environments 18.7 (95% CI: 6.0, 57.9) times greater than in open air	110 cases: 27 primary cases and 83 secondary cases
Number of super-spreading events and odds of transmission* [15]	SARS-CoV-2	1/7 super-spreading events	6/7 super-spreading events	Odds ratio of super spreading in closed environments: 32.6 (95%CI: 3.7, 289.5)	110 cases: 27 primary cases and 83 secondary cases
Number of cases [16]	SARS-CoV-2	95/10,926 cases	10,831/10,926 cases	<1% of transmissions happened outdoors	10,926 cases, totaling 201 events of transmission
Number of cases [20]	H1N1 2009 Influenza	0/3 cases	24/29 cases	Out of 32 total people in a holiday camp, 29 traveled together in a train wagon	32 people at a holiday camp
Mortality [19]	H1N1 1918 Influenza	28/820 deaths sleeping in hammocks outside, 34.1 persons/1,000	39/267, deaths sleeping in cabins inside, 146.1 persons/1,000	Risk Ratio of 4.28, 95% CI 2.69-6.81	Total of 1,217 people on the ship.

* superspreading defined as events where the number of secondary cases generated by a single primary case is greater than the 95th percentile of the distribution (i.e. transmission to three or more persons)

Table 2. Studies reporting outdoor SARS-CoV-2 transmission.

Year	Author	Location and Date	Sample Description	Design	Outcomes measured	Outdoor exposure	Outdoor findings	Indoor findings	Bias
2020	Qian et al.	320 prefectural cities in China. Between 4 January and 11 February 2020	7,324 cases, 318 outbreaks	Retrospective analysis of all public health reports from local Municipal Health Commission website to determine location of transmission.	Location of transmissions, clusters and outbreaks. Cluster was defined as 3 or more infections that appear linked to the same infection venue. An outbreak was defined as a cluster in which a common index patient is suspected. Outbreaks were organized by relationship and also by location.	Open air	One outdoor transmission involving two cases in Shangqiu, Henan: a 27-year-old man had a conversation outdoors with an individual who had returned from Wuhan.	Of 318 identified outbreaks that involved 3 or more cases, they all occurred in indoor environments.	Relied on heterogenous case reports of the local health department, which might have missed cases because of differential allocation of resources or internal biases. Additionally, the data was collected partly after lock-down (started January 23rd in Wuhan), after which most people were indoors. There was no effort to access exact locations of infection. Not peer-reviewed at the time of review.
2020	Nishiura et al.	Seven prefectures in Japan. Start date of 28 February 2020	110 cases (27 primary cases, 83 secondary cases). Seven superspreading events identified.	Retrospective case investigation using contact tracing data.	Location and number of transmissions from primary to secondary cases. Super-spreading events defined as: number of	Open air	Odds of transmission in a closed environment was 18.7 times greater compared to an open-air environment (CI:	Out of seven superspreading events, six of these events (85.7%) took place in closed environments.	Small sample size and no raw data provided to support calculations of odds. Limitations were not discussed in the manuscript.

Table 2. Studies reporting outdoor SARS-CoV-2 transmission.									
					secondary cases generated by a single primary case is greater than the 95th percentile of the distribution (i.e. transmission to three or more persons)		6.0, 57.9). The odds ratio of superspreading events in closed environments was as high as 32.6 (95% CI: 3.7, 289.5). One superspreading event occurred outdoors (not described).		Not peer-reviewed at the time of review.
2020	Leclerc et al.	Multiple world-wide locations, as of March 30th	201 events of transmission (clusters)	Review of all documented transmission clusters (world-wide) using literature review and open-source strategies	Settings of transmission clusters for 201 events	22 types of settings were determined. Outdoor locations were defined as "outdoor", while locations that were a mixture were defined as "indoor/outdoor". Indoor locations were defined as "indoor".	The transmissions in the only "outdoor" setting occurred in four outbreaks at outdoor construction sites in Singapore, totaling 95 cases. Updated results additionally revealed: - one transmission occurred while jogging in Codogno, Italy (non-peer re-viewed source) - Twenty cases in an outdoor park in Münster, Germany (non-peer reviewed source)	10/22 locations defined as indoor/outdoor, 11/ 22 defined as indoor. A total of 197 events occurred in these settings, totaling 10,831 cases.	Included reports from some non-peer reviewed sources (eg. local media outlets for the jogging and outdoor park transmission reports), which might have been individually influenced by recall bias and poor methodology. While the study conducted a systematic review, additional sources were collected using an open-source strategy which might have been affected by selection bias of respondents.
2020	Lan et al.	Six Asian	690 locally	Observational	Number of cases	Workplace largely	A total of 103	The five	The exact

Table 2. Studies reporting outdoor SARS-CoV-2 transmission.									
		regions: including Hong Kong, Japan, Singapore, Taiwan, Thailand, and Vietnam Between January 23, 2020 and March 14, 2020.	transmitted cases	study, extracted confirmed COVID-19 cases from governmental investigation reports. Only locally transmitted (non-imported) cases were included. Transmission period was extended to 40 days from primary case.	per occupation across country/area and stratified into early (first 10 days) and late (11-40th day) transmission periods.	outdoors	possible work-related cases were determined to be outdoors among a total of 690 local transmissions. Of workers that might be prevalently outdoors, 5% of cases were construction workers. Tour guides (5% of cases) might also be considered to have occurred partly outdoors.	occupation groups with the most cases were healthcare workers (22%), drivers and transport workers (18%), services and sales workers (18%), cleaning and domestic workers (9%) and public safety workers (7%).	outdoor/indoor makeup of the location of transmission was not described. This is in part due to the fact that the transmission source was not always known, and detailed occupational histories were also not always known. Also, none of the reports arose from systematic testing of high-risk occupations, rather from individual case reports, which might have been affected by biased and heterogenous reporting mechanisms from different regions.
2020	Szablewski et al.	Overnight camp in Georgia, USA. June 17-27 2020.	During June 17–20 the overnight camp held orientation for 138 trainees and 120 staff members; staff members remained for the first camp session, scheduled during June 21–27, and were joined by 363	Retrospective Case Investigation (MMWR)	Positive test result for SARS-CoV-2 (symptomatic and asymptomatic)	Camp attendees were cohorted by cabin and engaged in a variety of indoor and outdoor activities, including daily vigorous singing and cheering.	On June 24 a staff member tested positive to SARS-CoV-2. Test results were later available for 344 attendees; among these, 260 (76%) were positive. The percentage of transmission that	Median cabin attack rate was 50% among 28 cabins that had one or more cases (on average, each cabin housed 15 people). Attack rate was highest in the larger cabin, suggesting the	Attack rates are likely an underestimate because cases might have been missed among persons not tested or whose test results were not reported. Some cases may have

Table 2. Studies reporting outdoor SARS-CoV-2 transmission.									
			campers and three senior staff members on June 21. Children and adults attended.				developed solely outdoors was not investigated.	main location of transmission was in the cabins.	resulted from transmission occurring before or after camp attendance. Lastly, exact details of outdoor activities versus indoor were not described.

Table 3. Studies reporting other outdoor respiratory virus transmission ordered by infection identified.

Year	Author	Virus	Location and Date	Sample Description	Design	Outcomes measured	Outdoor exposure	Outdoor findings	Indoor findings	Bias
2017	Figueroa et al.	Respiratory disease outbreaks	United States, 2009-2014	18 mass gatherings in 8 states.	Data was collected on mass gathering related respiratory disease outcomes. 50 state health departments and 31 large local health departments were contacted via online assessment. 43 (53%) of 81 health jurisdictions responded.	Outbreak was defined as one or more cases of an infectious respiratory disease. Mass gathering (exposure) was defined as a planned or unplanned congregation of 1,000 or more persons in either an indoor or outdoor venue for a common purpose.	Mass gatherings were defined as indoors or indoor/outdoors.	All reported outbreaks occurred at multi-day mass gathering events. For Influenza A (H1N1) attack rates at two summer camps were of 1.4% and 4.8% respectively. Attack rate for a religious event was of 19.5%. At a sporting event in the spring, it was of 3.3% - but only included athletes. Attack rate of Inluenza A (H3) at another summer camp was of 0.02%.	At a professional conference in the winter, which was likely to be mostly indoors, attack rate was of 21.0%. Probable factors that affected attack rates were participant density and susceptibility, rather than gathering size alone. Use of non-pharmaceutical interventions (eg. handwashing, surface cleaning) might have been an additional factor.	Low response rate (around 50%) by state health departments, while there was no response from local health departments. There might be responded bias, given that departments which experienced mass gathering outbreaks might have been more willing to respond. Furthermore, the details of each mass gathering and their indoor/outdoor locations are not described.
2016	Rainey et al.	Respiratory disease outbreaks	United States, 2005-2014	21 published articles describing 72 mass gathering-related respiratory disease	Six medical, behavioral and social science literature databases were analyzed to extract relevant articles. NORS	Mass gatherings were defined as large events involving more than 1,000 persons in a specific	The authors did not specify outdoor vs indoor location of mass gathering.	Close social mixing and contact in communal housing/activities were associated with all other outbreaks identified. They	All reported outbreaks in summer camps had social contact and communal housing, none reported without	Search strategy might have not captured studies that did not use the word “outbreak”, and might have missed any outbreak not captured by surveillance systems

Table 3. Studies reporting other outdoor respiratory virus transmission ordered by infection identified.										
				outbreaks. 1,114 outbreaks reported to NORS (National Outbreaks Reporting System)	was also analyzed to estimate the frequency of mass gathering-related respiratory disease outbreaks.	location for a shared purpose. Definition of outbreak was deferred to the author's definition. Half of the reported outbreaks were related to a zoonotic source and were excluded. 38% of the outbreaks occurred at a variety of camps.		concluded that multiday mass gatherings with indoor residential overnight components can facilitate transmission.	a housing component.	(eg. smaller outbreaks, of diseases with longer incubation periods). Not much detail was shared on the indoor/outdoor locations and activities at the gatherings where outbreaks occurred.
2013	Botelho-Nevers et al.	Disease outbreaks (including respiratory disease)	"open air mass gatherings" worldwide, 1980-2012	9 published articles about respiratory infections at large, outdoor mass gatherings, festivals, or music festivals	Literature search using ProMed and MEDLINE database, with crossreferencing using search engines such as google and yahoo	Outbreaks in the setting of open-air gatherings.	Mass gatherings defined as "generally outdoors", but which may have onsite housing and food supply.	Four outbreaks of Influenza A (H1N1) and one of Influenza A and B were found. Overall, the estimated incidence of confirmed respiratory infections of influenza per 100,000 attendees ranged from 2 to 30. The discrepancy between sport events, which seem to have lower	No exclusively indoor events were included.	The infections related to large open air festivals may be under-reported, given difficulty in ascertaining exact location of transmission and sporadic surveillance systems. The search strategy of only using ProMed and MEDLINE might have limited the amounts of results that might otherwise be available on other reporting/surveillance agencies.

Table 3. Studies reporting other outdoor respiratory virus transmission ordered by infection identified.										
								incidence, and large scale open air festivals in terms of infectious diseases may also be the consequence of the relatively short duration of sports events which frequently last shorter than one day.		
2011	Pestre et al.	2009 H1N1 Influenza	Summer camp in France, August 2009	32 persons participated in the holiday camp. 29 of them traveled in the same train wagon.	Retrospective Case Investigation	Infection of H1N1 influenza.	Individuals who did not travel in the same train wagon.	The outbreak involved 21 children and 3 adults who had all travelled together in the same wagon. The three individuals that did not take the same train wagon and were immediately thereafter in contact with the 24 infected individuals at camp did not experience influenza symptoms.	Out of 29 individuals who took the same train wagon, 21 children and 3 adults experienced symptoms.	Conditions of outdoor versus indoor activities at camp were not described. Given this, the comparison between indoor (train wagon) and outdoor (camp) exposure assumes that a majority of time at camp, as compared to the train wagon, was outdoors. Measurement of cases might have been affected by timing of testing and/or presence of asymptomatic cases. Limitations were not discussed.
2010	Summers et al.	1918 Influenza	His Majesty's New Zealand Transport military troop ship in Sierra	1,217 persons onboard	Retrospective Historical Outbreak Analysis	Mortality	Sleeping in hammocks as opposed to cabins with bunks	Out of 1,217 persons onboard, over 1,000 suspected cases of influenza, 68 deaths. Mortality rate for persons that slept in	Mortality rate for persons that slept in cabins with bunks was of 39/267 (146.1 persons/1,000 population). The difference	Historical evidence used in this paper is subject to transcription and/or recording errors, lack of case definitions, and approximate estimates of case numbers. While it is

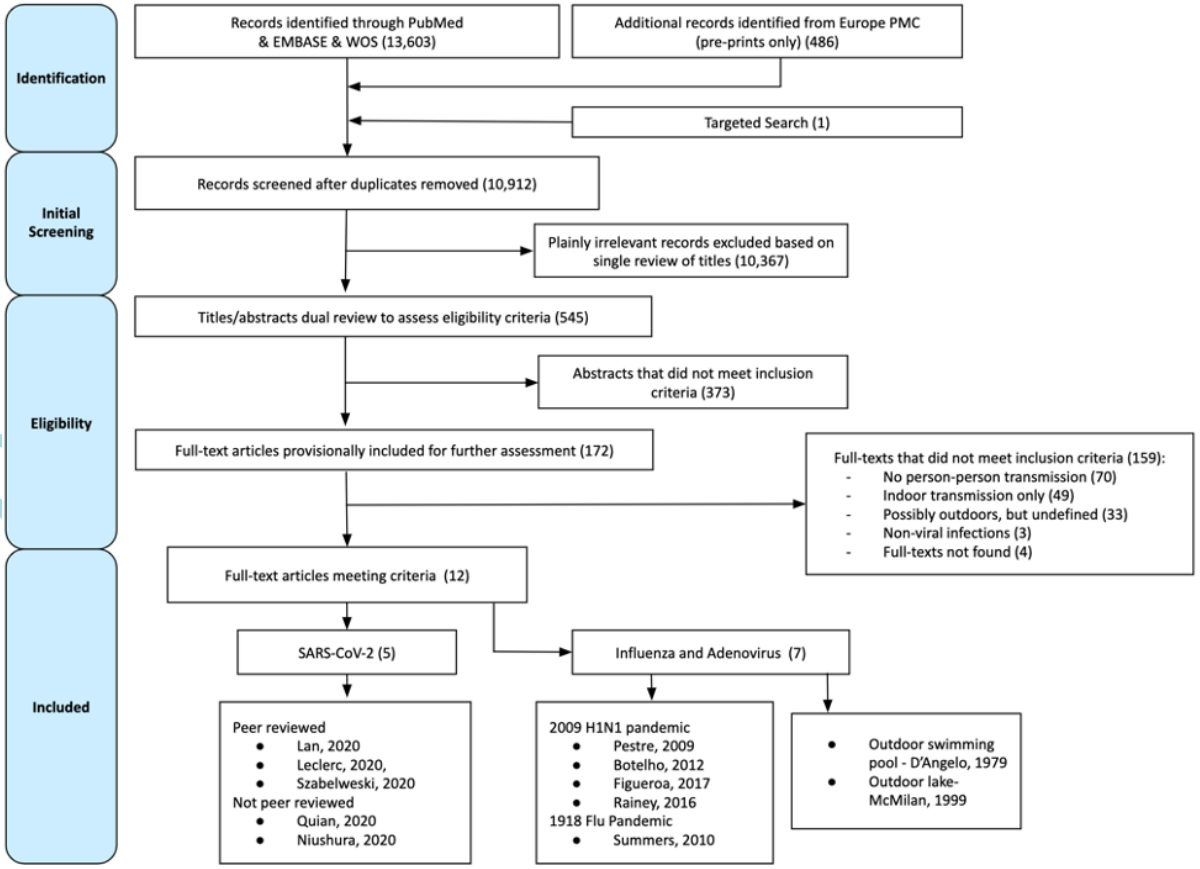
Table 3. Studies reporting other outdoor respiratory virus transmission ordered by infection identified.									
			Leone, July 1918					hammocks outdoors was of 28/820 or of 34.1 persons/1,000 population.	between hammocks was significant (crude RR 4.28, 95% CI 2.69–6.81). Density did not seem to be a contributing factor.	hinted that hammocks were in higher ventilated zones as compared to cabins, the exact location of hammocks was not described.

Table 4. Outdoor conditions where COVID-19 was transmitted

Setting	Description of transmission	Purely outdoors?	Use of Non-Pharmaceutical Interventions*
Overnight summer camp [18]	Outbreak of 260 cases during an overnight camp in Georgia. Everyone was tested negative for COVID less than or equal to 12 days prior to coming to camp. While exact outdoor activities were not described, the overnight component suggests that the attack rate increased with length of time spent at the camp. This was shown by staff members, who were present at camp the longest, having the highest attack rate (56%). Attack rate associated with being adult, length of stay, and being in a cabin together. Median attack rate in the cabins: 50%, overall attack rate 44%.	No	Yes. They state the NPI was not effective. The non-pharmaceutical interventions they tried was cohorting of attendees by cabin (less than or equal to 26 persons), staggering of cohorts for use of communal spaces, physical distancing outside of cabin cohorts, and enhanced cleaning and disinfection, especially of shared equipment and spaces. Cloth masks were required for staff members. Evidently, these interventions were not effective at preventing a majority of cases.
Conversation in outdoor setting [14]	One outdoor transmission involving two cases in Shangqiu, Henan: a 27-year-old man had a conversation outdoors with an individual who had returned from Wuhan. No secondary or tertiary cases from this transmission were reported	Yes	Unknown
Outdoor construction sites [16,17]	Four outbreaks at outdoor construction sites in Singapore, involving a total of 95 cases [16] Five cases of construction workers in Singapore [17]. Details of exact location of transmission were not described. Details of how "indoors" versus outdoors unknown. However, in Leclerc et al. building sites were described as "outdoor" settings.	Unknown	Unknown
Jogging outdoors [16]	One transmission while jogging in Codogno, Italy (reported by local news media, cited in Leclerc et al. open source database)	Yes	Unknown
Outdoor park [16]	Twenty cases in an outdoor park in Münster, Germany (reported by local news media, cited in Leclerc et al. open source database). The members of the extended family, who had been living in different houses in the Angelmodde district of Munster, were suspected to have met often on a playground in the Osthuesheide district. The activites of the family were not described, but it was described as a repeated exposure over days.	Yes	Unknown

* Such as masks, physical distance, cohorting.

