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EDITORIAL

Call for emergency action to limit global temperature increases, restore biodiversity, and protect health: wealthy nations must do much more, much faster

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The UN General Assembly in September 2021 will bring countries together at a critical time for marshalling collective action to tackle the global environmental crisis. They will meet again at the biodiversity summit in Kunming, China, and the climate conference (COP26) in Glasgow, UK. Ahead of these pivotal meetings, we—the editors of health journals worldwide—call for urgent action to keep average global temperature increases below 1.5°C, halt the destruction of nature, and protect health.

Health is already being harmed by global temperature increases and the destruction of the natural world, a state of affairs health professionals have been bringing attention to for decades (1). The science is unequivocal; a global increase of 1.5°C above the pre-industrial average and the continued loss of biodiversity risk catastrophic harm to health that will be impossible to reverse (2,3). Despite the world's necessary preoccupation with covid-19, we cannot wait for the pandemic to pass to rapidly reduce emissions.

Reflecting the severity of the moment, this editorial appears in health journals across the world. We are united in recognising that only fundamental and equitable changes to societies will reverse our current trajectory.

The risks to health of increases above 1.5°C are now well established (2). Indeed, no temperature rise is "safe." In the past 20 years, heat related mortality among people aged over 65 has increased by more than 50% (4). Higher temperatures have brought increased dehydration and renal function loss, dermatological malignancies, tropical infections, adverse mental health outcomes, pregnancy complications, allergies, and cardiovascular and pulmonary morbidity and mortality (5,6). Harms disproportionately affect the most vulnerable, including children, older populations, ethnic minorities, poorer communities, and those with underlying health problems (2,4).

Global heating is also contributing to the decline in global yield potential for major crops, falling by 1.8–5.6% since 1981; this, together with the effects of extreme weather and soil depletion, is hampering efforts to reduce undernutrition (4). Thriving ecosystems are essential to human health, and the widespread destruction of nature, including habitats and species, is eroding water and food security and increasing the chance of pandemics (3,7,8).

The consequences of the environmental crisis fall disproportionately on those countries and communities that have contributed least to the problem and are least able to mitigate the harms. Yet no country, no matter how wealthy, can shield itself from these impacts. Allowing the consequences to fall disproportionately on the most vulnerable will breed more conflict, food insecurity, forced displacement, and zoonotic disease—with severe implications for all countries and communities. As with the covid-19 pandemic, we are globally as strong as our weakest member.

Rises above 1.5°C increase the chance of reaching tipping points in natural systems that could lock the world into an acutely unstable state. This would critically impair our ability to mitigate harms and to prevent catastrophic, runaway environmental change (9,10).

Global targets are not enough

Encouragingly, many governments, financial institutions, and businesses are setting targets to reach net-zero emissions, including targets for 2030. The cost of renewable energy is dropping rapidly. Many countries are aiming to protect at least 30% of the world's land and oceans by 2030 (11).

These promises are not enough. Targets are easy to set and hard to achieve. They are yet to be matched with credible short- and longer-term plans to accelerate cleaner technologies and transform societies. Emissions reduction plans do not adequately incorporate health considerations (12). Concern is growing that temperature rises above 1.5°C are beginning to be seen as inevitable, or even acceptable, to powerful members of the global community (13). Relatedly, current strategies for reducing emissions to net zero by the middle of the century implausibly assume that the world will acquire great capabilities to remove greenhouse gases from the atmosphere (14,15).

This insufficient action means that temperature increases are likely to be well in excess of 2°C (16), a catastrophic outcome for health and environmental stability. Crucially, the destruction of nature does not have parity of esteem with the climate element of the crisis, and every single global target to restore biodiversity loss by 2020 was missed (17). This is an overall environmental crisis (18).

Health professionals are united with environmental scientists, businesses, and many others in rejecting that this outcome is inevitable. More can and must be done now—in Glasgow and Kunming—and in the immediate years that follow. We join health professionals worldwide who have already supported calls for rapid action (1,19).

Equity must be at the centre of the global response. Contributing a fair share to the global effort means that reduction commitments must account for the cumulative, historical contribution each country has made to emissions, as well as its current emissions and capacity to respond. Wealthier countries will have to cut emissions more quickly, making reductions by 2030 beyond those currently proposed (20,21) and reaching net-zero emissions before 2050. Similar targets and emergency action are needed for biodiversity loss and the wider destruction of the natural world.

To achieve these targets, governments must make fundamental changes to how our societies and economies are organised and how we live. The current strategy of encouraging markets to swap dirty for cleaner technologies is not enough. Governments must intervene to support the redesign of transport systems, cities, production and distribution of food, markets for financial investments, health systems, and much more. Global coordination is needed to ensure that the rush for cleaner technologies does not come at the cost of more environmental destruction and human exploitation.

Many governments met the threat of the covid-19 pandemic with unprecedented funding. The environmental crisis demands a similar emergency response. Huge investment will be needed, beyond what is being considered or delivered anywhere in the world. But such investments will produce huge positive health and economic outcomes. These include high quality jobs, reduced air pollution, increased physical activity, and improved housing and diet. Better air quality alone would realise health benefits that easily offset the global costs of emissions reductions (22).

These measures will also improve the social and economic determinants of health, the poor state of which may have made populations more vulnerable to the covid-19 pandemic (23). But the changes cannot be achieved through a return to damaging austerity policies or the continuation of the large inequalities of wealth and power within and between countries.

Cooperation hinges on wealthy nations doing more

In particular, countries that have disproportionately created the environmental crisis must do more to support low- and middle-income countries to build cleaner, healthier, and more resilient societies. High income countries must meet and go beyond their outstanding commitment to provide US$100 billion a year, making up for any shortfall in 2020 and increasing contributions to and beyond 2025. Funding must be equally split between mitigation and adaptation, including improving the resilience of health systems.

Financing should be through grants rather than loans, building local capabilities and truly empowering communities, and should come alongside forgiving large debts, which constrain the agency of so many low-income countries. Additional funding must be marshalled to compensate for inevitable loss and damage caused by the consequences of the environmental crisis.