Figure 1


Identification
Initial Screening
Eligibility
Included
Records identified through PubMed & EMBASE & WOS (13,603)
Additional records identified from Europe PMC (pre-prints only) (486)
Targeted Search (1)
Records screened after duplicates removed (10,912)
Plainly irrelevant records excluded based on single review of titles (10,367)
Titles/abstracts dual review to assess eligibility criteria (545)
Abstracts that did not meet inclusion criteria (373)
Full-text articles provisionally included for further assessment (172)
Full-texts that did not meet inclusion criteria (159):
- No person-person transmission (70)
- Indoor transmission only (49)
- Possibly outdoors, but undefined (33)
- Non-viral infections (3)
- Full-texts not found (4)
Full-text articles meeting criteria (12)
SARS-CoV-2 (5)
Influenza and Adenovirus (7)
Peer reviewed
Lan, 2020
Leclerc, 2020,
Szabelweski, 2020
Not peer reviewed
Quian, 2020
Niushura, 2020
2009 H1N1 pandemic
Pestre, 2009
Botelho, 2012
Figueroa, 2017
Rainey, 2016
1918 Flu Pandemic
Summers, 2010
Outdoor swimming pool - D'Angelo, 1979
Outdoor lake- McMilan, 1999

This is **"Exhibit BB"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

A Commissioner, etc.

BMC Infectious Diseases

RESEARCH ARTICLE

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A wind speed threshold for increased outdoor transmission of coronavirus: an ecological study

Sean A. P. Clouston[1,2*], Olga Morozova[1,2] and Jaymie R. Meliker[1,2]

Abstract

Background: To examine whether outdoor transmission may contribute to the COVID-19 epidemic, we hypothesized that slower outdoor wind speed is associated with increased risk of transmission when individuals socialize outside.

Methods: Daily COVID-19 incidence reported in Suffolk County, NY, between March 16th and December 31st, 2020, was the outcome. Average wind speed and maximal daily temperature were collated by the National Oceanic and Atmospheric Administration. Negative binomial regression was used to model incidence rates while adjusting for susceptible population size.

Results: Cases were very high in the initial wave but diminished once lockdown procedures were enacted. Most days between May 1st, 2020, and October 24th, 2020, had temperatures 16–28 °C and wind speed diminished slowly over the year and began to increase again in December 2020. Unadjusted and multivariable-adjusted analyses revealed that days with temperatures ranging between 16 and 28 °C where wind speed was < 8.85 km per hour (KPH) had increased COVID-19 incidence (aIRR = 1.45, 95% C.I. = [1.28–1.64], P < 0.001) as compared to days with average wind speed ≥ 8.85 KPH.

Conclusion: Throughout the U.S. epidemic, the role of outdoor shared spaces such as parks and beaches has been a topic of considerable interest. This study suggests that outdoor transmission of COVID-19 may occur by noting that the risk of transmission of COVID-19 in the summer was higher on days with low wind speed. Outdoor use of increased physical distance between individuals, improved air circulation, and use of masks may be helpful in some outdoor environments where airflow is limited.

Keywords: COVID-19, Infectious disease epidemiology, Risk factors, Quantitative modeling

Background

The novel severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) that causes a potentially deadly disease called coronavirus disease 2019 (COVID-19), began spreading in China [1], and Italy [2] before arriving in the United States (U.S.). COVID-19 first hit in the U.S. in regions, such as New York (N.Y.) and California, where global travelers often arrive into the U.S. [3]. Suffolk County, N.Y., experienced its first wave of infections early in March 2020, when the pandemic had just arrived in N.Y., causing a high degree of transmission and large numbers of COVID-related deaths.

COVID-19 transmits via aerosolized viral particles that begin shedding before symptoms are evident [4], making it difficult to trace patterns or locations where exposures are occurring. As a result, approximately half

*Correspondence: sean.clouston@stonybrookmedicine.edu
[1] Program in Public Health, Health Sciences Center, Stony Brook University, #3-071, Nichols Rd., Stony Brook, NY 11794-8338, USA
Full list of author information is available at the end of the article

of those diagnosed with COVID-19 report not knowing where they may have become infected [5]. One explanation for a lack of known exposures is that COVID-19 transmits in spaces that are believed to be safe. A handful of studies have made some headway in identifying such situations. For example, one study found that COVID-19 could transmit through the air over relatively long distances [6] and another highlighted the impact of air conditioning vents [7]. A third study found that a cluster of 17 cases were traced to indirect transmission in shared spaces at a shopping mall in Wenzhou, China [8]. Still other studies have revealed that individuals in a constricted space could spread COVID-19 via inhaled transmission over potentially large distances by following airflow within a restaurant [7] and the Diamond Princess cruise ship [6].

A recent review concluded that transmission within constricted indoor spaces is critically important [9]. However, outdoor exposures have been reported, yet relatively little is known about conditions that reduce safety of outdoor social contacts. There are reports of sporadic outbreaks in outdoor environments, including at a construction site in Singapore [10, 11], jogging [10], or during conversation [12]. Because of much lower risk outdoors [13], close outdoor contacts are often described as being risk-free, and exposure-mitigating strategies have focused on promoting the use of exterior spaces when conducting social activities in efforts to mitigate risk of exposure. Outdoor gatherings (for example, participating in events such as backyard barbecues, sitting near to others while watching outdoor events, standing in line outside, or socializing outdoors), may be sensitive to circumstances that may influence their protective features. If exposure occurs outside, simulation studies suggest that transmission may be hampered by the same factors as are commonly seen in studies of indoor transmission including the air turnover rate [13]. Indeed, one preliminary study reported evidence of an association globally between weather dynamics including lower temperatures and lower wind speed with small increase in COVID-19 incidence [14] that may be non-linear [15], with at least one locality in Indonesia reporting local findings supporting this pathway [16].

The present study examined data reported in Suffolk County, N.Y., a large suburban county (~1.5 million) that reported 96,057 cases between March and December 2020. The existence of a non-linearity in associations could imply that wind speed is moderated by another factor, potentially human activity. In the present study, we hypothesized that lower exterior wind speed would be associated with an increased risk of transmission during days ranging in temperature from 16 to 28 °C (degrees Celsius, equivalent to 60–84 degrees Fahrenheit [°F]) when individuals were most likely to be socializing outside.

Methods

Setting

Suffolk County is a large cousupplnty (2362 square-kilometers [km^2]) of approximately 1.5-million people that predominantly acts as an exterior suburban community serving New York City. The median age is 41.8 years; 66.6% are non-Hispanic White, 20.2% are Hispanic, 8.8% are Black, while the remainder predominantly reports being Asian or having two or more races. The median household income in Suffolk County is 54.6% higher than the national average. Overall, 6.8% of households fall below the national poverty line and 5.2% report lacking health insurance. Suffolk County is relatively densely populated with 645.6 people/km^2.

Measures

To examine the potential for exterior exposure risk, we modeled COVID-19 incidence using cases reported to the Suffolk County Department of Health from March 16th, when data first began being recorded reliably using an electronic interface, until December 31st, 2020. At that time, Suffolk County was enduring a second wave. Daily case counts were shared with Stony Brook University to support the COVID-19 modeling efforts at the local level. After cleaning, county-level data were published online to a publicly-accessible database (the Additional file 1 provides cleaned county-level data merged with other variables used in this study). We limited the analysis to dates following March 16th, 2020, with the opening of multiple drive-through testing sites throughout the area and the establishment of regular case-reporting routines. Susceptible population estimates integrate overall county residential estimates derived from the U.S. census and were updated for daily death counts, and for the reported number of COVID-19-related disease counts.

Since daily case counts exhibit temporal dependence that is primarily determined by the unobserved community force of infection, in secondary analyses we examined an alternative outcome measure of relative change in daily case counts compared to an 8-day forward/backward autoregressive moving average [17], as defined by:

$$\frac{\left(cases(t) - \frac{1}{8}\sum_{k=t-4}^{t+4} cases(k)\right)}{\left(\frac{1}{8}\sum_{k=t-4}^{t+4} cases(k)\right)} \forall k \neq t$$

The 8-day forward/backward moving average, when integrated into the model, serves as a proxy measure of underlying force of infection. This allows us to partially capture the variability in absolute case counts that is

due to "natural" transmission patterns rather than external shocks such as wind speed. It is important to note that, on average, this measure would be zero when case counts remain relatively constant over time, however, this measure will track the periods of exponential rise (where it will be positive) and decay (where it will be negative) of an epidemic's waves. It is therefore important to take these distinct behaviors into account.

Maximal daily temperature, as well as average wind speed, were derived from the U.S. National Oceanic and Atmospheric Administration data portal (w2.weather.gov). Data were recorded at a central location at the MacArthur Airport in Islip, N.Y. Total snowfall and rainfall were recorded in inches and converted to centimeters. While temperatures 16–28 °C are likely to be protective, reduced wind speed impact on these days may emerge because individuals are more likely to be socializing outdoors where risk is markedly lower. In the summer, higher wind speed increases airflow and may reduce risk versus in the winter when it may work to push outside social contacts to shelter in indoor spaces. When exterior temperatures are warm enough (16–28 °C) to allow for outdoor social contacts to occur comfortably, we anticipated that increased wind speed would reduce overall transmission risk. In contrast, on days where exterior temperatures were cooler, increased wind speed might cause individuals to retreat indoors for social occasions.

Covariates

We adjusted for the number of days since lockdown (March 16th, 2020) and days since reopening began (May 15th, 2020) in Suffolk County, N.Y. To account for differences in daily reporting patterns, we incorporated a categorical variable indicating the day of the week that cases were reported. Noting that there have been significant spread following holidays, we incorporated an indicator of holidays that also incorporated the most significant weekend nearby. We also included covariates measuring rainfall and snowfall because they may correlate with wind speed as well as social activities outdoors. In the primary analysis, we also adjusted for the 8-day forward/backward moving average daily case count.

Statistical modeling

Descriptive characteristics include time-related trends in maximal temperature, average daily wind speed, and daily case counts. Daily and smoothed trends in maximal temperature and in average wind speed were reported.

In the main analysis, the incidence of COVID-19 positive caseload was reported as case counts per day so multivariable-adjusted modeling relied on negative binomial regression [18]. Negative binomial regression was chosen over alternatives including Poisson because we were concerned about the potential for over-dispersion in the outcome [19] since the infectious disease caseload is highly variable and because COVID-19 appears to spread commonly through super-spreading clusters [20]. A nine-day lag between exposure and case registration was assumed, consistent with epidemiological estimates of the incubation period for COVID-19 [21, 22] coupled with a two-day testing and one-day reporting lag period that has been common in Suffolk County since testing became widely available. Unadjusted and multivariable-adjusted incidence rate ratios (IRR) and 95% confidence intervals (95% C.I.) were reported. The interval between infection and disease ascertainment is unobserved and varies geographically by local testing availability and reporting systems: it can be reduced in places where testing is easy to find and lengthened in places where testing is difficult or requires hospitalization. As such, we conduct a sensitivity analysis considering the range of values of time intervals between exposure and case reporting. For our lagging period, we allowed four days because our experience suggests that it takes two days to report testing results to the Department of Health, and an additional day to report those results publicly. Fifteen days was selected as a ceiling for index case analysis to reduce the risk of sequential outcomes from prior case/exposure cycles consistent with prior publications [23]. However, in sensitivity analyses we report results for a 4–13-day range to clarify the impact of those choices. We used the log-likelihood to compare model fit for different lags.

We analyzed the secondary outcome – a relative measure of daily case counts calculated as ln(incident cases/population * 100,000) – using linear regression with the same set of covariates as the primary outcome measure and exploring the results for a range of reporting lags.

Since we theorized that there is heterogeneity in association between wind speed and COVID-19 transmission may depending on temperature, cutoffs for "warm" days and for days when wind speed was sufficiently fast were determined by comparing Akaike's information criterion (AIC) across multiple models using different details as modeled parameters. We compared AIC between models to determine that 16 °C (60 °F) was an optimal lower bound in temperature, while follow-up analyses revealed an upper bound of 28 °C (84°F). To account for seasonality, we also adjusted for the maximal daily temperature. Because cutoffs may be useful when adjudicating risk at the local level, we used AIC to identify optimal cutoffs for wind speed. This resulted in identifying low wind speed to be < 8.85 KPH (kilometers per hour (KPH), equivalent to approximately 5.5 miles per hour).

Since the relative measure of daily case counts only partially adjusts for the community force of infection and underlying "natural" epidemic dynamics, we also

conducted additional stratified sensitivity analyses cut into periods when case counts were relatively flat (06/07/2020–11/03/2020) and when the epidemic was exponentially increasing (03/16/2020–04/10/2020 and 11/04/2020–12/31/2020) or decaying (04/11/2020–06/06/2020). We used two criteria: daily temperature and epidemic dynamics pattern (flat versus rising/falling) to determine subsets for stratified analyses. Analyses were completed using Stata 16/MP [StataCorp].

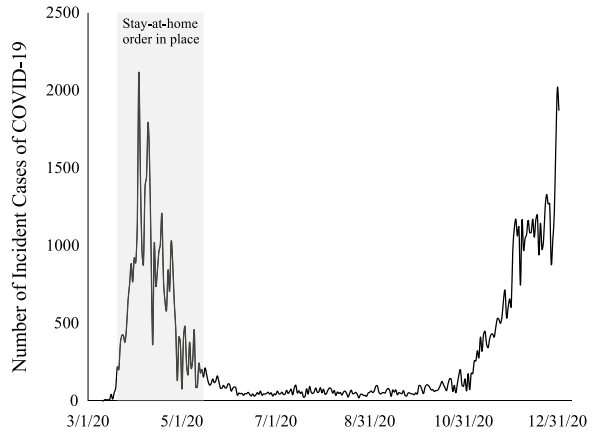

Fig. 1 Trends in daily COVID-19 cases identified in Suffolk County from March 16th–December 31st, 2020

Results

We begin by showing the number of daily cases over the entire observational window (Fig. 1). Cases were very high in the initial wave but diminished quickly once lockdown procedures were enacted.

The average temperature was 19.8 ± 8 °C and the average daily wind speed was 14.0 ± 5.8 KPH. Trends in daily temperature and wind speed are depicted throughout the analytic period (Fig. 2). Most days between May 1st, 2020, and October 24th, 2020, were characterized by temperatures 16–28 °C (solid red lines show this range). The trend in average wind speed (black dashed line) diminished slowly over time and then began to increase again in December 2020.