As health professionals, we must do all we can to aid the transition to a sustainable, fairer, resilient, and healthier world. Alongside acting to reduce the harm from the environmental crisis, we should proactively contribute to global prevention of further damage and action on the root causes of the crisis. We must hold global leaders to account and continue to educate others about the health risks of the crisis. We must join in the work to achieve environmentally sustainable health systems before 2040, recognising that this will mean changing clinical practice. Health institutions have already divested more than US$42 billion of assets from fossil fuels; others should join them (4).

The greatest threat to global public health is the continued failure of world leaders to keep the global temperature rise below 1.5°C and to restore nature. Urgent, society-wide changes must be made and will lead to a fairer and healthier world. We, as editors of health journals, call for governments and other leaders to act, marking 2021 as the year that the world finally changes course.

Competing interests

All authors have completed the ICMJE conflict of interest form. FG serves on the executive committee for the UK Health Alliance on Climate Change and is a Trustee of the Eden Project. RS is the chair of Patients Know Best, has stock in UnitedHealth Group, has done consultancy work for Oxford Pharmagenesis, and is chair of the Lancet Commission of the Value of Death. The other authors declare no competing interests.

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Note

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References

1. World Medical Association, International Council of Nurses, ISDE International, et al. In support of a #HealthyRecovery. May 26, 2020. https://healthyrecovery.net (accessed Aug 17, 2021).

2. Intergovernmental Panel on Climate Change. Summary for policymakers. Global warming of 1.5°C. An IPCC special report on the impacts of global warming of 1.5°C above pre-industrial levels and related global greenhouse gas emission pathways, in the context of strengthening the global response to the threat of climate change, sustainable development, and efforts to eradicate poverty. 2018. https://www.ipcc.ch/sr15/ (accessed Aug 17, 2021).

3. Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services. Summary for policymakers: the global assessment report on biodiversity and ecosystem services. 2019. https://ipbes.net/sites/default/files/2020-02/ipbes_global_assessment_report_summary_for_policymakers_en.pdf (accessed Aug 17, 2021).

4. Watts N, Amann M, Arnell N, et al. The 2020 report of the Lancet Countdown on health and climate change: responding to converging crises. Lancet 2021; 397: 129–70.

5. Rocque RJ, Beaudoin C, Ndjaboue R, et al. Health effects of climate change: an overview of systematic reviews. BMJ Open 2021; 11: e046333.

6. Haines A, Ebi K. The imperative for climate action to protect health. N Engl J Med 2019; 380: 263–73.

7. UN Environment Programme, International Livestock Research Institute. Preventing the next pandemic: zoonotic diseases and how to break the chain of transmission. 2020. https://72d37324-5089-459c-8f70-271d19427cf2.filesusr.com/ugd/056cf4_b5b2fc067f094dd3b2250cda15c47acd.pdf (accessed Aug 17, 2021).

8. Intergovernmental Panel on Climate Change. Summary for policymakers. Climate change and land: an IPCC special report on climate change, desertification, land degradation, sustainable land management, food security, and greenhouse gas fluxes in terrestrial ecosystems. 2019. https://www.ipcc.ch/srccl/chapter/summary-for-policymakers/ (accessed Aug 17, 2021).

9. Lenton TM, Rockström J, Gaffney O, et al. Climate tipping points—too risky to bet against. Nature 2019; 575: 592–95.

10. Wunderling N, Donges JF, Kurths J, Winkelmann R. Interacting tipping elements increase risk of climate domino effects under global warming. Earth Syst Dynam 2021; 12: 601–19.

11. High Ambition Coalition. 2021. https://www.hacfornatureandpeople.org (accessed Aug 17, 2021).

12. Global Climate and Health Alliance. Are national climate commitments enough to protect our health? https://climateandhealthalliance.org/initiatives/healthy-ndcs/ndc-scorecards/ (accessed Aug 17, 2021).

13. Thunberg G, Neubauer L, Charlier A, et al. Climate strikers: open letter to EU leaders on why their new climate law is "surrender". Carbon Brief, March 3, 2020. https://www.carbonbrief.org/climate-strikers-open-letter-to-eu-leaders-on-why-their-new-climate-law-is-surrender (accessed Aug 17, 2021).

14. Fajardy M, Köberle A, MacDowell N, Fantuzzi A. BECCS deployment: a reality check. Grantham Institute briefing paper 28. January, 2019. https://www.imperial.ac.uk/media/imperial-college/grantham-institute/public/publications/briefing-papers/BECCS-deployment---a-reality-check.pdf (accessed Aug 17, 2021).

15. Anderson K, Peters G. The trouble with negative emissions. Science 2016; 354: 182–83.

16. Climate action tracker. 2021. https://climateactiontracker.org (accessed Aug 17, 2021).

17. Secretariat of the Convention on Biological Diversity. Global biodiversity outlook 5. 2020. https://www.cbd.int/gbo5 (accessed Aug 17, 2021).

18. Steffen W, Richardson K, Rockström J, et al. Planetary boundaries: guiding human development on a changing planet. Science 2015; 347: 1259855.

19. UK Health Alliance. Our calls for action. 2021. http://www.ukhealthalliance.org/cop26/ (accessed Aug 17, 2021).

20. Climate Action Tracker. Warming projections global update: May 2021. https://climateactiontracker.org/documents/853/CAT_2021-05-04_Briefing_Global-Update_Climate-Summit-Momentum.pdf (accessed Aug 17, 2021).

21. UN Environment Programme. Emissions gap report 2020. Nairobi: United Nations Environment Programme, 2020.

22. Markandya A, Sampedro J, Smith SJ, et al. Health co-benefits from air pollution and mitigation costs of the Paris Agreement: a modelling study. Lancet Planet Health 2018; 2: e126–33.

23. Paremoer L, Nandi S, Serag H, Baum F. Covid-19 pandemic and the social determinants of health. BMJ 2021; 372: n129.

OVERVIEW

Decision analysis support for evaluating transmission risk of COVID-19 in places where people gather

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Abstract

Background: The coronavirus diseases 2019 (COVID-19) pandemic has presented an unprecedented public health challenge. Prior to vaccination, non-pharmaceutical interventions, including closures, were necessary to help control the epidemic. With the arrival of variants of concern and insufficient population vaccination coverage, ongoing evaluation of transmission risk in settings and the use of non-pharmaceutical interventions are necessary to help control the epidemic. This study aimed to produce a framework for evaluating transmission risk in settings where individuals gather and inform decision-making.

Methods: A multi-criteria decision analysis process was used to structure the framework. Fifteen criteria were identified as important to consider for COVID-19 transmission risk based on the literature. This list was ranked by experts and then categorized. The analysis was structured by the consensus list of criteria and relative positioning of each criteria within the list to produce sets of factors to consider when assessing transmission risk at gatherings.

Results: Fifteen experts from across Canada participated in ranking the criteria. Strong consensus was found on the relative importance of criteria and this relative consensus was used to create four categories: critical (3 criteria); important (6 criteria); good to consider (5 criteria); and if time permits (1 criterion).

Conclusion: The resulting consensus list and categories constitutes a set of important elements that can be applied to any setting as an objective and transparent framework to assess transmission risk in the venue. In conjunction with further consideration of the local epidemiology of COVID-19, an overall risk of transmission assessment can be established and uniformly implemented.

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Keywords: SARS-CoV-2, COVID-19, transmission risk, gatherings, systematic evaluation

Introduction

The emergence of the novel coronavirus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and the associated disease (coronavirus disease 2019; COVID-19) was initially observed as an outbreak in Wuhan, China in late 2019, and resulted in the ongoing pandemic (1). The virus was first detected in Canada in early 2020 and has caused 1,670,241 cases and 28,367 deaths (as of October 13, 2021) (2). The SARS-CoV-2 is a highly transmissible respiratory virus that can cause a range of symptoms from none to mild or severe disease and death (3). This has created an unprecedented disease management challenge for public health and numerous public health measures have been implemented with variable stringency in an attempt to slow the epidemic and reduce its impact. These include increased personal physical distancing and non-pharmaceutical interventions, such as case detection and isolation, tracing of contacts and quarantine and community masking (4), to reduce transmission opportunities in the community. However, when and where transmission is high, a range of restrictive closures have been imposed by provincial and local governments, including closures of schools, universities and non-essential businesses, bans or limitations on gatherings, limitations on travel within and between jurisdictions and encouragement of teleworking in

an attempt to limit transmission opportunities. Together these actions helped to minimize person-to-person contacts in Canada and resulted in the epidemic coming under control with low reported case incidence during summer 2020. However, the fall 2020 return to school and re-opening of businesses in many regions of Canada resulted in a resurgence of the epidemic and a second wave peaking higher in total cases, hospitalizations and deaths than the spring wave (2). As capacity for control of the epidemic by testing and tracing alone was surpassed, re-implementation of some levels of restrictive closures was deemed necessary to help reduce rates of contact between Canadians, regain previous levels of epidemic control and limit the risk of exceeding healthcare capacity. Closures of schools and businesses have important social and economic impacts on society. The challenge facing decision-makers is how to navigate the trade-off between preventing COVID-19 transmission and the negative potential health, social and economic impacts of restrictive measures (5–12). A full assessment that includes negative impacts of closures is outside the scope of this work, as at this time the focus is restricted to informing assessment of transmission risk.

The arrival of vaccine doses in Canada in December 2020 raised hopes that restrictive measures could be eased. However, the recent emergence of new, more transmissible and in some cases more virulent variants of concern (VOC) meant that caution was and will be needed when lifting restrictive measures and re-opening businesses and places where people gather—particularly until sufficient vaccination coverage and natural immunity of the Canadian population has been achieved. Even then, the capacity to inform decisions on restrictive closures will remain relevant with the continuing threat of immune escape VOC and the potential of waning immunity.

This project began in late 2020, prior to vaccine arrival in Canada, with the aim to explore available evidence on COVID-19 transmission in different settings and contribute to informing decision-making around closures. Settings are meant to broadly encompass all locations presenting a transmission risk for COVID-19 that a decision-maker may wish to assess. These include transmission at private gatherings in people's homes, as well as transmission in public places such as schools, grocery stores, retail stores, concerts and bars among others. The explicit consideration of high-risk populations can also be included in the assessment. While the potential cascading effects of closures are numerous and still being studied, characteristics of a setting contributing to transmission risk remains independently important to evaluate, even as vaccination is being rolled out since the presence of variants of concern continues to pose an important transmission risk. The objective of this project was to produce a framework to assist in ranking settings by the risk they pose for COVID-19 transmission, and potentially identify areas where mitigating measures can be targeted to help reduce transmission risk in these same settings in order to help inform decision-making.

Methods

Multi-criteria decision analysis (MCDA) is part of a family of decision aid tools from the field of operations research and used in numerous sectors to systematically evaluate alternatives over multiple criteria (13). Multi-criteria decision analysis approaches help to structure reflection around a decision problem by allowing the integration of multiple types of evaluations and the highlighting of strengths and weaknesses of the alternatives under evaluation. Participatory MCDA processes generally consist of a multi-step problem structuring phase where the problem is defined, stakeholders identified, criteria defined and weighted, items to be ranked identified and evaluated over the criteria, followed by a decision analysis phase where the multi-criteria analysis is carried out along with a sensitivity analysis and interpretation of results (**Table 1**). In this article, a "rapid and light" version of a participatory MCDA process was used to structure a framework for the evaluation of settings at risk for COVID-19 transmission, while taking into account time constraints of stakeholders and considerable data gaps in the literature. The objective was to identify criteria and indicators that would be most informative for assessing transmission risk in settings and produce a consensus ranking of these criteria by experts. The results of this exercise are presented along with a discussion of how the results could be used to help assess settings for transmission risk.