Further interrogating the functional shape of the relationship between the wind speed and incidence of COVID-19 (Fig. 3) we found that during periods where temperatures ranged from 16 to 28 °C, reduced wind speed was associated with increased incidence. However, on cooler days, when very high wind speeds were most common, incidence of COVID-19 appears to increase slightly as a function of wind speed though this was not evident in multivariable analyses. Using the logarithmic transformation to capture tapering threshold effects in a multivariable-adjusted model examining the impact of wind speed only on days that were 16–28 °C. Exploring the implications of this threshold effect we found that while an increase in wind speed from 5 to 6 KPH was associated with a 12.56% caseload reduction, a similar increase from 15

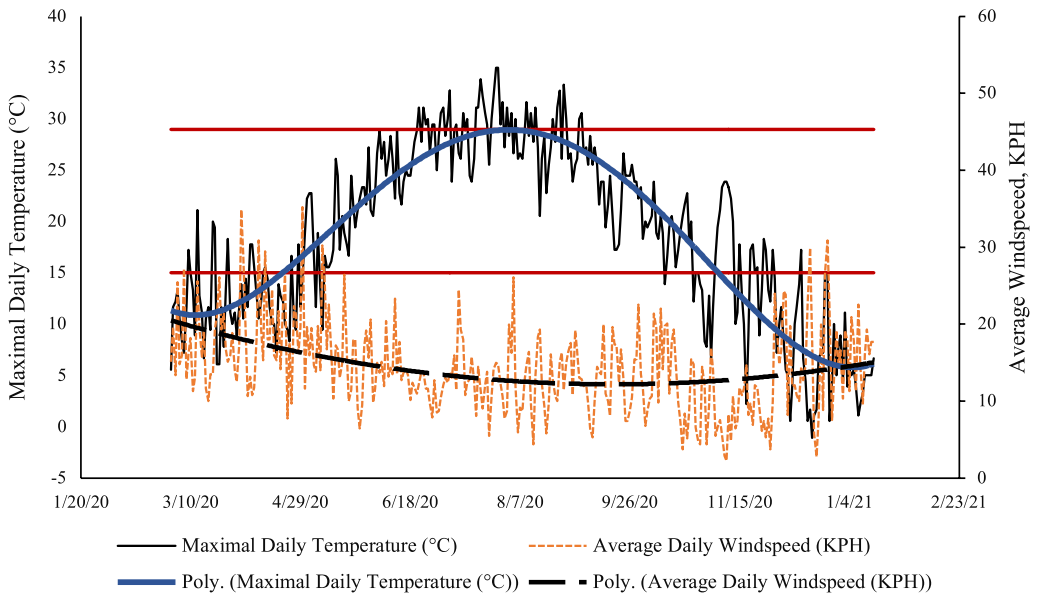

Fig. 2 Trends in maximal daily temperatures, expressed in °C, and mean daily wind speed expressed in kilometers per hour in Suffolk County, NY, from March 16th–December 31st, 2020. The horizontal red lines show temperatures in the 16–28 °C range

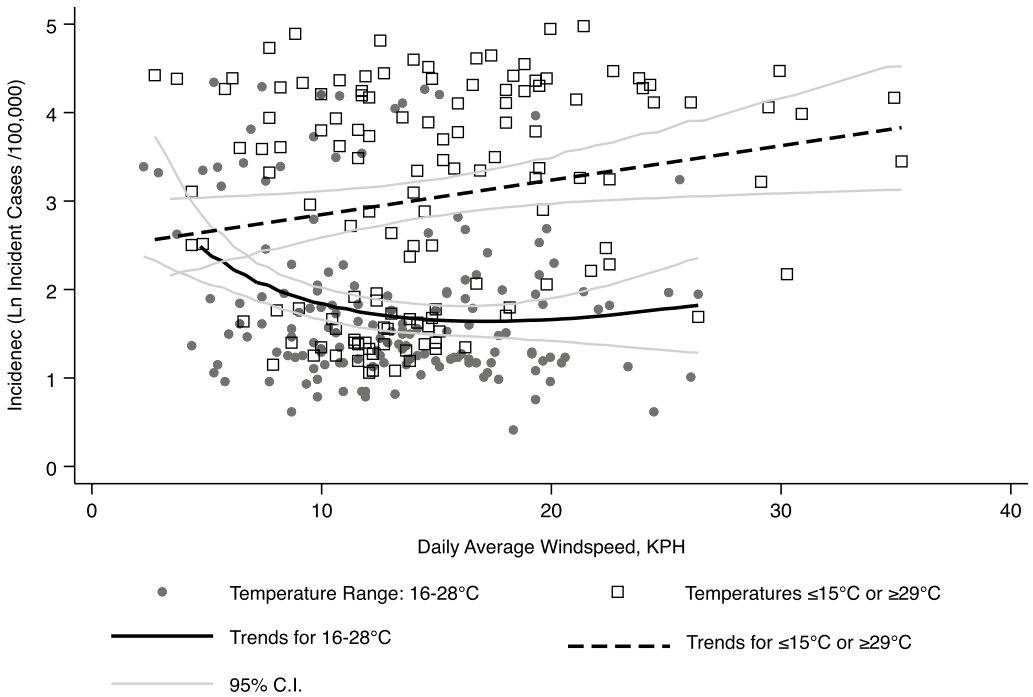

Fig. 3 Average wind speed versus number of incident cases of COVID-19 in Suffolk County from March 16th–December 31st, 2020. The natural log function was selected because it performed better (AIC = 4055.4) than alternative specifications including linear (AIC = 4105.3), inverse (AIC = 4298.5), and quadratic (AIC = 4057.3). Unadjusted and multivariable-adjusted models are shown in Table 2. Note that the incidence of COVID-19 was lagged from wind speeds by nine days

to 16 KPH was only associated with a 1.16% decrease in caseload. Visual inspection showed that on warm days (temperatures ranging from 16 to 28 °C) with very high wind speed (above 20 KPH) increasing wind speed was associated with increased transmission. However, using a quadratic transformation we did not find this association to be statistically significant (P = 0.071).

Unadjusted analyses revealed statistically significant associations between higher COVID-19 incidence and lower wind speed in 16–28 °C weather (Table 1). Multivariable-adjusted analyses similarly revealed that results remained statistically significant upon adjusting for confounders.

As noted in the Methods section, optimal temperature cutoffs were 16–28 °C in temperature, and < 8.85 KPH in wind speed. Using these cutoffs, in Table 2 we examined the risk associated with lower wind speed (< 8.85 KPH) on days with maximal temperatures in the 16–28 °C range. Analyses revealed that on days with temperatures from 16 to 28 °C, exposures to wind speed < 8.85 KPH was associated with a 45% increase in incidence in multivariable-adjusted models.

Sensitivity analysis

We examined the sensitivity of the results to analytic choices by first examining whether reliance on different outcomes made differences to the results. For the relative change in daily case counts compared to an 8-day forward/backward moving average, the results were substantively similar (B = − 16.12 [− 27.78, − 4.45], P = 0.007) on days with temperatures from 16 to 28 °C; in other words, days where wind speed was < 8.85 KPH were attributed with 16.12% increases in relative incidence (Additional file 2: Table S1). We also examined whether choices in the lag between exposure and case reporting changed our results. While the results shown theoretically represent the appropriate timing, we also examined variation in periods between exposure and case recording from 4 to 13 days. We found that while the nine-day reporting average was the best performing within our hypothesized observational window (Additional file 2: Figure S1). Across all lags, we identified a consistent association between slower wind speed days and lower follow-up case counts (Additional file 2: Table S2). We examined whether holidays were more impactful depending on temperature but found that while the effect sizes

Table 1 Incidence rate ratios for COVID-19 derived from negative binomial regression showing both unadjusted and multivariable-adjusted analyses from March 16th–December 31st, 2020

	Unadjusted	**Multivariable-adjusted**
Variable	IRR [95% C.I.]	aIRR [95% C.I.]
Wind speed (Ln–KPH) when temperature 16–28 °C	1.85 [1.67–2.06] P < 0.001	1.17 [1.09–1.26] P < 0.001
Wind speed (Ln–KPH) when temperature ≤ 15 or ≥ 29 °C	1.04 [0.79–1.36] P = 0.798	0.93 [0.81–1.06] P = 0.248
Maximal exterior temperature, °C		1.00 [0.99–1.01] P = 0.677
Days since lockdown		0.95 [0.93–0.97] P < 0.001
Days since reopening		1.06 [1.04–1.08] P < 0.001
Holiday adjustment		1.11 [0.92–1.33] P = 0.264
Snowfall, cm		0.98 [0.92–1.04] P = 0.540
Rainfall, cm		1.01 [0.94–1.09] 1.02 P = 0.776
Eight-day forward/backward moving average		1.22 [1.20–1.25] P < 0.001
α	0.98 [0.85–1.13]	0.17 [0.14–0.2]

IRR incidence rate ratio, *95% C.I.* 95% confidence interval. All models additionally adjust for day of the week in which cases were reported and for the size of the county population adjusted for reductions due to death or recovery from COVID-19 during the period of observation. α is a measure of dispersion. P-values derived from Student's T-tests

Table 2 Incidence rate ratios for COVID-19 derived from negative binomial regression showing both unadjusted and multivariable-adjusted analyses comparing days where wind speed < 8.85 KPH to days with ≥ 8.85 KPH wind speeds from March 16th–December 31st, 2020

	Unadjusted	**Multivariable adjusted**
Variable	IRR [95% C.I.]	aIRR [95% C.I.]
Wind speed < 8.85 KPH when temperature 16–28 °C	4.09 [3.16–5.28] P < 0.001	1.45 [1.28–1.64] P < 0.001
Wind speed < 8.85 KPH when temperature ≤ 15 or ≥ 29 °C	1.45 [1.04–2.03] P = 0.029	1.03 [0.88–1.20] P = 0.717
Maximal exterior temperature, °C		0.99 [0.99–1.00] P = 0.021
Days since lockdown		0.94 [0.93–0.96] P < 0.001
Days since reopening		1.07 [1.05–1.09] P < 0.001
Holiday adjustment		1.12 [0.94–1.34] P = 0.208
Snowfall, mm		0.93 [0.82–1.06] P = 0.274
Rainfall, mm		1.02 [0.88–1.20] P = 0.774
Eight-day forward/backward moving average		1.21 [1.19–1.24] P < 0.001
α	1.02 [0.88–1.17]	0.16 [0.13–0.19]

*KPH: kilometers per hour; °C: degrees Celsius; IRR: incidence rate ratio; 95% C.I.: 95% confidence interval. All models adjust for day of the week in which cases were reported and for the size of the county population adjusted for reductions due to individuals who had died or become immune due to COVID-19 during the period of observation. α is a measure of dispersion. P-values derived from Student's T test

were slightly smaller on days with temperatures from 16 to 28 °C (interaction B = − 0.18, P = 0.142), these differences were not statistically significant. Finally, we stratified analysis dates into periods characterized by rising, falling, and stable transmission. This analysis resulted in the same overall association ($aIRR_{>8.85\ KPH} = 0.87$ [0.75–1.03]; $aIRR_{Ln\text{-}KPH} = 0.88$ [0.75–1.05]) though insufficient observations to achieve statistical power (power = 0.65).

Discussion

The COVID-19 pandemic has caused an immense toll on the American population and has inflicted enormous economic damage. Current evidence suggests that COVID-19 is airborne and is predominantly spread indoors. The present study examined variations in wind speed under the hypothesis that higher winds may disperse COVID-19 viral particles away from people socializing outdoors, thereby offering increased protection among individuals who may have been exposed to COVID-19 outdoors. We found that slow average wind speed (< 8.85 KPH) was associated with increased incidence of COVID-19 on days that had temperatures supporting socializing outdoors (16–28 °C; aIRR = 1.45 [1.28–1.64], P < 0.001). This study supports the view that while transmission was lowest when days were in comfortable ranges (from 16 to 28 °C), on these days the risk was highest when wind speed was slow.

This study suggests that low wind speed may reduce the protective impact of weather ranging from 16 to 28 °C. Results align with anecdotal reports from local Departments of Health and from the Centers for Disease Control and Prevention [24], who have noted that gatherings of increased risk include outdoor social gatherings such as "Backyard Barbecues". One interpretation of this evidence may be that airborne transmission in shared outdoor spaces is feasible on days when the wind is insufficient to disperse viral particles. For example, wind speed in weather outside of the 16–28 °C temperate zone may make social activities less pleasant or may increase the risk of transmission in outdoor settings with stale air.

The present study represents a step forward to understanding the regional role of outdoor wind and temperature dynamics, and their interrelationships when trying to understand COVID-19 infection dynamics. The next steps in this research area might include the study of microclimate dynamics within regions to determine the relevance of architectural design, fencing, and wind flow within roads in determining geographical differences in disease transmission and exposure dynamics. Understanding the geographical distribution of cases resulting on wind-less compared to similar windy days may help determine other factors, such as population density or housing density, that modify impact of reduced wind speed. Additionally, multilevel analyses might examine the extent to which social activities might be affected most by reduced wind speed. Yet, while geographic targets are critical, further research is also needed to determine the extent to which reduced wind speed is more, or less, impactful with novel COVID variants or with other respiratory diseases. One potential output of such information may be to inform the creation of a weather warning system so that individuals or policymakers could issue guidelines or warning systems when masking usage might be recommended outdoors or in outdoor spaces at risk of reduced wind speed.

Limitations

Despite examining a large population (~ 1.5 million) that identified many cases (96,057 between March-December 2020), this study is limited in examining the experience of a single U.S. County. Although there is little reason to think that shared indoor spaces would increase on days of lower wind speed in the 16–28 °C temperature range, we cannot conclusively state that higher wind speed protected any individuals. Our results were strongly influenced by covariates as evidenced by the change in IRR observed in unadjusted *versus* adjusted models; it is always possible that key confounders were missing from our model. For example, we could not address the potential for non-independence that may emerge when individuals who have previously survived COVID-19 may be re-infected. However, sensitivity analyses examining the percent change of new cases on a given day relative to the eight-day backward/forward average case count attempted to address temporal changes in incidence patterns directly within the outcome variable, and our results were similar. Follow-up research is necessary to determine specifics about exposures, including distances that COVID-19 viral particles can travel and reliably infect individuals and microclimate differences that may affect specific geographic differences that may moderate these results.

To obtain a measure of wind speed for this analysis, we relied on data from a central airport. While this provided consistent measures of wind speed across the island, these measures may not be generalizable to microclimates occurring in the fenced-in backyards, lea of hills and dunes, or forests. Notably, this choice may mean that cutoffs used here may not apply in other situations. More analysis is necessary if weather data are going to be relied upon to help understand caseload in other areas. We reported a nine-day exposure-test positive reporting lag structure; however, sensitivity analyses suggested that a 16-day lag structure may work better. The 16-day lag is outside of the expected lag period for cases in our area. Still, we felt that it might indicate that case dynamics

could proceed from asymptomatic younger individuals to cause secondary cases in older individuals reported 16 days later. As such, future work should anticipate that different cutoffs will be necessary when wind speeds are measured in other places and in locations where wind is highly sensitive to local geography.

Conclusions

Throughout the U.S. epidemic, the role of outdoor shared spaces such as parks and beaches has been studied, and ultimately beaches and parks remained open because outdoor gatherings are considerably less risky than indoor ones. This analysis does little to suggest that either should be closed, since the level of risk due to outdoor exposures should be weighed in relation to the much higher risk of exposure in shared interior spaces such as houses, restaurants, or public transport. Instead, this study may suggest that individuals socializing outdoors may not be completely safe by being outdoors and should remain vigilant, especially on days where airborne particles may be less likely to disperse due to contextual factors such as reduced wind speed, that may reduce the benefits of socializing outside. In this case, outdoor use of increased physical distance between individuals, improved air circulation, and use of masks may be helpful in some outdoor environments where airflow is limited.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-021-06796-z.

Additional file 1: Data file 1. County-level data used in this study.

Additional file 2. Supplemental Tables and Figures showing results from foundational and sensitivity analyses. Table S1. Multivariable-adjusted regression coefficient, 95% confidence interval, and P-values examining association between wind speed (<8.85 KPH) on days with temperatures of 16-28°C and percentage increases in case numbers. **Table S2.** Multivariable-adjusted incidence rate ratio (aIRR), 95% confidence interval, and P-values examining association between wind speed (Ln-KPH) on days with temperatures from 16-28°C and increases in case numbers only in samples where a 13-day lag was observed to maintain predictive stability. **Figure S1.** Gaussian-smoothed fit characteristics for the model presented in Table 1 relying on different lag structures examining possible lags of 4-13 days. Note that the best fitting lag (9 days) was shown using a red diamond.

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None.

Authors' contributions
SC analyzed data and drafted the manuscript. OM provided scientific oversight, edited the manuscript, and provided topical expertise. JM provided scientific oversight and critically edited the manuscript. All authors read and approved the final manuscript.

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Availability of data and materials
All data analyzed during this study are included in this published article and its supplementary information files.

Declarations

Ethics approval and consent to participate
Data used in this study are secondary analyses of daily case counts reported on publicly available websites, and therefore was not human subject's research. All identifiers were removed from the data prior to publication online. No administrative privileges were needed to access the data used in this study.

Consent for publication
Not applicable.

Competing interests
None.

Author details
[1]Program in Public Health, Health Sciences Center, Stony Brook University, #3-071, Nichols Rd., Stony Brook, NY 11794-8338, USA. [2]Department of Family, Population, and Preventive Medicine, Renaissance School of Medicine at Stony Brook, Stony Brook, NY, USA.

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Publisher's Note

This is **"Exhibit CC"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

A Commissioner, etc.

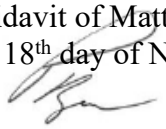
In **Sweden**, from **3 January 2020** to **11:38am CEST, 14 July 2021**, there have been **1,092,540 confirmed cases** of COVID-19 with **14,643 deaths**, reported to WHO. As of **4 July 2021**, a total of **8,713,499 vaccine doses** have been administered.

Sweden Situation

Daily Weekly

1,092,540
confirmed cases

This is **"Exhibit DD"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



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A Commissioner, etc.

World Health Organization

Search by Country, Territory, or Area

Covid-19 Response Fund

Donate

Global > Brazil

Overview Data Table Explore

In **Brazil**, from **3 January 2020** to **3:19pm CEST, 29 June 2021**, there have been **18,769,808 confirmed cases** of COVID-19 with **524,417 deaths**, reported to WHO. As of **2 July 2021**, a total of **95,647,172 vaccine doses** have been administered.

This is **"Exhibit EE"**
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022

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A Commissioner, etc.

These are days with a reporting anomaly. Read more here.

Tests

Hospitalized

Deaths

	AVG. ON JUN. 25	14-DAY CHANGE	TOTAL REPORTED
Cases	1,578	-4%	2,321,929
Tests	47,643	+8%	—
Hospitalized	1,840	-7%	—
Deaths	31	-22%	37,772

▸ About this data

	AT LEAST ONE DOSE	FULLY VACCINATED
All ages	53%	45%
18 and up	64%	54%
65 and up	90%	78%

See more details ›

▸ About this data

Restrictions ›

Reopened

Masks not required

Gov. Ron DeSantis, a Republican, suspended all local coronavirus restrictions and mandates until July 1, after which they will be permanently invalidated. Mr. DeSantis has barred businesses from requiring patrons to provide proof of Covid-19 vaccination, and in June he issued a full pardon for all non-violent offenses related to local government restrictions. More details ›

This is **"Exhibit FF"**
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Epidemiology and Infection

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Review

*These authors contributed equally to the work.