Table 1: Summary of steps in participatory and "light" multi-criteria decision analysis process

Phase	#	Steps included in the participatory process	Steps included in the "light" process[a]
Problem structuring	1	Definition of the problem of interest	x
	2	Identification of stakeholders	x
	3	Identification of alternatives[b]	–
	4	Definition of criteria	x
	5	Weighting of criteria	x
	6	Evaluation of alternatives[b] based on criteria	–
Decision analysis	7	Decision analysis	–
	8	Sensitivity analysis	–
	9	Interpretation of results	–

[a] Steps included in the "light" process are marked with an "X". Dashes, "-", indicate step not included
[b] "Alternatives" in this context would be the settings (e.g. bars, indoor concerts, etc.) under evaluation

Four steps from a participatory MCDA methodology were adapted to allow for the construction of an expert-ranked consensus list of criteria that could be used as a decision-aid. A quick scan of the literature was conducted to search for broad

factors contributing to COVID-19 transmission risk and produce a preliminary list of key criteria. The scan was conducted in an evergreen database of COVID-19 literature maintained within the Public Health Agency of Canada that compiles citations daily from seven databases. The search was used to draft an initial list of twenty-three criteria, and indicators for their rapid evaluation. A limited number of studies were available and consisted primarily of rapid reviews of reports where clusters had occurred with many of the early outbreaks reported having occurred before widespread use of public health measures. Preliminary criteria related to common factors present in settings where outbreaks had occurred. Droplet and aerosol transmission was thought to account for most transmissions and pointed towards elements favoring close contact in closed and crowded spaces as primary drivers of transmission.

The preliminary list of criteria was presented to a group of 62 provincial public health experts for review and comment. The list was condensed to 15 criteria, including 10 site and event characteristics, one participant-level characteristic and four potential mitigation measures (**Table 2**). In order to keep the final number of criteria manageable, a number of criteria from the original list were combined (e.g. indoor/outdoor location and ventilation) and criteria to evaluate secondary activities at settings were not included (e.g. shared dining or break rooms). This list was then presented to a group of experts within the Pan-Canadian Public Health Network involved in the COVID-19 response, for ranking during December 2020 via an online tool created explicitly for this purpose. The individual expert-ranked lists were combined using general Mallows models (14) to produce a consensus ranking (see **Appendix** for more details on the general Mallows models). The R package PerMallows (15) was used to analyze the rankings.

Table 2: Criteria for evaluating transmission risk in settings

Criteria	Level (from lower to higher risk)	Summary: What is known	Examples	References
Location and ventilation	1. Outdoors 2. Indoors good ventilation (well-designed mechanical - HVAC) 3. Indoors with moderate ventilation (windows) 4. Indoors poor ventilation	Risk of transmission generally thought to be lower outdoors depending on nature of setting, activity type, duration, circulation and providing physical distancing at or around 2 meter can be maintained. Weed *et al.* report limited evidence of outdoor transmission based on reviewed studies. Some outdoor transmission has occurred when physical distancing was breached or in high density conditions, low circulation, large size of gatherings over extended duration has taken place (e.g. outdoor concerts, festivals, some physical activities, sporting events). Risk of transmission in closed environments reported to be higher than in open-air environments (OR 18.7 (6.0–57.9)). Note: cases in study occurred when social interactions were unrestricted. ECDC concluded that well maintained HVAC systems adapted for use in COVID-19 pandemic may help to decrease airborne transmission. HVAC - contamination in air samples and HVAC system surfaces in healthcare settings indicate possible spread but virus viability not established. Some early case clusters were attributed to air conditioning units and air recirculation. Air jets from AC and recirculation of indoor air considered likely modes of transmission. Other coronavirus infections have been associated with poor ventilation (insufficient movement and clearance of contaminated indoor air).	**Indoor examples:** Gyms, fitness class, recreational sports, workplaces. Nightclubs with poor ventilation, crowding and loud music leading to attendees potentially yelling and leaning very close together to communicate; Karaoke rooms Parties, restaurants, healthcare facilities **Outdoor examples:** Local festivals, events with tented eating spaces with poor ventilation	(16–23)
Duration of event (time)	1. Interaction less than 5 minutes 2. 5–14 minutes 3. 15–60 minutes 4. More than 60 minutes	In a review of outdoor transmission events, crowding was a common factor among outbreaks, but circulation (mixing) of participants, close range interactions with loud conversations, shouting or singing and duration were found to be important factors (Weed & Foad). A rapid synthesis by found that large clusters occurred in settings where individuals were confined for prolonged periods of time (e.g. shared accommodations, food processing plants, religious services).	N/A	(21,24,25)

Table 2: Criteria for evaluating transmission risk in settings (*continued*)

Criteria	Level (from lower to higher risk)	Summary: What is known	Examples	References
Contact between participants during activity	1. No physical contact 2. Within 2 meter 3. Some physical contact, within 1 meter of participants, sharing of surfaces 4. Close physical contact, skin contact	Transmission of SARS-CoV-2 is primarily via prolonged close contact and exposure to respiratory secretions. Close proximity contacts between individuals increases the likelihood of transmission of virus with contact interactions ranging from face-to-face interactions to direct physical contact either. Transmission risk can be mitigated to some extent by use of masks, and other PPE. Workplace infections have been facilitated by close contact and duration of interaction. For example, grocery store employees with direct customer exposure, paramedics and firefighters with physical contact with potentially infected individuals at higher risk.	N/A	(24,25)
Density of crowd	1. Low (more than 2 meter distancing regularly maintained) 2. Medium (2 meter distancing) 3. High (less than 2 meter between participants)	Dalton *et al*. suggest an 8-fold increase in risk of viral dose excretion and inhalation from communicating at a distance of 30 cm vs 1 meter. Settings where physical distancing at or around 2 meter not possible linked with increased risk of transmission.	Nightclubs with poor ventilation, crowding and loud music leading to attendees potentially yelling and leaning very close together to communicate; Karaoke rooms	(17,21)
Mixing of networks/ bubbles at event (closed small groups vs random participants every time)	1. Closed small group with no outside contacts 2. Closed group with some outside contacts 3. Random mixing of large groups	From predictive modeling studies: - Small closed community networks where groups of people only interact with a chosen group of other people and there is limited interaction outside network have lower risk. Risk increases with bridges to other networks. - Random mixing events (e.g. public transport, bars and sporting events) are higher risk because of mixing from many small networks. - Could also include settings where exposed to multiple clients (for example transport workers, sales people, cleaners). A review of workplace related transmission risk found that drivers and transport workers, service and sales workers, food industry, personal care occupations, food production, preschool occupations, community and social services, construction and related trades occupations and public safety workers were most at risk of infection (these groups are highly exposed to random individuals/clients in their line of work).	Ski resorts due to their attraction of global travellers	(26–28)
Mixing of participants (circulation and mixing of participants within the event)	1. None 2. Moderate 3. High	In a review of outdoor transmission events, crowding (number and density) was a common factor among outbreaks, but circulation (mixing) of participants, close range interactions with loud conversations, shouting or singing and duration were important factors.	N/A	(21)

Table 2: Criteria for evaluating transmission risk in settings (*continued*)

Criteria	Level (from lower to higher risk)	Summary: What is known	Examples	References
Number of individuals (per gathering or event or venue)	1. 1 2. 1-2 3. Less than 5 4. Less than 10 5. Less than 100 6. Less than 1,000 7. More than 1,000	Large crowd size increases the probability that an infected individual is present, increases crowding, contact and thus transmission likelihood, even in outdoor settings. Of fifty-five studies reviewed in recent PHAC evidence brief, clear relationship found between increased gathering size and risk, but size threshold was inconsistent. When physical distancing breached, density is high, circulation of participants occurs and gathering takes place over extended duration of time, risk of transmission increases. An ecological study estimated a 36% reduction in R_o if the cut-off for gathering size was 10 people, compared to 21% if it was 100 people, and a 2% reduction in R_o if the cut-off for gathering size was 1,000 people. In an evaluation of NPIs at a global scale, Esra *et al*. estimated overall 10% reduction in infections associated with gathering size restrictions. In indoor environments in particular, larger numbers of individuals increases the potential concentration of airborne virus-carrying particles and number of individuals that can be exposed at any given time.	Carnival outbreak in Germany with 1,700 cases Sporting events also associated with outbreaks Weddings, religious gatherings, bars linked to clusters in Hong Kong	(21,22,24, 29–33)
Related activity (e.g. shared/ group travel to setting)	1. None 2. Yes, related activity with transmission risk	Congregate work and living increase the risk of transmission.	N/A	(34)
Ease of contact tracing should an outbreak occur	1. Participants' details available and can be easily reached should the need arise 2. Inconsistent tracking of participants may be difficult to follow-up 3. None	Timely test, trace and isolation have been shown to be important NPI strategies for working to contain transmission of COVID-19. Modelling studies show delays in tracing (three or more days) fail to bring Rt under 1.	N/A	(21,35,36)
Cohorting and physical distancing to reduce contacts	1. Cohorting to reduce mixing of networks and density/numbers 2. None	Successful prevention of transmission in the workplace linked to limited physical contact, including cohorting or staggering of employees.	N/A	(37,38)
Level of expelled air	1. Silent 2. Talking 3. Singing or shouting 4. Moderate to intense physical exercise 5. Aerosol-forming medical procedures	Dalton *et al*. suggest a 3 to 10-fold increase in risk of viral dose excretion due to louder vocalization (yelling or singing) in environments with loud music. Dalton *et al*. further suggest a 3-fold increase in risk of viral dose excretion due to light exercise (compared to talking).	Example of transmission in singing group/choir Gyms	(17,39–45)
Age structure of the participant population	1. Low risk—mostly children 2. Medium risk—mixed adults and children 3. High risk—all adults	Analysis of data from Wuhan found greatest model fit for testing of hypothesis that children show more mild symptoms. Infection fatality rate estimates close to zero for children and younger adults and rise exponentially with age.	N/A	(46–49)
Environmental cleaning/other transmission mitigation efforts	1. Yes, use of plexiglass or other non-permeable barrier between individuals; hand washing and consistent cleaning of shared surface and environment after every individual use 2. None	Public health interventions most effective when combined. Modelling shows hand hygiene, use of masks, and limiting individual contacts help to reduce transmission in larger gatherings of random individuals.	N/A	(26)

Table 2: Criteria for evaluating transmission risk in settings (*continued*)

Criteria	Level (from lower to higher risk)	Summary: What is known	Examples	References
Use of masks or face coverings	1. Masks or face coverings consistently used properly 2. Masks or face coverings poorly used 3. No masks nor face coverings worn	Much of the research on use of face masks was done prior to COVID-19 and the use of surgical masks. Observational studies on the use of protective effects of face masks against influenza like illness have been demonstrated. Studies on healthcare worker use of non-medical masks has demonstrated protection compared to no mask. Modelling shows hand hygiene, use of masks, and limiting individual contacts help to reduce transmission in larger gatherings of random individuals	Shared transport by bus example in China where infected traveller wore no mask during first bus ride and infected five other travellers, but wore mask during second bus ride with no secondary cases arising from last trip (Liu & Zhang)	(26,50,51)
Shared equipment or surfaces	1. None 2. Some shared equipment or surfaces but disinfected regularly 3. Some shared surfaces (e.g. elevator buttons, door handles, pens), individuals encouraged to disinfect self before use 4. Activity entails shared equipment and surfaces that cannot be disinfected continuously for practical reasons	Transmission of SARS-CoV-2 is primarily via prolonged close contact and exposure to respiratory secretions. However, SARS-CoV-2 can survive on various surfaces for limited amounts of time. Fomite transmission is known to occur with MERS-CoV and SARS. SARS-CoV-2 virus survival shown to be dependent on relative humidity and nature of contact surface (survival likelihood greater on plastic and stainless steel versus copper or cardboard surfaces). Transmission via contaminated surfaces appears possible. Environmental samples taken from an infected patient's room (door handle, toilet bowl, sink, air outlet fans) in Singapore found to be positive for SARS-CoV-2. Two other infected patient's room samples all negative. First patient had higher viral load than later two. Tests did not assess virus viability from samples.	Religious gatherings can present opportunities to pass around offerings, sacramental objects or sharing of food and refreshments. Outbreaks reported in South Korea and Arkansas, United States. Note that singing, indoor facility and ventilation also described as having taken place in Arkansas outbreak	(17,52–54)

Abbreviations: COVID-19, coronavirus disease 2019; ECDC, European Centre for Disease Prevention and Control; HVAC, heating, ventilation, and air conditioning; MERS-CoV, Middle East respiratory syndrome coronavirus; N/A, not applicable; NPI, non-pharmaceutical interventions; PHAC, Public Health Agency of Canada; PPE, personal protective equipment; R_o, reproduction number; SARS, severe acute respiratory syndrome; SARS-CoV-2, severe acute respiratory syndrome coronavirus