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Author for correspondence:
Y. Ma, E-mail: ym48@bu.edu

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Quantifying TB transmission: a systematic review of reproduction number and serial interval estimates for tuberculosis

Y. Ma[1], C. R. Horsburgh Jr[2], L. F. White[1,*] and H. E. Jenkins[1,*]

[1]Department of Biostatistics, Boston University School of Public Health, Boston, MA 02118, USA and [2]Department of Epidemiology, Boston University School of Public Health and Department of Medicine, Boston University School of Medicine, Boston, MA 02118, USA

Abstract

Tuberculosis (TB) is the leading global infectious cause of death. Understanding TB transmission is critical to creating policies and monitoring the disease with the end goal of TB elimination. To our knowledge, there has been no systematic review of key transmission parameters for TB. We carried out a systematic review of the published literature to identify studies estimating either of the two key TB transmission parameters: the serial interval (SI) and the reproductive number. We identified five publications that estimated the SI and 56 publications that estimated the reproductive number. The SI estimates from four studies were: 0.57, 1.42, 1.44 and 1.65 years; the fifth paper presented age-specific estimates ranging from 20 to 30 years (for infants <1 year old) to <5 years (for adults). The reproductive number estimates ranged from 0.24 in the Netherlands (during 1933–2007) to 4.3 in China in 2012. We found a limited number of publications and many high TB burden settings were not represented. Certain features of TB dynamics, such as slow transmission, complicated parameter estimation, require novel methods. Additional efforts to estimate these parameters for TB are needed so that we can monitor and evaluate interventions designed to achieve TB elimination.

Introduction

Tuberculosis (TB), an airborne bacterial infection caused by the organism *Mycobacterium tuberculosis* (*Mtb*), has surpassed HIV/AIDS as the leading cause of death due to a single infectious organism worldwide [1]. It primarily attacks the lungs but can also infect other areas of the body [2, 3]. Those exposed to *Mtb* often develop latent TB infection (LTBI) and have a 5–10% lifetime risk of progressing to active TB [4, 5]. Worldwide, 2–3 billion people are infected with TB; an estimated 10.4 million people developed active TB disease in 2015 [4]. Major innovations in strategies and tools to monitor the success of new strategies are needed to achieve the World Health Organisation (WHO)'s ENDTB goals of reducing TB deaths by 95% and new cases by 90% by 2035 [4].

The reproductive number and serial interval (SI) are two key quantities in describing transmission of an infectious disease. The reproductive number is defined as the average number of secondary cases a primary infectious case will produce. In a totally susceptible population, it is referred to as the basic reproductive number (R_0); it is referred to as the effective reproductive number (R_e) if the population includes both susceptible and non-susceptible persons [6]. An $R_e > 1$ indicates that the disease will continue to spread while an $R_e < 1$ indicates that the disease will eventually die out. Although the reproductive number is usually defined as the average number of secondary cases, it is occasionally defined as the average number of secondary infections [7–10], a distinction that is important for a disease with a long incubation period (the time between infection and developing symptomatic disease) and/or only a fraction of infections progressing to disease. Depending on the setting, the reproductive number can be expressed as a function of parameters such as infection rate, contact rate, recovery rate, making it useful in determining whether or not a disease can spread through a population.

The serial interval (SI), defined as the time between disease symptom onset of a case and that of its infector [11], is a surrogate for the generation interval – an unobservable quantity defined as the time between the infection of a case and the time of infection of its infector [12]. The SI is an important quantity in the interpretation of infectious disease surveillance data, in the identification of outbreaks and in the optimisation of quarantine and contact tracing.

These two quantities have been used to inform control policies during outbreaks [13] by quantifying the transmission of infectious diseases such as influenza A (H1N1) [11, 12, 14], Severe Acute Respiratory Syndrome (SARS) [12, 15] and Ebola [16, 17], where progression to disease upon transmission occurs quickly. For example, Wallinga and Teunis [18] in

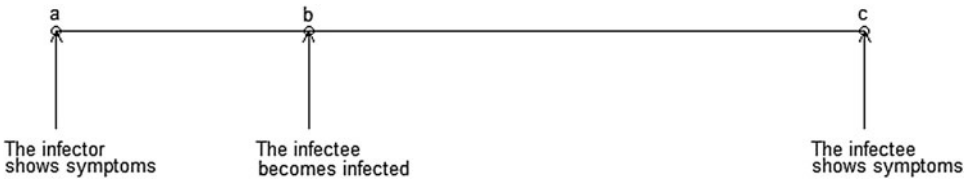

Fig. 1. Important infectious disease intervals. The time between a and c is the serial interval; the time between b and c is the incubation period.

2004 demonstrated the impact of the first global alert against SARS on the change of the effective reproductive number.

TB has a slower transmission rate due to its much longer incubation period. Of the 5–10% of infections that develop into active (symptomatic and infectious) TB disease, it is thought that the majority occur within the first 2 years after infection [2, 5, 19], although active TB disease can develop decades after initial infection [20]. This is much longer than the aforementioned infectious diseases where cases show symptoms within days of infection. Although there is an increasing consensus that some transmission events may occur before the infector shows symptoms, many likely occur after the infector is symptomatic, therefore, the longer the incubation period is, the longer the SI (Fig. 1).

Development of TB disease can be caused by *de novo* infection, reactivation of the same bacterial strain as a previous infection [5, 21] or by infection with a bacterial strain different from the original infection (reinfection TB). This complicates estimation of the serial interval, unless molecular techniques are used to distinguish reinfection and reactivation [21]. To our knowledge, there has been no systematic review of methods to estimate the serial interval and reproductive number for TB. Therefore, in this paper we systematically review the literature to examine the methods applied to the estimation of TB transmission parameters and the estimates obtained from these methods. This compilation informs the gaps in our understanding of TB and identifies areas where further research is needed to develop methods to better understand TB transmission.

Methods

We conducted two searches in PubMed for publications in English – one for TB and serial interval; one for TB and reproductive number.

Tuberculosis and serial interval

('Tuberculosis'[MeSH] OR '*Mycobacterium tuberculosis*'[MeSH] OR 'tuberculosis'[TI]) and ('serial interval'[tiab] or 'generation interval'[tiab] or 'serial distribution' [tiab] or 'secondary infections' [tiab] or 'secondary cases' [tiab]).

TB and reproductive number

('Tuberculosis'[MeSH] OR '*Mycobacterium tuberculosis*'[MeSH] OR 'tuberculosis'[TI] OR 'pulmonary, tuberculosis [MeSH]') and ('reproductive number'[tiab] or 'reproduction number'[tiab] or 'reproductive rate'[tiab] or 'reproduction rate'[tiab] or 'reproduction ratio'[tiab] or 'reproductive ratio'[tiab] or 'reproduction value'[tiab] or 'reproductive value'[tiab] or 'R_0'[tiab] or 'secondary infections'[tiab] or 'secondary cases'[tiab]).

Titles and abstracts of the publications referenced in the articles we found were reviewed for inclusion for either parameter. For the SI, as limited number of publications met our inclusion criteria, we also reviewed the titles and abstracts of publications that cited the serial interval articles that we included in a full-text review.

Two reviewers (two of YM, HEJ, LFW) independently screened all titles and abstracts, resolving discrepancies by consensus. Each publication was then independently reviewed by two reviewers (two of YM, HEJ, LFW) for inclusion. From the included articles, the same pairs of reviewers extracted the following details for all parameter estimates (if available): point estimates, confidence intervals, ranges, sample size and location/setting. We summarised the methods for analysis and aggregated those with similar estimation approaches.

Results

Serial interval

The serial interval query returned 171 articles (Fig. 2), of which 163 were excluded as they did not present any estimates. Leung *et al.* [22] reported the serial interval as the time from identification of primary case to secondary case as median 1.4 years (range: 0.4–5.2 years). This study used household transmission data from Hong Kong and focused on MDR- and XDR-TB. Vynnycky and Fine [23] analysed a population of white males in England and Wales in the 20th century using a mathematical compartmental model to estimate the SI as dependent on the age when infection occurred, distinguishing reinfection and reactivation in the model. In this model, the risk of developing disease was calibrated on incidence data. The estimates were presented as a frequency distribution. The most frequent time to develop disease was estimated at: between 20 and 30 years due to reinfection for those infected in the first year of life; between 10 and 14 years due to reinfection for those infected at age 10; <5 years due to recent infection for those infected at age 20 and those infected at age 40. ten Asbroek *et al.* [24] analysed genetic data for a Dutch sample from 1993 to 1996 to link infectors and infected people using DNA fingerprinting based on restriction fragment length polymorphism (RFLP) and estimated the serial interval at a geometric mean of 0.57 years (95% confidence interval (CI) 0.44–0.73). In this 4-year study, the probability of observing both the infector and the infected person depended on the time interval between isolates – the shorter this time interval was, the more likely that this couple was observed. Therefore, the observed serial intervals were weighted by the inverse of the difference between the length of the study period and the time between isolates of the infector and the infected person, allowing a rough correction for underrepresentation of longer SIs (Table 1).

Two articles that cited the articles that met our inclusion criteria in the PubMed search reported estimates of the SI and were included for full-text review. Borgdorff *et al.* [25] used the same method on genetic data as [24] to estimate the median SI

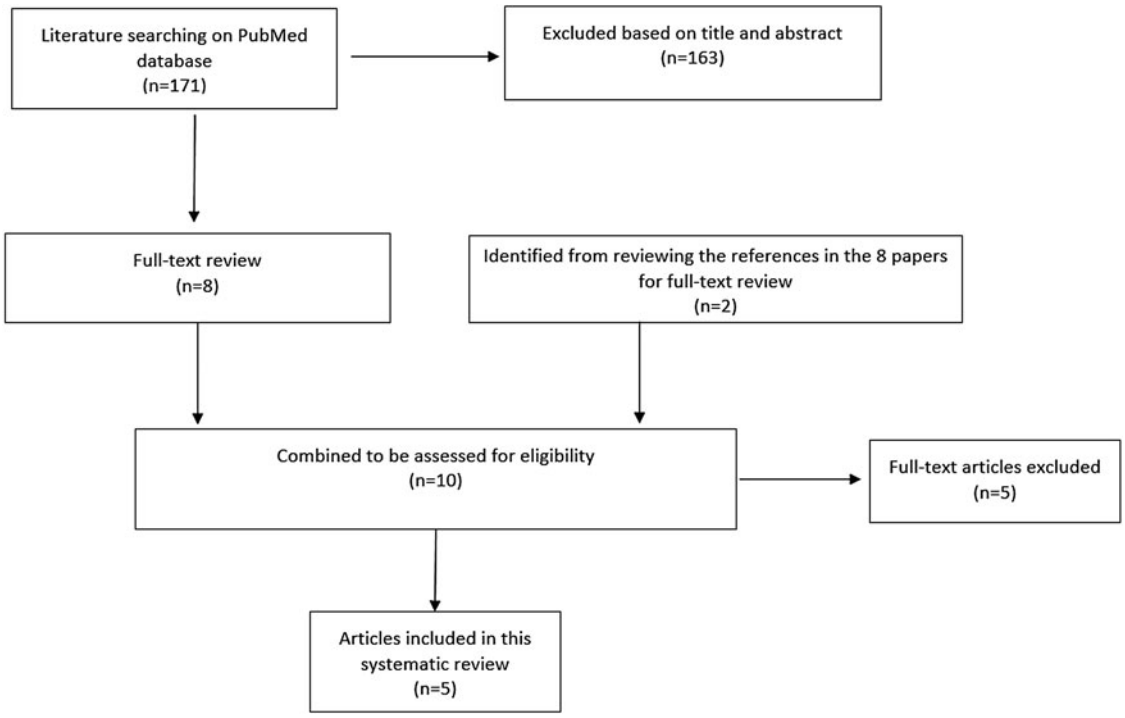

Fig. 2. Flow diagram of articles included in the search of estimates of the serial interval.

Table 1. Estimates of the Serial Interval

Name of first author [publication]	Objective	Method	Assumptions	Estimated serial interval
Leung [22]	Study household transmission of MDR-TB	Data on all MDR-TB in Hong Kong 1997–2006. Did contact investigations and DNA fingerprinting and linked index to secondary cases	No censoring in this estimate, not clear how long people were followed up for	1.4 (0.4–5.2) years (median)
Vynnycky [23]	Demonstrate how the lifetime risk of disease, the incubation period and the serial interval changed	An age-dependent compartmental model	Assumed values for model input parameters such as the annual risk of infection	Estimated as dependent on age of infection and summarised as frequency distributions
ten Asbroek [24]	To determine the serial interval and incubation period of tuberculosis within 4 years of transmission	Descriptive approach on RFLP data (used to link infectors and infected people)	One source of infection for each infected cluster	0.57 years (95% CI 0.44–0.73)
Borgdorff [25]	Same as [24]	Same as [24]	NA	Median: 1.44 years (95% CI 1.29–1.63)
Brooks-Pollock [26]	Estimate the relative contributions of household and community transmission, the serial interval and the immunity afforded by a previous TB infection	Descriptive approach for the serial interval	All members of the study cohort have been exposed to TB by living with someone with active disease	Mean serial interval: 3.5 years; median serial interval 1.65 years

as 1.44 years (95% CI 1.29–1.63 years) for a Dutch sample from 1993–2007. Brooks-Pollock [26] in 2011 analysed cross-sectional household data for a sample in Lima, Peru from 1996 to 2002 and reported the time between the diagnosis of the infector and the infected person as an estimate for the SI with mean at 3.5 years and the median at 1.65 years.

Reproductive number

Two hundred and thirty-seven articles were identified for the reproductive number of TB. Additionally, six articles were included based on reviewing titles and abstracts of the articles that were referenced in the 237 articles, making the total number

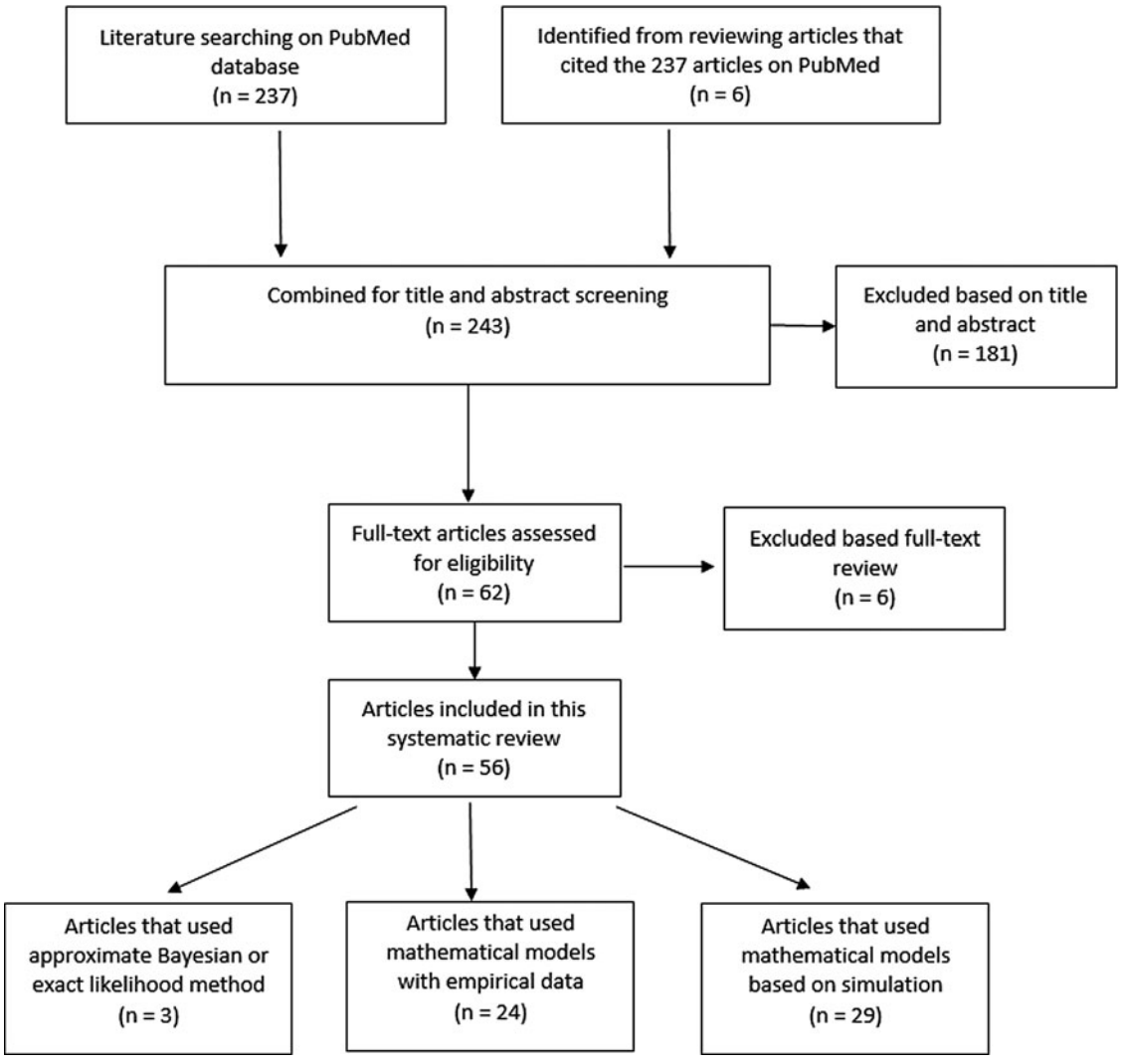

Fig. 3. Flow diagram of articles included in the search of estimates of the reproductive number.

of articles 243. Fifty-six articles met our inclusion criteria and are described below. Three articles used either approximate Bayesian or exact likelihood methods, 24 articles used either a mathematical model fit with empirical data or a descriptive/regression approach on empirical data, and 29 articles used a simulation-based mathematical model (Fig. 3). Explicit estimates were extracted and summarised in Fig. 4. The estimates range from as low as 0.26 for the Netherlands in 1993–2007 to as high as 4.3 in China in 2012.