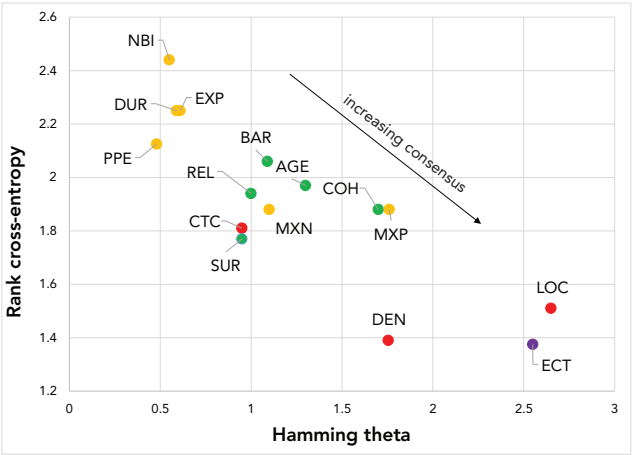
Results

Fifteen characteristics (i.e. criteria) were presented to a set of experts for ranking from highest to lowest level of importance when evaluating transmission risk of COVID-19 in various settings. Fifteen experts returned rankings by the deadline, and while the number of respondents was low, the respondents represented the geographic regions in Canada most affected by COVID-19 at the time.

Consensus ranking by means of generalized Mallows models

A generally good consensus emerged among experts on the relative importance of the criteria with some individual variations in specific ranking positions (**Figure 1**). **Table 3** shows the rankings created by each participant. The consensus ranking resulting from the generalized Mallows models with the Kendall and Hamming distance is shown in **Table 4**. While there was broad agreement between the two consensus rankings, differences emerged as a result of wider variation in respondent rankings for some criteria.

Figure 1: Rank cross-entropy and Hamming theta[a] from the generalized Mallows model[b]



Abbreviations: AGE, age structure of participants; BAR, engineering controls—use of physical barriers and environmental cleaning; CTC, contact between participants; COH, use of cohorting; DEN, density of crowd; DUR, duration of event; ECT, ease of contact tracing; EXP, level of expelled air; LOC, location and ventilation; MXN, mixing of networks; MXP, mixing of participants; NBI, number of households; PPE, personal protective equipment; REL, related activity; SUR, shared equipment or surfaces

[a] Hamming theta ($\theta_{i=1:15}$)

[b] Criteria are color coded by category: critical criteria in red, important criteria in orange, good to consider criteria in green and if time permits criterion in purple. Consensus among respondents on the absolute ranking positions of criteria increases for criteria located in the lower right quadrant

Table 3: Expert rankings of COVID-19 transmission criteria[a]

Expert	Criteria ranking														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	LOC	DUR	CTC	DEN	MXN	MXP	NBI	REL	ECT	COH	EXP	AGE	BAR	PPE	SUR
2	LOC	AGE	CTC	MXN	NBI	MXP	EXP	ECT	SUR	PPE	DUR	REL	BAR	DEN	COH
3	LOC	ECT	EXP	DUR	NBI	REL	CTC	SUR	AGE	COH	MXN	MXP	PPE	DEN	BAR
4	AGE	MXP	LOC	DUR	EXP	COH	CTC	ECT	SUR	BAR	NBI	REL	MXN	DEN	PPE
5	MXN	CTC	NBI	DUR	REL	DEN	LOC	AGE	SUR	BAR	ECT	PPE	COH	MXP	EXP
6	NBI	DEN	DUR	LOC	MXN	MXP	ECT	REL	PPE	BAR	COH	SUR	EXP	CTC	AGE
7	MXP	MXN	LOC	DUR	ECT	REL	DEN	SUR	EXP	COH	CTC	AGE	PPE	NBI	BAR
8	MXP	NBI	DUR	LOC	ECT	DEN	MXN	CTC	BAR	AGE	REL	EXP	PPE	SUR	COH
9	COH	DEN	LOC	DUR	MXP	MXN	REL	NBI	SUR	BAR	CTC	EXP	AGE	PPE	ECT
10	CTC	DUR	MXN	LOC	REL	NBI	MXP	ECT	SUR	BAR	DEN	PPE	AGE	COH	EXP
11	LOC	EXP	NBI	DEN	ECT	REL	COH	PPE	AGE	CTC	MXP	SUR	DUR	MXN	BAR
12	LOC	NBI	CTC	DEN	MXN	EXP	DUR	AGE	SUR	ECT	REL	PPE	MXP	COH	BAR
13	LOC	EXP	MXP	CTC	NBI	REL	DEN	AGE	SUR	MXN	COH	PPE	ECT	DUR	BAR
14	LOC	COH	DUR	CTC	BAR	REL	ECT	SUR	AGE	PPE	DEN	NBI	MXP	MXN	EXP
15	LOC	MXP	DUR	DEN	REL	ECT	BAR	EXP	SUR	NBI	MXN	COH	AGE	CTC	PPE

Abbreviations: AGE, age structure of participants; BAR, engineering controls—use of physical barriers and environmental cleaning; CTC, contact between participants; COH, use of cohorting; DEN, density of crowd; DUR, duration of event; ECT, ease of contact tracing; EXP, level of expelled air; LOC, location and ventilation; MXN, mixing of networks; MXP, mixing of participants; NBI, number of households; PPE, personal protective equipment; REL, related activity; SUR, shared equipment or surfaces

[a] Responses correspond to individual expert rankings

Table 4: Consensus ranking (mode) of criteria under generalized Mallows models using the Kendall and Hamming distance

Category	Code	Criteria	Kendall	Hamming
Critical	DEN	Density of crowd	1	2
	CTC	Contact between participants	2	3
	LOC	Location and ventilation	3	1
Important	NBI	Number of households (or individuals)	4	4
	EXP	Level of expelled air (of activity)	5	10
	DUR	Duration of event	6	6
	PPE	Personal protective equipment—use of masks or face coverings	7	5
	MXP	Mixing of participants	8	8
	MXN	Mixing of networks	9	7
Good to consider	BAR	Engineering controls—use of physical barriers and environmental cleaning	10	12
	REL	Related activity (e.g. shared group travel)	11	9
	COH	Administrative scheduling—use of cohorting to stagger participants and reduce contacts	12	13
	AGE	Age structure of participants in population	13	14
	SUR	Shared equipment or surfaces	14	11
If time permits	ECT	Ease of contact tracing should an outbreak occur	15	15

Abbreviations: AGE, age structure of participants; BAR, engineering controls—use of physical barriers and environmental cleaning; CTC, contact between participants; COH, use of cohorting; DEN, density of crowd; DUR, duration of event; ECT, ease of contact tracing; EXP, level of expelled air; LOC, location and ventilation; MXN, mixing of networks; MXP, mixing of participants; NBI, number of households; PPE, personal protective equipment; REL, related activity; SUR, shared equipment or surfaces

Location and ventilation and ease of contact tracing were the criteria on which experts most strongly agreed in terms of absolute rank ordering (i.e. most important and least important criteria). Location and ventilation appears exclusively in the first seven ranks and almost always (n=14/15 times) in the first four ranks. Criteria with stronger disagreement among experts regarding absolute rank position were number of households or individuals and level of expelled air.