Three articles (Table 2) used the same genetic RFLP data from TB diseased individuals during an outbreak in San Francisco in 1991–1992 [33]. They all estimated the effective reproductive number in a Bayesian framework. Tanaka *et al.* [30] used an approximated computation method to obtain an estimate of 3.4 (95% CI 1.4–79.7). Stadler [31] in 2013 used an exact likelihood method to obtain an estimate of 1.02 (95% CI 1.01–1.04) and claimed that the difference from the estimate in [30] was due to the lack of precision in the approximation of the posterior distribution in [30]. Aandahl *et al.* [32] in 2014 reconciled the two methods by specifying an informative prior for two parameters in [30] and improving the convergence performance of the Markov chain Monte Carlo (MCMC) sampler in [31]. The reconciled estimates were: 2.1 (95% CI 1.54–2.66) for the approximate method in [30] and 2.05 (95% CI 1.55–2.63) for the exact method in [31]. These papers used the same model but differed in the methods used to obtain the estimates. The assumptions of the model are listed in Table 2.

Twenty-four articles analysed the reproductive number with empirical data (Table 3). Seventeen articles reported explicit estimates, with five estimating the effective reproductive number and 12 estimating the basic reproductive number. The majority of these articles used mathematical compartmental models with different variations in structure and parameterisation to address issues such as seasonality [43], the effect of age [46, 51] and HIV–TB co-epidemics [9].

Two articles [7, 40] used the Wells–Riley model or a modified version of the model. In these models, the reproductive number was expressed as a function of infection risk, which was further expressed as proportionate to environmental factors such as the number of infectious people in a given space, per-person breathing rate and inversely proportionate to germ-free ventilation rate. One article derived the reproductive number as a function of the transmission index – defined as the ratio of the number of secondary cases to the sum of the number of source cases (infectors)

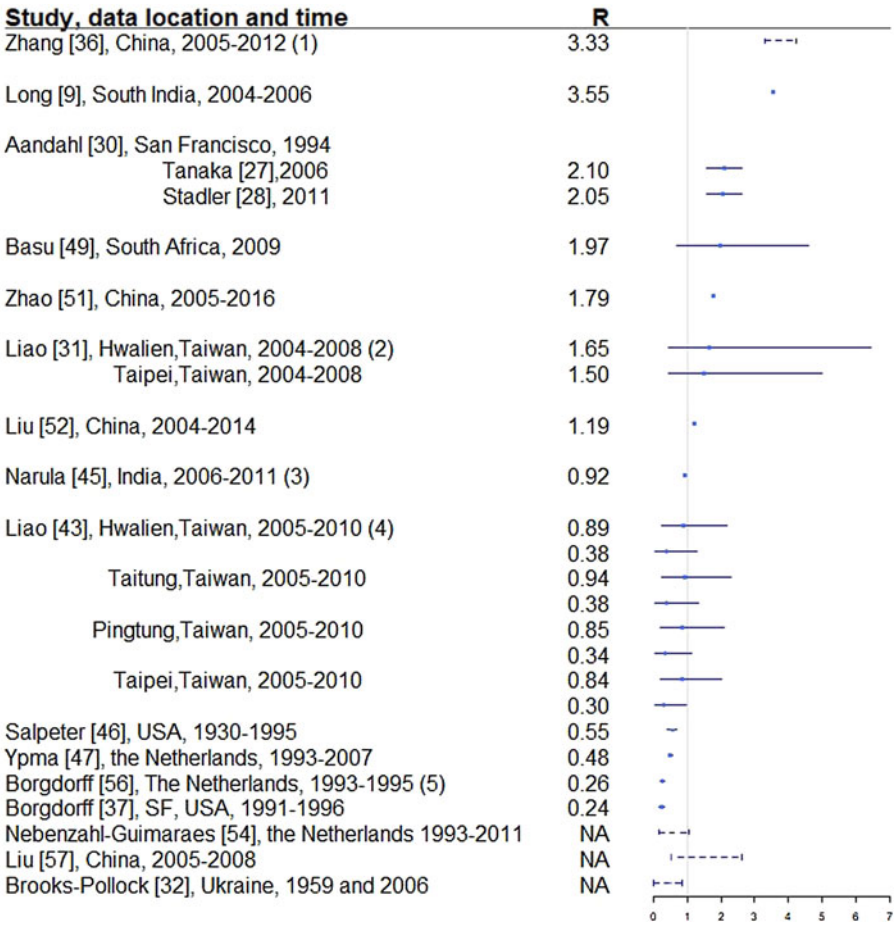

Fig. 4. Reproductive number from studies with explicit *R* estimate from empirical data. Notes: (1) The range is for years 2005-2012, with the reproductive number estimated at 3.33, 3.72, 3.38, 3.97, 4.29, 3.32, 3.92 and 4.30, respectively. (2) For each location, the first *R* corresponds to drug-sensitive population and the second correspond to drug-resistant population. (3) *R* estimated for 35 states and union territories of India with estimates ranging from 0.72 to 0.98; 0.92 is the overall estimate for India. (4) For each location, the first R corresponds to drug-sensitive population and the second correspond to drug-resistant population. (5) Bordgorff in [27–29] estimated the reproductive number for the Netherlands from 1993 to 2007 at around 0.26 with lower bound of the 95% CI around 0.20 and upper bound around 0.32. (6) Broken lines indicate range; solid lines indicate 95% confidence interval. (7) Vynnycky and Fine [23] in 1998 estimated the basic reproductive number to decline from about 3 in 1900 to 2 in 1950 and to below 1 in about 1960 for England and Wales, which is not included in this graph.

and non-clustered cases where clusters are defined as groups of patients that had isolates with identical fingerprints [27]. The largest reproductive number (effective) was estimated in [38] using the Chinese Centre for Disease Control and Prevention (CDC) data from 2005 to 2012, where the annual reproductive number ranged between 3.33 and 4.30 for years 2005–2012 in China. The lowest (effective) reproductive number was estimated at 0.24 (95% CI 0.17–0.31) using RFLP data in San Francisco, USA from 1991 to 1996 [49]. Vynnycky and Fine [51] in 1998 used an age-structured mathematical model and estimated the effective reproductive number to be around 1 from 1900 to 1950 in England and Wales; the basic reproductive number was estimated to have declined from about 3 in 1900 to 2 by 1950, and first fell below 1 in about 1960. The assumptions of these models are listed in Table 3.

One article defined the reproductive number as the number of secondary infections caused by an infectious case [7]. As only a fraction of the infected people develops active disease, the estimated reproductive number was larger than those in the other papers. The median of the reproductive number in this article ranged from 14 to 45 as exposure time increased from 1 to 5 months.

Twenty-nine articles analysed the reproductive number through simulation based on a mathematical modelling framework (Table 4). These articles all used mathematical compartmental models with different variations to address issues such as reinfection [68], the interaction between HIV and TB [64], and drug-resistant and drug-sensitive TB [60]. The majority of them focused on studying the effect of these issues on TB transmission dynamics through simulations that were not based on a specific population. In this case, parameters for the model were based on estimates from studies performed in diverse settings or sampled over a range of feasible values. The analytical expression of the basic reproductive number was derived to study the disease-free equilibrium and endemic-persistent state of TB in these papers. Five articles [10, 60, 64, 73, 76] included drug-resistant TB cases as a compartment and four articles [58, 68, 72, 75] included HIV + TB cases as a compartment.

Discussion

We found very few publications that reported estimates for the serial interval of TB. Estimates of the reproductive number were limited to seven countries, with the majority of the publications using mathematical compartmental models that did not base estimates on actual data. This indicates a need for a better understanding of these crucial parameters of TB transmission, which can help inform public health decisions in order to reach the WHO's End TB goals [4] of reducing TB deaths by 95% and incident cases by 90% by 2035.

Serial interval

We found only five articles that discussed the estimation of the SI for TB and presented explicit estimates. ten Asbroek [24] estimated the serial interval over 4 years as a geometric mean of

Table 2. Estimates of the reproduction number using approximate Bayesian computation and exact likelihood methods (all methods used data from San Francisco on cases reported in 1994)

Name of first author [publication]	Objective	Method	Assumptions	Estimated reproductive number (95% credible interval)
Tanaka [30]	Estimate TB transmission parameters: net transmission rate, doubling time and reproductive number	Approximate Bayesian computation	Constant supply of susceptible people; all genotypes are selectively neutral; mutation and transmission are independent; infinite alleles; epidemic spreads until *N* individuals are infected	3.4 (1.4–79.7)
Stadler [31]	Estimate TB transmission parameters: net transmission rate and reproductive number	Exact likelihood	Constant birth-death rate; infinite alleles; epidemic started at a random time in the past; an isolate is sampled from an individual with probability *P*	1.02 (1.01–1.04)
Aandahl [32]	Reconcile the different estimates in [30, 31]	Improved the method in [30] by specifying informative priors; improved convergence performance of the MCMC sampler in [31]	Fixed mutation rate; used Gaussian prior for the death/recovery rate	1) 2.1 (1.54–2.66) in [30] 2) 2.05 (1.55–2.63) in [31]

0.57 years (95% CI 0.44–0.73). Using the same method over a longer study period (15 years compared with 4 years in [24]), the estimated median was 1.44 years, which is comparable with the median serial interval of 1.65 years in [26] with a 6-year study period. This indicates that the study period could potentially bias the serial interval estimates, even though the method in [24] corrected for the underrepresentation of longer serial intervals. In contrast with other infectious diseases that progress much faster and have SIs measured in days, the SI of TB can be weeks, years and even decades [23]. This unique feature of TB makes it difficult to obtain an unbiased estimate of the SI as lengthy follow-up is required to observe the long period between presence of symptoms of the infector and the infected person. Additionally, uncertainty regarding the presence and impact of multiple infection events further complicates the observation of this interval. Currently, the most common way of monitoring TB is by looking at annual incidence rates in studies that are often no longer than 5 years [79, 80]. This creates two issues: right censoring as symptoms of the infected people can develop long after the end of studies, and interval censoring as the symptom onset time can fall during long intervals between two observed time points. Another issue is patients' and doctors' delay. Patients may not seek medical assistance immediately after symptoms develop and diagnosis may require lab-processing time which causes delay in establishing the diagnosis [24], creating a left censoring issue. Survival analysis techniques can be considered to address these issues but may need substantial modification. Further ambiguity exists due to the inconsistent availability of genetic typing of strains to link cases, and the further uncertainty about how to best link strains when genetic information is available, as such information may not account for mutation rate, or infection with multiple bacterial strains.

Reproductive number

The majority of the articles used mathematical compartmental models (a brief introduction can be found in the appendix) to describe the transmission dynamics of TB. These models have been widely used to understand the dynamics of infectious diseases including SARS, influenza and TB, and they either use empirical data to estimate the parameters in the model or are based on simulation.

The compartmental models using empirical data are distinguished from simulation-based models in two key ways. First, empirical models use data to estimate some of the model parameters, while others are taken directly from the literature or assumed. Simulation-based models do not use empirical data to parameterise the models. For example, in [42] where empirical data was used, the mortality rate due to drug susceptible TB was estimated from Taiwanese Centre of Disease Control data and the effective contact rate for TB was estimated based on the literature; in [41] where simulation was used, the recruitment rate was taken from the literature and awareness rate of TB was estimated from data.

A second distinction between models based on empirical data and simulation-based models is that the former often report explicit estimates of the reproductive number for a specific region, while the latter usually focus on studying the impact of a certain feature on TB transmission dynamics. For example, in [37] where empirical data were used, the reproductive number was reported for India overall and by regions; in [60] where a simulation-based approach was used, the impact of drug-sensitive and drug-susceptible strains mixed together on TB transmission dynamics was studied.

In developed countries, the reproductive number was sometimes estimated to be well below 1: for example, 0.55 in the USA from 1930 to 1995 [52] and 0.26 in the Netherlands from 1993 to 1995 [27]. In developing countries, the reproductive number was as high as 4.3 in China in 2012 [38] and 3.55 in Southern India from 2004 to 2006. In the Netherlands, the reproductive number has been consistently estimated at well below one, ranging from 0.24 [49] to 0.48 [39].

The same dataset in San Francisco, USA in 1991–1992 (published in 1994) was used to estimate the effective reproductive

Table 3. Estimates of the reproductive number from mathematical models with empirical data

Name of first author [publication]	Location, time of data	Type of data	Objective	Methods	Assumptions	Reproductive number type	Estimated reproductive number
Zhao [34]	China, 2005–2016	CDC data	To investigate the impact of age on TB transmission	SEIR model with age structure; use least squares to get parameters that align with TB data in China; use Latin hypercube sampling to get CI	Although the susceptible compartment was stratified by age, the other compartments were not age-stratified thus assuming no difference in age for those compartments	Basic	1.786 (95% CI 1.775–1.796)
Liu [35]	China, 2004–2014	Annual TB case data	To use modelling to investigate the impact of different vaccination strategies (constant or pulse BCG) on TB transmission	Compartmental models with vaccination compartments	Assumptions made for all parameter values	Basic	1.19
Yang [36]	Shaanxi, China, 2004–2012	Notifiable active TB cases by month	Study the seasonality impact on TB transmission dynamics	A seasonality TB compartmental model: subjects either entered latent or diseased compartment; contact rate, reactivation rate and disease-induced death rate are periodic continuous functions	Parameter values for recruitment rate, natural death rate, recovery rate	Basic	Dependent on parameter values
Nebenzahl-Guimaraes [28]	The Netherlands, 1993–2011	Surveillance and RFLP data	Determine if mycobacterial lineages affect infection risk, clustering and disease progression among *Mycobacterium tuberculosis* cases	Descriptive and regression approach; DNA fingerprinting to link cases	All secondary cases captured in surveillance data; genetic matching accurately reflects transmission patterns	Effective	Range: 0.17–1.04
Narula [37]	India, 2006–2011	Quarterly reported data from Central TB Division	Estimate basic R_0 for TB	Compartmental model with Bayesian melding technique to estimate parameters; Susceptible, latent, infected compartments instead of SIR	Some parameter values assumed with reference in the differential equations	Basic	0.92, averaged for India overall with range 0.72–0.98
Zhang [38]	China, 2005–2012	Monthly case reporting data from CDC	Estimate effective R_0 of TB by year	Compartmental model adding hospitalised compartment; Chi-square test for optimal parameters	An upper bound for number of initially susceptible people, natural death rate, initial number of latent individuals	Effective	Range from 3.318 to 4.302 from year 2005 to 2012

Ypma [39]	The Netherlands, 1993–2007	RFLP data	Explore the high heterogeneity in the number of secondary cases caused per infectious individual for TB	Model 'superspreading' parameter as a negative binomial distribution	Immigrants who have been in the country for less than 6 months at diagnosis are index cases themselves	Fingerprint reproductive number as a function of the effective reproductive number and the probability that the fingerprint of the infected person is different than its infector	0.48 (95% CI 0.44–0.59)
Andrews [40]	Cape Town, South Africa, 2011	Carbon dioxide data, public transit usage data from national survey	Estimate risk of TB transmission on 3 modes of public transit	Modified Wells-Riley model for airborne disease transmission	Duration of infectiousness of 1 year; used TB and HIV parameters from studies in the same area; natural history parameters from the literature	Basic	Dependent on duration of infectiousness and frequency of transit usage
Okuonghae [41]	Benin city, Nigeria, 2008	Survey data	Assess how control strategies on addressing TB transmission parameters can minimise incidence	Compartmental model adding compartments of disease awareness level, identified infectiousness	Model parameter values such as recruitment rate, recovery rate from the literature	Basic, under treatment	Dependent on parameter values
Liao [42]	Taiwan, 2005–2010	Monthly data from CDC	Estimate MDR-TB infection risk	Mathematical probabilistic two-strain model with compartments for drug-sensitive and drug-resistant subjects; dose–response model for relationship between R_0 and total proportion of infected population	Some model parameter values from data, some from the literature; assumed 0.99 of people latently infected were drug sensitive and 0.01 were drug resistant	Basic	**Hwalien County**: 0.89 (95% CI 0.23–2.17) for drug sensitive; 0.38 (95% CI 0.05–1.30) for multi-drug resistant; **Taitung County**: 0.94 (95% CI 0.24–2.28) for drug sensitive; 0.38 (95% CI 0.05–1.33) for multi-drug resistant; **Pingtung County**: 0.85 (95% CI 0.21–2.08) for drug sensitive; 0.34 (95% CI 0.04–1.13) for multi-drug resistant; **Taipei City**: 0.84 (95% CI 0.21–2.00) for drug sensitive; 0.30 (95% CI 0.04–0.97) for multi-drug resistant;

(*Continued*)

Table 3. (*Continued.*)

Name of first author [publication]	Location, time of data	Type of data	Objective	Methods	Assumptions	Reproductive number type	Estimated reproductive number
Liao [43]	Taiwan, 2004–2008; selected three areas with the highest incidence, one with the lowest incidence	Monthly disease burden TB data from Taiwan CDC	Examine TB population dynamics and assess potential infection risk	Compartmental model with susceptible, latently infected, infectious, non-infectious and recovered compartments; incorporated reactivation, relapse and reinfection	Some parameter values taken from the literature, some estimated from data	Basic, estimated as sum of fast, slow and relapse	Highest R_0 total in Hwalien: 1.65 with 95th percentile range 0.45–6.45; Taipei lowest at 1.5 (0.45–4.98); Taitung: 1.72; Pingtung: 1.65
Liu [44]	China, 2000–2008	Data from the National Bureau of Statistics	Incorporate migration to study TB transmission	SEIR compartments for rural residents, migrant workers and urban population	Model parameters calculated from website data; migration rates	Basic	No explicit estimate
Borgdorff [29]	The Netherlands, 1993–2007	RFLP data	Determine to what extent tuberculosis trends in the Netherlands depend on secular trend, immigration and recent transmission	DNA fingerprinting to link cases	All secondary cases captured in surveillance data; genetic matching accurately reflects transmission patterns	Basic	0.24 (95% CI 0.21–0.26)
Liu [45]	China, Jan, 2005–Dec, 2008	Monthly notification data from Ministry of Health	Develop a model incorporating seasonality and define basic reproduction ratio	Used periodic infection rate and reactivation rate to incorporate seasonality in the compartmental model; considered fast and slow progression	Parameters such as recruitment rate, natural death rate were assumed to be constants; some parameter values assumed and some taken from the literature	Basic	Dependent on parameter values with range 0.4–2.6
Brooks-Pollock [46]	Ukraine, 1959 and 2006	Mortality data	Explore the effect of age structure on TB infection and disease prevalence, basic reproductive number and impact of intervention	Basic SEIR mathematical model with assumptions about survivorship	A survivorship function which could be described in terms of age and life expectancy	Basic	Dependent on progression rate with range 0–0.85
Basu [47]	KwaZulu-Natal, South Africa	Extensively drug-resistant TB data (XDR-TB)	Model XDR-TB transmission dynamics	Model XDR-TB incorporating the existing XDR detection rate and treatment system	Even mixing of air; range of key parameters in the model	Effective	1.97, range 0.7–4.6; 1.23, range 0.4–3.1 when combining screening and therapy; 1.38, range 0.6–3.3 with South African strategic plan alone.

Furuya [7]	Japan, 2000–2005	Exposure data	Quantify the risk of TB infection in an internet café where people without homes stayed overnight	Wells-Riley model to estimate the reproductive number	Patients stayed in a confined space for 150 days; some values in the Wells-Riley equation assumed, others from the literature	Estimated as a function of exposure period	Dependent on exposure period
Long [9]	Southern India, 2004–2006	HIV-TB co-epidemics data	Model HIV-TB co-epidemics and explore hypothetical treatment effect	First model: susceptibility to either or both diseases compartments; second model: SII*SEI	A linear relationship between treatment levels and the associated parameters; model parameters from the literature	Basic	R = 3.55 when no active treatment for TB
Borgdorff [48]	The Netherlands, 1995–2002	RFLP data	Assess progress towards TB elimination	DNA fingerprinting to link cases; survival analysis	All secondary cases captured in surveillance data; genetic matching accurately reflects transmission patterns	Basic	Dutch index cases: 0.23, non-Dutch index cases: 0.25
Borgdorff [49]	San Francisco, USA, 1991–1996	RFLP data	Determine tuberculosis transmission dynamics in San Francisco and its association with country of birth and ethnicity	Define effective reproductive number as a function of transmission index, which is a function of number of secondary cases and potential source cases in a given subgroup	Each cluster originates from a single source case in the database; either the first case of a cluster was its source case, or that the probability of being a source case declined exponentially over time by 0.77% per day	Effective, recent transmission	0.24 (95% CI 0.17–0.31)
Davidow [50]	New York City, 1989–1993	TB and AIDS surveillance data	Evaluate the importance of recent M. tuberculosis transmission	Estimated # of TB infectious cases 1 year ago and computed short-term R_0; R_0 = the average # of new infections caused by each case per year of infectiousness*the average duration of infectiousness*the probability of progressing to active TB within 1 year after infection	Some clinical assumptions; parameter values in equation taken from the literature or calculated from neighbourhood-specific data	Short-term	No explicit estimates; focused on percentage of TB cases due to infection 1 year ago
Vynnycky [51]	England and Wales, 1900	Surveillance data; age and time-specific mortality rates	Describe transmission dynamics of all forms of pulmonary TB	Age-structured mathematical model with compartments for endogenous and exogenous diseases	General relationship between: first primary episode and age at infection, risk of exogenous disease and age at reinfection, endogenous disease and current age; risk of reinfection and first infection are identical; parameter values from the literature	Basic and net which is the same as effective	Net R at about 1 from 1900–1950; basic R_0 declined from about 3 in 1900, reached 2 by 1950, and first fell below 1 in about 1960

(*Continued*)

Table 3. (*Continued.*)

Name of first author [publication]	Location, time of data	Type of data	Objective	Methods	Assumptions	Reproductive number type	Estimated reproductive number
Salpeter [52]	USA, 1930–1995	Case rates, correction for rates before 1975	Estimate time delay from infection to disease and R	Estimate *R* as a function of case rate and the shape of the delay function	*R* and case rate constant with calendar time t; incidence rate of latent infection is independent of the age	Effective	0.55, range 0.4–0.7 in sensitivity analysis
Borgdorff [27]	Netherlands, 1993–1995	RFLP data	Quantifying transmission of TB between and within nationalities	Effective R_0 estimated as a function of transmission index	Probability of a patient being the source of a cluster was proportional to the incidence rate of potential sources times the probability that a potential source would give rise to a cluster	Effective	0.26, 95% CI (0.20–0.32); also estimated for different nationalities

number in two separate studies [30, 31] that yielded disparate results. The estimates from these two papers were reconciled in [32] to an estimated effective reproductive number of approximately 2.1 by specifying an informative prior for two parameters in [30] and improving the convergence performance of the MCMC sampler in [31]. One can contrast this estimate with other estimates for the USA to see the range of values obtained. A study of the entire USA in [52] estimated the reproductive number to be 0.55 using case rates of active TB in USA from 1955 to 1994. As shown in [81], TB incidence in San Francisco peaked between 1991 and 1993, due to the TB/HIV co-epidemic, which is consistent with the higher estimated reproductive number (around 2.1) in [30–32]. When using TB case rates in the entire USA from 1955 to 1994 as in [52], the potential geographical and temporal heterogeneity in the estimates is not well represented, resulting in an estimated reproductive number of 0.55. We would expect a lower reproductive number, and in particular, a reproductive number below one, when using data from 1955 to 1994 because by 1955, effective antibiotics were in use and BCG had also been developed, both leading to a reduction in TB incidence across the USA. In addition, Borgdorff [49] reported an effective reproductive number of 0.24 using RFLP data in San Francisco from 1991 to 1996. In this paper, the ratio of secondary cases and source cases was used to estimate the reproductive number, which may be an oversimplified estimator of the reproductive number. Issues such as linking the secondary cases and the sources cases have not been addressed. These divergent results indicate the need for the use of whole genome sequencing (WGS), which can be used to effectively link source and secondary cases.

Similar to the more statistical analysis of the San Francisco and the entire USA data, we observe that mathematical models lead to inconsistent results, at least partially attributable to the varying assumptions they make in their structure and parameterisation. For example, even though both [38] and [42] used mathematical compartmental models with different variations for similar regions (China and Taiwan), they have quite different estimates: between 3.3 and 4.3 in China from 2005 to 2012 as compared with 0.9 for drug-sensitive TB, around 0.38 for multidrug-resistant TB (defined as a TB strain resistant to at least isoniazid and rifampicin) in Taiwan from 2005 to 2010. Both articles used incidence data from Chinese and Taiwanese CDC but formulated the compartments in the models differently. In [38], compartments 'exposed', 'infectious and hospitalised' and 'infectious but not hospitalised' were included; in [42], compartments 'latent', 'infected' were used for two sub-populations: drug-sensitive and multidrug-resistant. The model parameters were also differently specified: in [38], some parameters were assumed while others were estimated using minimum sum of square; in [42], some parameters were given a probabilistic distribution and estimated with a root-mean-squared error method while others were assumed. The difference between the estimated reproductive numbers produced from these two modelling exercises is striking, as the two regions and populations are quite comparable in terms of demographics, economic status and access to healthcare. One could similarly contrast the modelling approaches and estimates obtained in [34] and [43], two other studies from China and Taiwan from similar time periods that produced different estimates. The differing model structures, as well as the parameter estimates, including the recruitment rate, incidence rate, and mortality rate, likely drive these observed differences. It is difficult to say which model might be a more accurate reflection of reality.

The example above illustrates the challenges of interpreting and using mathematical models for estimation of the reproductive

Table 4. Estimates of the reproductive number from mathematical models based on simulation

Name of first author [publication]	Objective	Methods, setting	Assumptions	Basic or effective R_0	Estimated R_0
Ren [53]	Develop SEIR model for imperfect treatment with age-dependent latency and relapse	SEIR model	TB infectious in latent period; age-dependence	Basic	Dependent on parameters
Jabbari [54]	To set up a model that can examine two TB strains (DS and DR) with multiple latent stages	Mathematical compartmental model with compartments for latency stages	The drug-sensitive strain will not play a role in the process of exogenous reinfection for the drug-resistant strain	Basic	Dependent on parameters
Okuonghae [55]	Study the effects of additional heterogeneities from the level of TB awareness on TB transmission dynamics and case detection rate	Expanding [34] by dividing both susceptible and latently infected compartment by level of TB awareness	Reasonable values and bounds for parameters such as transmission rate, recovery rate from the literature	Effective	Dependent on parameters such as active case finding rate and treatment rate
Liu [56]	Evaluate effect of treatment for TB	Compartmental model with treatment and two latent periods incorporated	Once the treatment of active TB cases is interrupted, there is no more treatment; specified model parameter values and their relationship with one another	Basic	Dependent on transmission coefficients
Silva [57]	Study optimal strategies for the controlling active TB infectious and persistent latent individuals	Compartmental model considering reinfection and post-exposure interventions with the addition of early latent and persistent latent compartments	Parameter values taken from the literature	Basic	Dependent on transmission coefficient
Hu [58]	Study the threshold dynamics of TB	Compartmental model with periodic functions for reactivation rate and infection rate; include additional compartment for treated people that do not return to the hospital for examination	NA	Basic	Dependent on transmission coefficient
Emvudu [59]	Address the problem of optimal control for TB transmission dynamics	Compartmental model with an additional compartment for loss to follow-up	Half of the parameter values were assumed; others taken from the Cameroon literature	Basic	Dependent on parameters such as transmission rate
Sergeev [60]	How drug-sensitive and drug-resistant strains mixed together can impacts long-term TB dynamics	Compartmental with the three compartments for both latent and infected: drug-resistant, drug-sensitive and mixed strains	Reasonable values for many parameters; few data exist to inform model parameters	Basic; estimated for drug-resistant, drug-sensitive and mixed strains	Dependent on model parameters
Roeger [61]	Model TB and HIV co-infection	Compartmental model for joint dynamics of TB and HIV and compute independent reproductive numbers for the two diseases	Probability of infection is the same for those treated with TB and those susceptible; assumed relationship among model parameters	Overall R_0 as the max of R_0 for TB and HIV	Dependent on model parameters
Gerberry [62]	Study the trade-off between BCG and	Compartmental model with additional compartments for latently	Throughout the duration of the vaccine's efficacy,	Basic	Dependent on model parameters

(*Continued*)

Table 4. (*Continued.*)

Name of first author [publication]	Objective	Methods, setting	Assumptions	Basic or effective R_0	Estimated R_0
	detection, treatment of TB	infected and unvaccinated, latently infected and vaccinated; establish thresholds for basic R_0	latent TB completely undetectable		
Bhunu [63]	Model HIV/AIDS and TB coinfection	Compartmental model for TB, HIV separately without intervention; full model with intervention	Parameter values from Central Statistics Office of Zimbabwe and literature; relationship amongst parameters in the model	Basic	Dependent on model parameters
Bhunu [8]	Model the effect of pre-exposure and post-exposure vaccines	Compartmental model with additional compartments for susceptible (vaccinated or not) and latent (history of vaccine or not)	Homogeneous mixing; recovered people would not develop disease from reinfection, but could be re-infected; parameter values taken from Central Statistics Office and literature	Basic	Dependent on model parameters
Sharomi [64]	Address the interaction between HIV and TB	TB-only, HIV-only and full model analysed with both susceptible and latent compartments divided according to TB and HIV status	Dually infected people could not transmit both diseases; some parameters taken from the literature, others assumed	Basic	Dependent on model parameters
McCluskey [65]	Address global stability of high dimensional TB model	Use Lyapunov function to demonstrate the stability of the endemic equilibria in mathematical models for TB: SEIR, SEIS and SIR; fast and slow progression incorporated		Basic	No explicit estimate
Martcheva [66]	Address the issue of an infected person being subject to further contacts with infectious individuals—'super infection'	Subdivide the latent stage into one where the disease progresses and one where the disease development is on hold	Relationship among model parameters	Basic	No explicit estimate
Aparicio [67]	Express basic R0 as a function of cluster size	Divide individuals into either active clusters or otherwise	Homogeneous mixing	Basic	No explicit estimate; expressed as a function of household size
Feng [68]	Examine how exogenous reinfection changes the TB transmission dynamics	Include additional parameters in the mathematical model to model exogenous reinfection	Constant per capita removal rate to focus on the role of reinfection	Basic	No explicit estimate; analytical expression
Beatriz [69]	Assess the effects of heterogeneous infectivity	Divide infective period into k stages	Homogenous mixing; bilinear incidence rate	Basic	No explicit estimate; analytical expression
Castillo-Chavez [70]	Use an age-structure model to study the dynamics of TB	Use age-specific parameters in the compartmental model; transmission dynamics studied for with and without vaccine	Mixing between individuals is proportional to their age-dependent activity level; disease-induced death rate neglected	Net and basic	No explicit estimate; analytical expression
Lietman [71]	Test the hypothesis that exposure to TB		Cross-immunity is symmetric: same	Basic	

(*Continued*)

Table 4. (*Continued.*)

Name of first author [publication]	Objective	Methods, setting	Assumptions	Basic or effective R_0	Estimated R_0
	leads to disappearance of leprosy	Add in leprosy compartment in the mathematical model	immunity for TB and leprosy		Dependent on R_0 of leprosy and cross-protection rate
Sanchez [72]	Evaluate the effects of parameter estimation uncertainty on the value of R_0	Latin hypercube sampling used on parameters in the compartmental model in Blower [72] to evaluate uncertainty of R_0	Range for parameters in the compartmental model	Sum of R_0 for fast, slow and relapse	Dependent on parameters in the model
Gumel [10]	Study the transmission dynamics of TB with multiple strains, in the presence of exogenous reinfection	Included drug-sensitive and resistant strains in the compartmental model; exogenous reinfection incorporated	Homogenous mixing	Effective R_0 for the two strains	Dependent on parameters in the model
Singer [73]	Study the impact of different reinfection levels of latently infected individuals on TB transmission dynamics	Compartmental model for heterogeneous population: one group more susceptible to infection than the other	Parameter range uniformly distributed according to previous papers	Basic	No explicit estimate
Trauer [74]	Model TB transmission for highly endemic regions of the Asia-Pacific where HIV-coinfection is low	Compartmental models with compartments for immunisation, latency, reinfection, drug-resistance, etc.	Parameters fixed values according to papers and WHO	Basic	Dependent on parameters; computed as 8.34 for drug-susceptible and 5.84 for drug resistant at baseline
Dye [75]	To establish criteria for MDR-TB control	Compartmental models with compartments for drug-susceptible, drug-resistant, treatment failure, etc.	Parameters calculated from different populations	Basic	Dependent on parameters; best estimated of the model parameters yielded $R_0 = 1.6$ (95% CI 1.02–2.67)
Blower [76]	Track the emergence and evolution of multiple strains of drug-resistant TB	Non-compartmental mathematical model	NA	Basic	Dependent on drug susceptibility of TB
Blower [77]	Model the transmission dynamics of TB	Compartmental models with latently infected, infectious, non-infectious, recovered compartments	Some model parameters assumed; some taken from references	Basic; defined as the sum of slow progression, recent transmission and relapse	Median of 4.47, range: 0.74–18.58
Blower [78]	Understand, predict and control TB	Compartmental models with drug-sensitive and drug-resistant compartments	NA	Basic	Dependent on model parameters
Aparicio [67]	Evaluate homogeneous mixing and heterogeneous mixing models for TB	Three types of compartmental models: a standard incidence homogenous mixing mode; a heterogeneous mixing model; an age-structured model	Assumptions on model parameters	Basic	Dependent on model parameters

number. However, most estimates to date make use of this approach. One shortcoming of these models is that they require assumptions about parameter values that may be difficult to estimate, such as the transmission rate, the treatment rate and the recovery rate, which are often unobservable and not reliably estimated. As a result, most of the articles assume values for the parameters in the model based on evidence in the published literature, where it exists, sometimes without measures of uncertainty (e.g. standard errors). Model structure also varies substantially from study to study, with no generally agreed upon

Fig. 5. Shaded areas and stars indicate countries and cities with reproductive number estimates. Multiple estimates: China, Taiwan, USA, India; one estimate: Ukraine, the Netherlands, South Africa, the UK. *indicates San Francisco corresponding to data used in [30–32].

approach to model TB and estimate parameters. For example, in [35], compartments of different vaccine strategies were included in the model and in [38], a compartment of hospitalisation was included in the model. These models also often require assumptions about the parameters used to run the models, which are likely to differ by country and time period. Sometimes sufficient data are unavailable to parameterise a model and generalisations need to be made that may not always be appropriate. The majority of the existing publications use mathematical compartmental models, which are not often ideal for statistical inference and estimation due to strong assumptions for the model structure and parameters used to run the models. While these models have the flexibility of using different compartments to evaluate the impact of policies, they are not ideal for real-time analysis where the appropriate model structure and parameter values required fitting the model may not be clear. The complexity of the natural history of TB and important factors such as HIV and drug resistance complicate these models and require additional parameters for which the data are sometimes not available. We believe that it is important to develop, as a complementary approach to compartmental models, likelihood-based data-driven analytic tools. Ideally, these estimators can be used with datasets using minimal assumptions. In addition, as WGS data become more ubiquitous [82], it will be important to develop methods that use these data to estimate the reproductive number (Fig. 5).

This review found that the reproductive number estimates for TB are very divergent – in reality, we would expect different results in different parts of the world, reflecting diversity in TB epidemics geographically. Therefore, it is important to have estimates from a wide range of settings. An ultimate goal of methods to estimate the reproductive number should be to use routinely collected data (including potentially WGS data) to be able to monitor the reproductive number in 'real-time' and evaluate interventions through this process.