Criteria categorization based on combined consensus rankings

Criteria were placed into categories based on their level of agreement between experts and combined Kendall and Hamming rank orderings (Table 4). Four categories were created as a result of these ranking agreements among experts: "critical"; "important"; "good to consider"; and "if time permits".

Categories 1 and 2: Critical and important criteria

The first set of criteria ("critical") consisted of three criteria that were consistently ranked within the first few positions by experts: 1) density of the crowd; 2) contact between participants; and 3) location and ventilation.

The second set of criteria ("important") were almost consistently ranked within the top half of the ranking by experts (with the exception of level of expelled air), though some variability in specific rank positioning was observed among experts: 1) number of households; 2) level of expelled air (of activity); 3) duration of the event or activity; 4) use of personal protective equipment; 5) mixing of networks; and 6) mixing of participants. While level of expelled air showed wide variation in expert ranking (present in the top half for some experts and the bottom half for others); given available literature data on this criterion, it was placed in the "important" category.

Categories 3 and 4: Good to consider and if time permits criteria

The third set ("good to consider") consisted of five criteria. Experts generally ranked these criteria in the lower half of their rankings, though relative importance attributed to each criteria varied between experts. This set included the following: 1) the use of engineering controls and environmental cleaning; 2) related activity; 3) administrative scheduling; 4) age structure of participants; and 5) shared equipment or surfaces. Finally, given very strong agreement for the rank positioning of the last criterion, ease of contact tracing, which was almost consistently ranked last among experts, this criterion was placed in the "if time permits" category.

Discussion

This project aimed to identify key factors (criteria) to consider when making decisions around COVID-19 transmission risk in various settings where people gather. The use of generalized Mallows models allowed for the analysis and quantification of the consensus among experts on the rank importance of different transmission risk factors (criteria). A lack of approximate consensus on a given criterion can lead to large differences between models with different metrics; however, using the Kendall and Hamming metrics, broad consensus was found among the most important and least important criteria.

The consensus-ranked list of transmission criteria and corresponding categories resulting from this exercise contribute to a framework for ranking settings for COVID-19 transmission risk based on criteria identified from both the literature and expert opinion. How a setting is evaluated or scored with respect to a specific criterion will depend on a range of factors specific to the local community where the evaluation is undertaken, including local transmission, public health measures in place, current adoption of those measures by the local population and setting-specific characteristics.

Although this framework is intended to assist in evaluating transmission risk, all risk assessments should be performed in the context of the local epidemiology and with consideration of the specific characteristics of the gathering/event/venue being evaluated. A ranking of transmission risk of settings produced in one geographical location will not necessarily be the same as that performed in another geographical location due to local epidemiological variation even if the same criteria are used.

Based on the formative research conducted, the consensus list captures elements that are most directly related to transmission risk. When evaluating settings and their risk for transmission, it is important to keep in mind the activities performed on site and their related contexts since related activities may affect transmission risk; e.g. shared transport to the setting or shared accommodations. These related activities may present additional opportunities for transmission that may be important to consider for inclusion in the risk assessment.

Many of the criteria presented are inter-related or synergistic and, as a result, may be difficult to evaluate individually (e.g. the number of participants at an event and the density of the crowd). The use of scenarios may help tease apart some of these factors. For example, a scenario could be defined to evaluate transmission risk when a certain percentage of the population is vaccinated, and a separate scenario defined to consider a different target vaccination percentage. Alternate scenarios could be defined to consider different levels of community transmission as local prevalence of COVID-19 will change the likelihood of encountering an infected individual. Expert review

and discussion of the evaluations is also important as it will promote cross-examination and consideration of a broad set of local factors.

Operationalization of this list and resulting categories is left to the discretion of regional public health experts, though some suggestions are discussed. Assessment as part of a multi-step MCDA process would enable a systematic evaluation between settings; however, a full illustration of this approach is beyond the scope of this article.

Variant of concern considerations

Transmission risk evaluation will continue to be necessary until sufficient vaccination coverage can be reached to achieve herd immunity. With the emergence of VOCs across the country, additional waves of cases may continue to threaten healthcare capacity in Canada despite vaccine rollout. As such, our experts were consulted once again in March 2021 to see if their rankings of the criteria would change given the emergence of VOCs. Given a lack of evidence that VOCs affect transmission risk differently, the experts that responded (n=10/15) left their rankings unchanged. This should be monitored as further knowledge is gathered on the subject.

Using the criteria for evaluation of settings and gatherings and limitations

Although a full multi-criteria evaluation of settings is outside of the scope of the current paper, some guidelines on the use of the criteria for evaluating settings are suggested below. Software packages exist for MCDA analysis, including a recently developed free package for R (https://cran.r-project.org/web/packages/MCDA/MCDA.pdf) and other academic or paid software options. These software packages allow MCDA analysis without the need for statistical experts to carry out the evaluations.

Before undertaking an evaluation of settings, the scope and scale of the assessment should be clearly defined. For example, it is important to define whether the evaluation is being performed to assess the daily exposure of individuals to transmission at any given setting versus assessment of the daily exposure of individuals working all day at a setting since a setting may pose different risks to a casual visitor versus an employee who is exposed over several hours. It is important to consider whether specific subgroups are to be considered in the assessment; for example, are clinically-vulnerable individuals included in the scope or is a separate assessment required to properly assess this subgroup? As settings are considered for inclusion, creating a description of the setting in the context being assessed is useful (e.g. in a grocery store—where a typical visit generally lasts approximately 15 minutes—masks are currently mandatory). Additional variations of settings can be added to assess variations that may be relevant to consider (e.g. variations where mask use is not mandatory, etc.). A quick review of the criteria should be undertaken by the experts participating in the process to assess whether all proposed criteria remain relevant to the local context (e.g. a criterion for which all settings have the same score is not discriminating and may be omitted from the evaluation).