Our review is subject to a number of limitations. It is possible that some useful papers could have been excluded due to our selection of search terms and our inclusion of reports in only English. These limitations are difficult to avoid in systematic reviews, in which the potential for increased yield from a wider search must be weighed against the increased feasibility of a tighter search. Additionally, our query was limited to searching in abstracts and titles, making it possible that we excluded articles where the keywords only appear in the text [25].

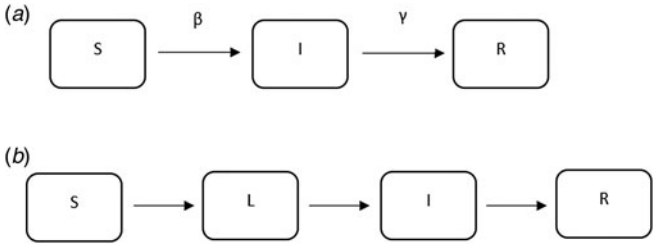

Fig. 6. Examples of mathematical compartmental models.

In conclusion, a limited number of studies have yielded explicit estimates for the serial interval and reproductive number of TB. When estimating the serial interval, it is difficult to observe the symptom onset of the infector and infected person with precision. Estimates of the reproductive number were limited geographically (Fig. 6) with estimates only available for seven countries. Settings with high TB burdens, especially high drug-resistant TB burdens such as the former Soviet Union [83] are not included in these papers. In addition, there was only one estimate from a high TB and high HIV burden country [47]. The lack of estimates could be because incidence and mortality rates are currently used to monitor TB control. These rates are not suitable for monitoring transmission; reductions in mortality could be attributed to improvements in treatment outcomes rather than any change in transmission and, due to the long incubation period of TB, changes in transmission could take years to impact incidence rates. In contrast, the reproductive number can provide a direct estimate of TB transmission

itself. Most studies used mathematical models with various assumed model structures and parameters, making it difficult to compare the estimates and draw useful conclusions about the TB transmission dynamics by evaluating the reproductive number.

The WHO End TB goals [4] include reducing TB deaths by 95% and incident cases by 90% by 2035. To achieve these goals, it is necessary to obtain improved estimates of the reproductive number and the SI as they can be used for monitoring and evaluating the effect of interventions on TB transmission. For example, the serial interval of TB can be used to determine how long one must monitor contacts of an infectious TB case to see if they will develop symptoms [84]. The effective reproductive number can be used to monitor the efficacy of interventions in reducing transmission. As interventions decrease transmission, estimates of the reproductive number should correspondingly decrease [41]; in particular, if the reproductive number can be maintained below one, the disease can potentially be eliminated.

The limited number of articles that we found and the lack of geographic representation, demonstrate a substantial gap in our understanding of these crucial parameters of TB transmission in diverse settings.

Supplementary material. The supplementary material for this article can be found at https://doi.org/10.1017/S0950268818001760

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Conflict of interest. None.

Ethical standards. The authors assert that all procedures contributing to this work comply with the ethical standards of the relevant national and institutional committees on human experimentation and with the Helsinki Declaration of 1975, as revised in 2008.

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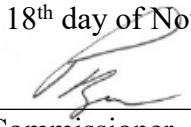
to the Affidavit of Matthew Hodge,
affirmed this 18th day of November, 2022



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BMC Infectious Diseases

RESEARCH ARTICLE Open Access

Serial interval and incubation period of COVID-19: a systematic review and meta-analysis

Muluneh Alene[1], Leltework Yismaw[1], Moges Agazhe Assemie[1], Daniel Bekele Ketema[1], Wodaje Gietaneh[1] and Tilahun Yemanu Birhan[2*]

Abstract

Background: Understanding the epidemiological parameters that determine the transmission dynamics of COVID-19 is essential for public health intervention. Globally, a number of studies were conducted to estimate the average serial interval and incubation period of COVID-19. Combining findings of existing studies that estimate the average serial interval and incubation period of COVID-19 significantly improves the quality of evidence. Hence, this study aimed to determine the overall average serial interval and incubation period of COVID-19.

Methods: We followed the PRISMA checklist to present this study. A comprehensive search strategy was carried out from international electronic databases (Google Scholar, PubMed, Science Direct, Web of Science, CINAHL, and Cochrane Library) by two experienced reviewers (MAA and DBK) authors between the 1st of June and the 31st of July 2020. All observational studies either reporting the serial interval or incubation period in persons diagnosed with COVID-19 were included in this study. Heterogeneity across studies was assessed using the I^2 and Higgins test. The NOS adapted for cross-sectional studies was used to evaluate the quality of studies. A random effect Meta-analysis was employed to determine the pooled estimate with 95% (CI). Microsoft Excel was used for data extraction and R software was used for analysis.

Results: We combined a total of 23 studies to estimate the overall mean serial interval of COVID-19. The mean serial interval of COVID-19 ranged from 4. 2 to 7.5 days. Our meta-analysis showed that the weighted pooled mean serial interval of COVID-19 was 5.2 (95%CI: 4.9–5.5) days. Additionally, to pool the mean incubation period of COVID-19, we included 14 articles. The mean incubation period of COVID-19 also ranged from 4.8 to 9 days. Accordingly, the weighted pooled mean incubation period of COVID-19 was 6.5 (95%CI: 5.9–7.1) days.

Conclusions: This systematic review and meta-analysis showed that the weighted pooled mean serial interval and incubation period of COVID-19 were 5.2, and 6.5 days, respectively. In this study, the average serial interval of COVID-19 is shorter than the average incubation period, which suggests that substantial numbers of COVID-19 cases will be attributed to presymptomatic transmission.

Keywords: COVID-19, Serial interval, Incubation period, Meta-analysis

* Correspondence: yemanu.tilahun@gmail.com
[2]Department of Epidemiology and Biostatistics, Institute of Public Health, College of Medicine and Health Science, University of Gondar, Gondar, Ethiopia
Full list of author information is available at the end of the article

Background

The 2019 Coronavirus Disease (COVID-19) continues to be one of the potential clinical and public health issues in the global population [1]. Globally, from the outbreak of the virus up to August 5, 2020, 18 million total confirmed cases and 700, 000 deaths were reported [2]. Rapid spread of COVID-19 causes an enormous impact on social, economic and health care system in the world [3]. Effective treatment to block the spread of COVID-19 is not developed yet, hence countries implement non-treatment intervention such as social distancing, isolation, face mask and quarantine to reduce its rapid transmission [4, 5].

Existing evidence showed that most of the COVID-19 cases are missed by screening due to they are unaware they were exposed, and not developed symptoms yet [5]. In the absence of strong public health interventions, preliminary estimates showed that the basic reproduction number of Severe Acute Respiratory Syndrome Coronovirus-2 (SARS-CoV-2) ranged from 2.8 to 5.5 [6]. Serial interval and incubation period are the two main epidemiological parameters that determine the transmission dynamics of infectious diseases [7]. Serial interval is defined as the time from illness onset in the primary case to illness onset in the secondary case, while incubation period is the time from infection occurred to the onset of signs and symptoms.

Previous studies reported that the average serial interval of COVID-19 is shorter than the average incubation period, which suggests that a substantial proportion of presymptomatic transmission [8, 9]. This makes it difficult to trace contacts due to the rapid turnover of case generations. An observational study that aimed to provide the epidemiological parameters of COVID-19 using seven countries data revealed that the mean incubation period and serial interval were 7.44 days and 6.70 days, respectively [10]. A study that compares the incubation period of SARS-CoV-2, severe acute respiratory syndrome coronavirus (SARS-CoV), and middle east respiratory syndrome coronavirus (MERS-CoV) reported that no observable difference in the incubation was noted between them [11].

Globally, a number of studies were conducted to estimate the average serial interval and incubation period of COVID-19. However, the reported estimate of serial interval and incubation period in these fragmented studies vary depending on the number of study participants recruited, the type of design employed, the data collection period, and the country in which the study conducted. Combined findings of existing studies significantly strengthen the quality of evidence investigating the average estimate of serial interval and incubation period of COVID-19. Thus, this meta-analysis was aimed to determine the overall pooled mean serial interval and incubation period of COVID-19 using available evidences. The findings of this study are intended to improve policies and strategies for better prevention and control of COVID-19.

Methods

Source of information

We identified relevant studies through searching electronic databases and gray literatures. Additionally, we were searched from the reference lists of all the included studies to identify any other studies that may have been missed by our search strategy.

Searching for studies

We followed the preferred reporting items for systematic review and meta-analysis (PRISMA) checklist for this study [12]. A comprehensive search strategy was performed from international electronic databases (Google Scholar, PubMed, Science Direct, Web of Science, CINA HL, and Cochrane Library) by two experienced review (MAA and DBK) authors between 1st of June and the 31st of July 2020. The following searching terms are used from the above databases: “serial interval” OR “generation time” AND “incubation period” OR “infectious period” AND “COVID-19” OR “SARS-CoV-2” OR “novel coronavirus”.

Inclusion criteria

Design

All observational studies either reporting the serial interval or incubation period of COVID-19.

Study setting

Worldwide.

Population

All age group.

Publication status

All published and unpublished articles.

Language

Only studies reporting using the English language.

Publication date

Published from the 1st of January 2020 to the 30th of June, 2020.

Exclusion criteria

Articles that were not fully accessed after at least two email contacts of the principal investigator were excluded. In addition, we excluded case reports, letters, and review articles.

Study selection

The eligibility assessment was undertaken by two (WG and TYB) authors, independently. The disagreement between two reviewers were fixed by consensus.

Outcome measures and data extraction

This study has two outcome variables. The first is the average estimate of serial interval. The serial interval is defined as the time from illness onset in the primary case to illness onset in the secondary case. It also measured from pairs of cases with a clear infector–infectee relationship. The second outcome variable is the average estimate of the incubation period. Incubation period is defined as the time from infection occurred to the onset of signs and symptoms. It was measured with cases of a well-defined period of exposure and symptom onset. Screening of studies and all essential data from the included studies were extracted independently by two (MA and LY) of the authors. This form includes the last name of the first author, country, data collection period, sample size, average estimate, standard deviation, and 95% confidence intervals. The same data extraction form was used for both outcomes. Discrepancies between the two reviewers was resolved by consensus involving all authors.

Assessing the risk of bias

Two experienced reviewers (MA and DBK) were assessed the risk of bias of the included articles. The Newcastle-Ottawa Scale (NOS) adapted for cross-sectional studies was used to evaluate the quality of studies [13]. This tool includes three categories with a maximum score of 9 points. The first is the "selection" category, which accounts for a maximum of 4 points, the second is the "Comparability" category, which accounts for a maximum of 2 points, and the third is "outcome" which accounts a maximum of 3 points. Based on the composite score from this three categories, the studies were classified as good quality if the score ≥ 6 points, fair quality 2 to 5 points inclusively and poor quality ≤1 point.

Data processing and analysis

A meta-analysis of continuous outcomes was employed for this study. We analyzed the data sets for each outcome variable (serial interval and incubation period). After extracting all essential data using Microsoft Excel, data were exported to R 4.0.2 statistical software for meta-analysis. In order to pool the results of included studies in a consistent format, we estimated the sample mean and standard deviation for studies that report median and interquartile range [14]. To determine the extent of variation between the studies, we did a heterogeneity test using the Higgins method, that was quantified by I^2 value [15]. Weighted average using the inverse variance method was used to estimate the pooled average. A random-effect meta-analysis with an estimation of DerSimonian and Laird method was performed. The publication bias was also assessed using a funnel plot and Egger's tests [16]. The pooled average estimates with 95%CI confidence interval was presented using forest plots.

Results

Search results

Figure 1 indicates the overall flow of study selection, literature search and number of the included studies. During electronic literature search 14,247 articles were identified and 14, 140 duplicated articles were removed. After meticulous review of the whole articles, 28 studies that fulfill the suitability standards were included. From the included studies, a single study might report both outcomes (serial interval and incubation period). Accordingly, a total of 23 and 14 studies were combined to estimate the mean serial interval, and incubation period of COVID-19, respectively.

Description of the included studies

All the included studies are cross-sectional, and half of them were preprints. Majority of studies included in this study are conducted in China. We included a total of 23 articles to pool the mean of serial interval of COVID-19. The minimum and maximum pairs of COVID-19 patients among the included studies were 6 [17] and 1407 [18], respectively. Among the included studies, the mean serial interval of COVID-19 was ranged from 4. 2 days [19] to 7.5 days [17] (Table 1).

Similarly, to pool the mean incubation period of COVID-19, a total of 14 articles were included. Among those, the minimum sample size was 10 [17] and the maximum was 183 [20]. The mean incubation period of COVID-19 ranged from 4.8 days [20] to 9 days [19] (Table 2).

Pooled average estimate of serial interval and incubation period

In this study, a total of 3924 pairs of COVID-19 patients were included to pool the mean serial interval. Accordingly, the weighted overall mean serial interval of COVID-19 was 5.2 (95%CI: 4.9–5.5) days (Fig. 2). Likewise, a total of 1, 453 COVID-19 patients were included to pool the overall incubation period of COVID-19. Consequently, the weighted pooled mean incubation period of COVID-19 was 6.5 (95%CI: 5.9–7.1) days (Fig. 3).

Of the included studies to pool the mean serial interval of COVID-19, our summary quality assessment showed that nearly three-fourth (73.9%) of the studies

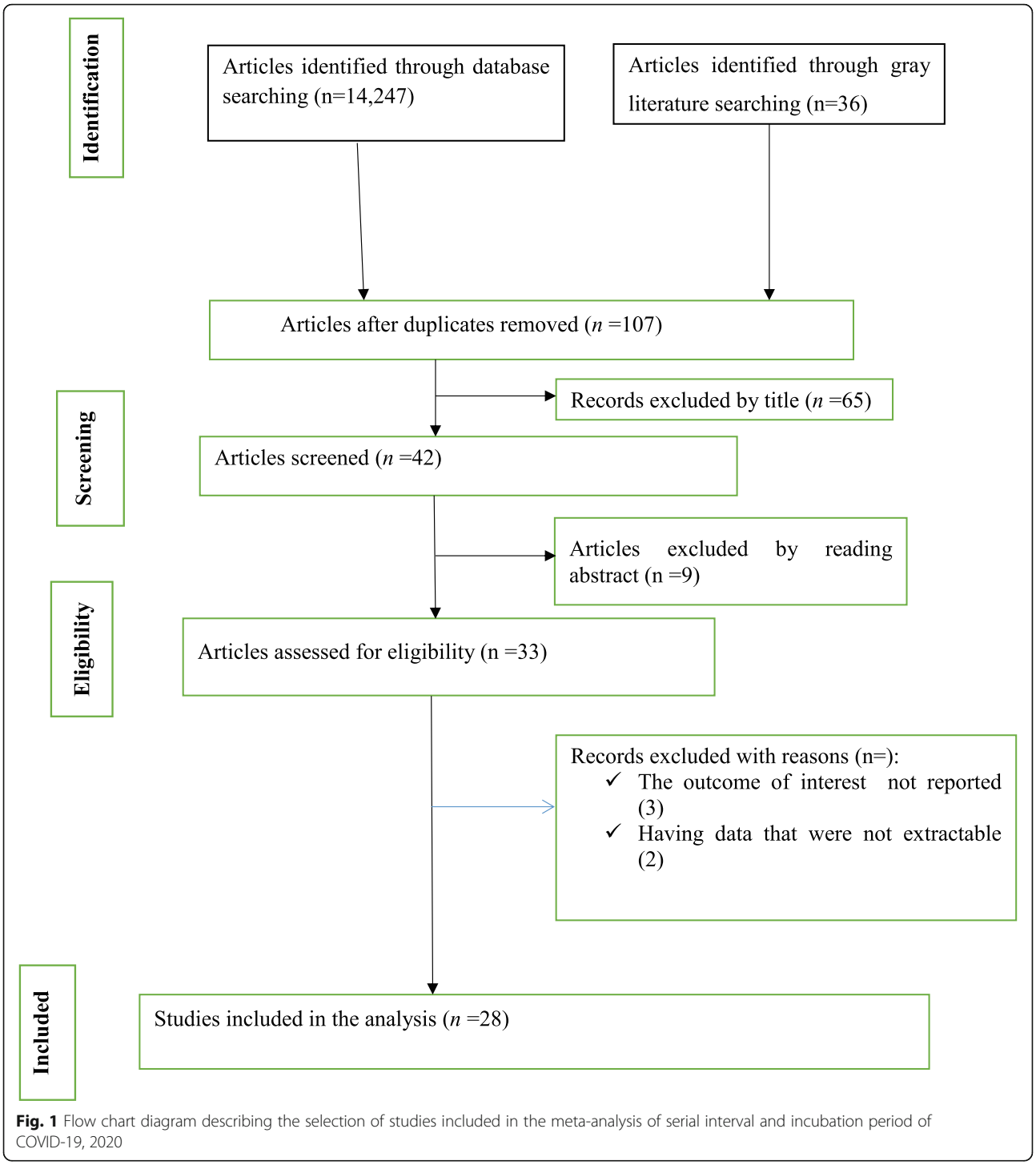

Fig. 1 Flow chart diagram describing the selection of studies included in the meta-analysis of serial interval and incubation period of COVID-19, 2020

had a good quality (Table S1). Similarly, among the included studies to pool the mean incubation period of COVID-19, about 71.4% of studies had a good quality (Table S2). We assessed the issue of publication bias by visual inspection of funnel plot and by using Egger's regression test. Though the funnel plot looks asymmetrical the Egger's test showed that no relationship between the effect size and its precision (Fig. 4).

Discussion

The current study has two main objectives. The first objective is to determine the overall mean serial interval of

Table 1 Descriptions of the included studies conducted on the average estimate of serial interval of COVID-19, 2020

No.	First author	Country	Study period	Sample size (in pairs)	Mean in days	Standard deviation	95%CI for mean
1.	Aghaali et al	Iran	February 20,2020	37	4.55	3.3	NR
2.	Ali et al	China	January 9 to February 13, 2020	677	5.1	5.3	4.7–5.5
3.	Bi et al	China	Jan 14 to February 12, 2020	48	6·3	4.2	5.2–7·6
4.	Bui et al	Vietnam	January 29 to March 24,2020	9	5.8	3.6	NR
5	Cereda et al.	Italy	March 82,020	90	6.6	28	0.7–19
6.	Chan et al	China	January 23 to April 6, 2020	47	6.5	4.7	NR
7.	Cheng et al	Taiwan	January 15 to February 26,2020	12	7.0	5.8	3.7–13.2
8.	Du et al	China	January 20 to February 19, 2020	339	5.3	5.3	4.7–5.9
9.	He et al	China	January 21 to March 6, 2020	77	5.8	4.5	4.8–6.8
10.	Li et al	China	January 21, 2020, to February 29, 2020.	337	5.8	3.9	5:4–6:2
11.	Li et al	China	January 22, 2020	6	7.5	3.4	5.3–19
12.	Liu et al	China	January 1, to March 12, 2020	116	5.8	3.2	
13.	Najafi et al	Iran	February 22 to March 29, 2020	21	5.7	3.9	NR
14.	Nishiuraa et al	Japan	February 12, 2020	28	4.7	2.9	3.7–6.0
15.	Kowk et al	China	February 13,2020	26	4.6	3.3	3.4–5.9
16.	Tindale et al	Singapore	January 19 to February 26,2020	93	4.6	0.9	2.7–6.4
17.	Tindale et al	Tianjin	January 21 to February 27,2020	135	4.2	4.0	3.4–5.0
18.	Viego et al	Argentina	March 20 to May 8, 2020	13	5.5	5.0	2.8–8.1.
19.	Xu et al	China	January 15 to February 29, 2020	1407	5.2	5.3	4.6, 5.8
20.	Yang et al	China	January 20, 2020	152	4.6	4.4	3.7–5.5
21.	You et al	China	March 31, 2020	198	4.6	5.5	NR
22.	Zhang et al	China	after Jan. 20, 2020	35	5.1	3.4	1·3–11·6
23.	Zhao et al	China	February 15,2020	21	4.4	3	2.9–6.7

Table 2 Descriptions of the included studies conducted on the average incubation period of COVID-19, 2020

No.	First author	Country	Study period	Sample size	Mean in days	Standard deviation	95% CI
1.	Backer et al	China	January 20 to 28, 2020	88	6.4	3.8	5.6–7.7
2.	Bi et al	China	Jan 14 to Feb 12, 2020	183	4·8	0.9	4·2–5·4
3.	Cheng et al	Taiwan	January 15 to February 26,2020	32	4.9	6.3	2.7–8.4
4.	Han et al	China	December 29, 2019, to February 5, 2020.	59	5.8	2.9	5.1–6.5
5.	Kong	China	January 22 to February 15, 2020	136	8.5	4.1	7.8–9.2
6.	Lauer et al	China	January 4 to February 24, 2020.	181	5.1	0.97	4.5–5.8
7.	Li et al	China	January 22, 2020	10	5.2	1.9	4.1–7.0
8.	Linton et al	China	January 31, 2020	158	5.6	2.8	5.0–6.3
9.	Tindale et al	Singapore	January 19 to February 26,2020	93	7.1	4.9	6.1–8.3
10.	Tindale et al	Tianjin	January 21 to February 27,2020	135	9 .0	6.5	7.9–10.2
11.	Viego et al	Argentina	March 20 to May 8, 2020	12	7.5	5.9	4.1–10.9
12.	Yang et al	China	January 20, 2020	178	8.5	3.8	4.8–6.0
13.	You et al	China	March 31, 2020	139	8	4.8	NR
14.	Zhang et al	China	after Jan. 20, 2020	49	5.2	12.1	1·8–12·4

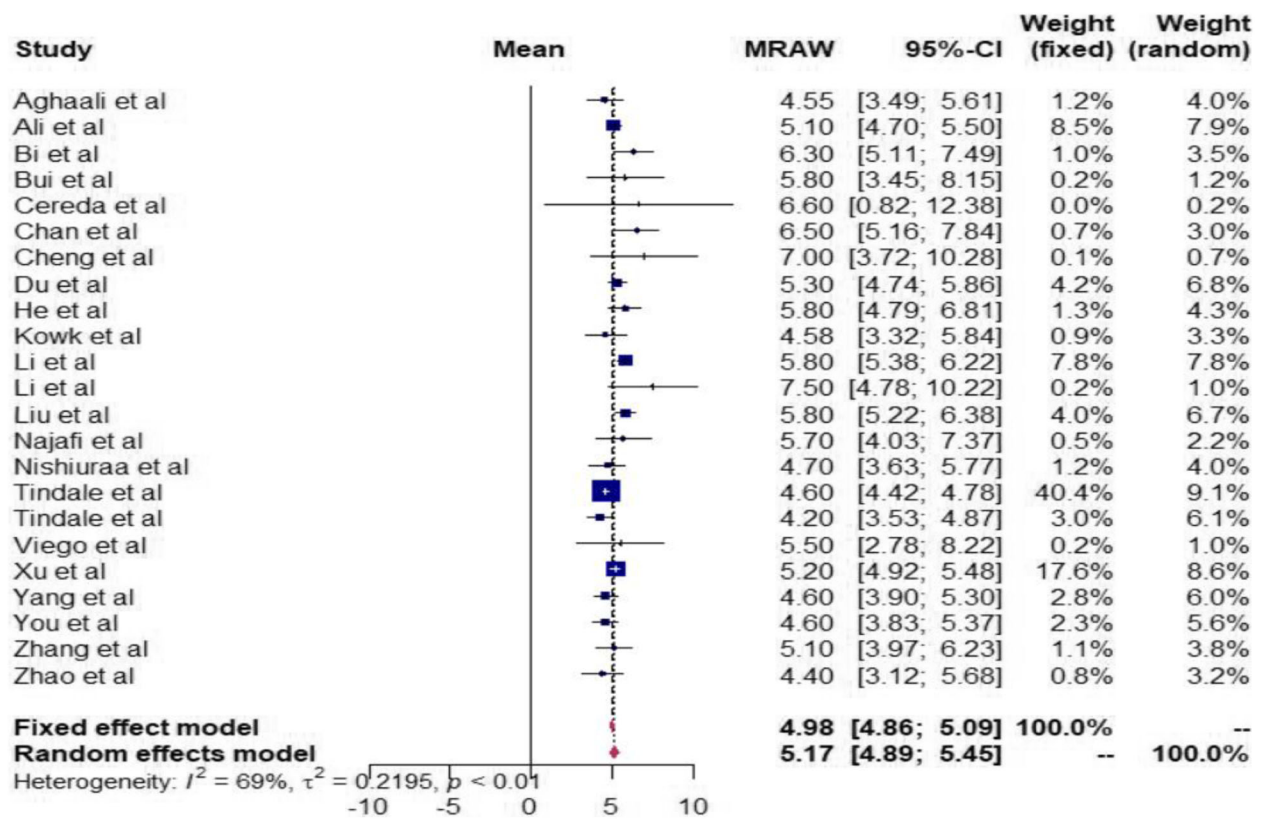

Fig. 2 Forest plot that shows the pooled mean serial interval of COVID-19 using available studies, 2020

COVID-19. In this study, we found that the weighted pooled mean serial interval of COVID-19 was 5.2 (95%CI: 4.9–5.5) days. This result is consistent with a study conducted in China [21], which reported that the mean serial interval of 5. 35 (95%CI: 4:63; 6:07) days. Another systematic review and meta-analysis study that combines 11 studies reported that the mean serial interval of 5.19 (95%CI: 4.37, 6.02) [22]. A study that compares the epidemiology of COVID-19, SARS-CoV, and MERS-CoV showed that COVID-19 had a short serial interval than SARS and MERS [23]. In addition, the pooled mean serial interval of COVID-19 obtained in this study is shorter than the mean serial interval of MERS and SARS reported in South Korea, and Singapore [24, 25].

The second objective of this study was to determine the overall mean incubation period of COVID-19. Consequently, the weighted pooled mean incubation period of COVID-19 was found 6.5 (95%CI: 5.9–7.1) days. This result is consistent with a study conducted in Hong Kong [26]. A result obtained from a rapid systematic review and meta-analysis showed that median incubation period of COVID-19 is 5.1 (95% CI: 4.5–5.8) days. Furthermore, the average incubation period of COVID-19 obtained in this study is longer than the average incubation period of SARS that reported in Toronto, Hong Kong, and Beijing [24, 27]. In addition, the average incubation period of COVID-19 obtained in the current study is longer than a systematic review study that reported the average incubation period of SARS [28].

Moreover, the average incubation period of COVID-19 obtained in the current study is longer than the mean incubation period of MERS reported in Hong Kong, and the Middle East [29, 30]. The possible explanation for this result might be the associations between shorter incubation periods and greater severity of infectious disease [31]. A longer incubation period was associated with a reduction in the risk of death [32]. The estimated fatality rate of COVID-19, SARS, and MERS are 2.3, 9.5, and 34.4%, respectively [33–35]. Conversely, another study showed that there is no observable difference between the incubation periods for SARS-CoV-2, severe acute respiratory syndrome coronavirus (SARS-CoV), and MERS-CoV. This study reported that the estimated incubation periods for SARS-CoV-2, SARS-CoV, and MERS-CoV were 4.9, 4.7, and 5.8 days, respectively [11].

In the current study, we included more studies by making longer searching date than the previous published articles. As the number of studies in meta-analysis

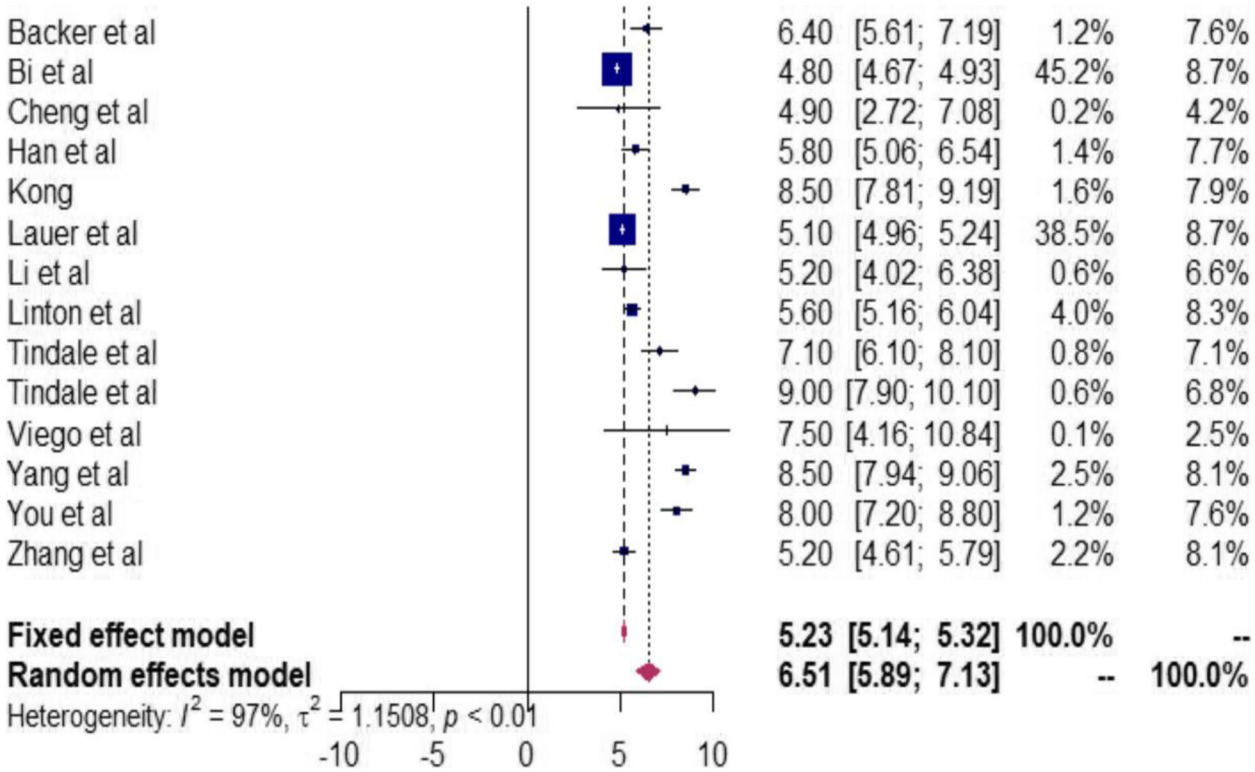

Fig. 3 Forest plot that shows the pooled mean incubation period of COVID-19 using available studies, 2020

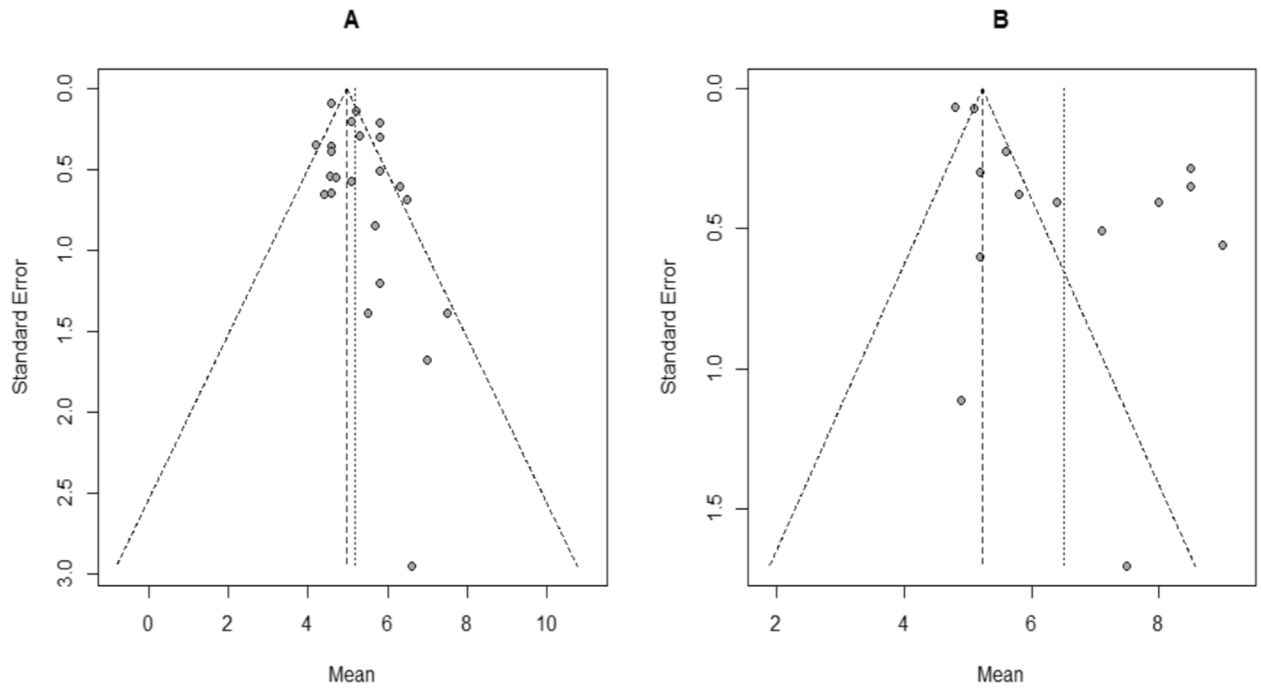

Fig. 4 Funnel plots to check publication bias. **a** The included studies to pool the mean serial interval of COVID-19. **b** The included studies to pool the mean incubation period of COVID-19

increases, the power of estimating the pooled serial interval and incubation period of COVID-19 will be improved.

Limitations

The current study has a number of limitations. Firstly, the overall estimate of serial interval and incubation period were computed with in a considerable heterogeneity. The source of heterogeneity might be difference in study population, data collection period, and method of analysis. Secondly, the majority of the included studies had relatively small study participants which may decrease the power of the study. Thirdly, the review was limited to only articles published in the English language. Lastly, since the included articles are limited to few countries, it may not represent the global figure.

Conclusions

This systematic review and meta-analysis showed that the weighted pooled mean serial interval and incubation period of COVID-19 were 5.2, and 6.5 days, respectively. The average serial interval of COVID-19 is shorter than the average incubation period, which suggests that substantial numbers of COVID-19 cases will be attributed to presymptomatic or asymptomatic transmission.

Abbreviations

MERS-CoV: Middle East respiratory syndrome coronavirus; COVID-19: novel coronavirus disease 2019; SARS-CoV-2: Severe Acute Respiratory Syndrome Coronavirus 2

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-021-05950-x.

Additional file 1: Table S1. Assessing the risk of bias for the included studies to estimate the pooled avarage of serial interval of COVID-19, 2020.

Additional file 2: Table S2. Assessing the risk of bias for the included studies to estimate the pooled avarage incubation period of COVID-19, 2020.

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Authors' contributions

MA, LY, and MAA: conceived the design; DBK and WG develop the search strategy; MA, LY, MAA and TYB: searched, screened, and appraised the studies, and extract the data: MA analyze the data; MAA, LY, MAA and TYB: drafted the manuscript. All authors read and approved the final manuscript for publication.

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Availability of data and materials

All the materials and data on which the findings of this review based are presented within the manuscript.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests
All authors declared that there is no competing interest.

Author details
[1]Department of Public Health, Debre Markos University, Debre Markos, Ethiopia. [2]Department of Epidemiology and Biostatistics, Institute of Public Health, College of Medicine and Health Science, University of Gondar, Gondar, Ethiopia.

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