Depending on the data available to a decision-maker for assessing settings, and taking into account levels of uncertainty, variability and missing data, the essential and important criteria should be evaluated where possible as a first level of assessment of COVID-19 transmission risk between settings. Expert judgement and opinion can be used to fill in missing data. If sufficient information is available or can be appropriately assessed by experts, a more complete MCDA-style assessment of settings can be undertaken. A systematic evaluation process, such as offered by an MCDA evaluation, can be used to better understand the relative transmission risk between settings and, in particular, to highlight the strongest contributing factors as well as strongest protective factors for transmission risk between settings. This type of evaluation could help inform where mitigation measures should be considered to help reduce transmission risk. A setting that has criteria that score as poor or insufficient should be considered for mitigation and potential monitoring of transmission risk. As previously suggested, the use of scenarios can also be used to consider the changing epidemiology and its impact on transmission. For example, scenarios with different levels of vaccination, new levels of dominance of a VOC and levels of community transmission can be defined and used to evaluate how they may affect relative transmission risk of settings.

Depending on the data available and levels of uncertainty around these data, any resulting ranking will not represent a strict absolute assessment or ranking of settings, but rather a working local evaluation that reflects the information available and the relevant experts participating in the process.

As a reminder, the use of this framework is meant to help inform decision-making around transmission risk rather than make decisions, since other factors should be considered in a decision-making process around closures. To conduct a more complete assessment of closures/re-openings, additional dimensions beyond transmission risk factors alone such as social considerations, economic and other health factors could be considered for inclusion in a multi-step participatory MCDA process.

Conclusion

This project drew upon the latest evidence concerning transmission risk factors for COVID-19 in venues from which criteria for the evaluation of transmission risk was developed and then evaluated by experts. The resulting consensus list constitutes a set of important generic elements that can be applied to any setting as an objective and transparent framework to assess transmission risk in the venue. With further

consideration of the local epidemiology of COVID-19, an overall risk of transmission assessment can be established. This work focused on the factors most directly related to COVID-19 transmission as a first level of concern in evaluating settings. Depending on the decision-making context (e.g. decisions around closures or re-openings) additional factors should be considered for inclusion in the decision-making process, including economic and social impacts. Additional layers of information could be added to the participatory MCDA process to include economic, social and health criteria so that trade-offs could be more fully examined, allowing for more informed decisions by decision-makers around closures and re-openings to reduce the transmission risk of COVID-19.

Authors' statement

VH — Conception and design, data acquisition and interpretation, writing–original draft, review and editing
DM & JL — Data acquisition, data analysis, writing–review and editing
AF, AO, PT and NHO — Conception and design, revising and editing of writing and critical review
LW — Interpretation, revising and editing of writing and critical review

Competing interests

None.

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References

1. World Health Organization. Novel coronavirus (2019-nCoV) Situation Report. Geneva, Switzerland: WHO; 21 January 2020 (accessed 2021-03-01). www.who.int/docs/default-source/coronaviruse/situation-reports/20200121-sitrep-1-2019-ncov.pdf

2. Government of Canada. COVID-19 daily epidemiology update. Ottawa (ON): Government of Canada; (updated 2021-09-15; accessed 2021-04-26). https://www.canada.ca/en/public-health/services/diseases/2019-novel-coronavirus-infection/health-professionals/epidemiological-summary-covid-19-cases.html#a4

3. Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, Zhang L, Fan G, Xu J, Gu X, Cheng Z, Yu T, Xia J, Wei Y, Wu W, Xie X, Yin W, Li H, Liu M, Xiao Y, Gao H, Guo L, Xie J, Wang G, Jiang R, Gao Z, Jin Q, Wang J, Cao B. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet 2020;395(10223):497–506. DOI PubMed

4. Detsky AS, Bogoch II. COVID-19 in Canada: experience and Response. JAMA 2020;324(8):743–4. DOI PubMed

5. Adams-Prassl A, Boneva T, Golin M, Rauh C. Inequality in the impact of the coronavirus shock: Evidence from real time surveys. J Public Econ 2020;189:104245. DOI

6. Blundell R, Costa Dias M, Joyce R, Xu X. COVID-19 and Inequalities. Fisc Stud 2020. DOI PubMed

7. Brodeur A, Gray D, Islam A, Bhuiyan S. A literature review of the economics of COVID-19. J Econ Surv 2021. DOI PubMed

8. Calderón-Larrañaga A, Dekhtyar S, Vetrano DL, Bellander T, Fratiglioni L. COVID-19: Risk accumulation among biologically and socially vulnerable older populations. Ageing Res Rev 2020;63:101149. DOI PubMed

9. Engzell P, Frey A, Verhagen MD. Learning inequality during the COVID-19 pandemic. 2020; SocArXiv ve4z7, Center for Open Science. https://osf.io/preprints/socarxiv/ve4z7/

10. Nicola M, Alsafi Z, Sohrabi C, Kerwan A, Al-Jabir A, Iosifidis C, Agha M, Agha R. The socio-economic implications of the coronavirus pandemic (COVID-19): A review. Int J Surg 2020;78:185–93. DOI PubMed

11. Rossi R, Socci V, Talevi D, Mensi S, Niolu C, Pacitti F, Di Marco A, Rossi A, Siracusano A, Di Lorenzo G. COVID-19 pandemic and lockdown measures impact on mental health among the general population in Italy. Front Psychiatry 2020;11:790. DOI PubMed

12. Serafini G, Parmigiani B, Amerio A, Aguglia A, Sher L, Amore M. The psychological impact of COVID-19 on the mental health in the general population. QJM 2020;113(8):531–7. DOI PubMed

13. Behzadian M, Kazemzadeh RB, Albadvi A, Aghdasi M. PROMETHEE: A comprehensive literature review on methodologies and applications. Eur J Oper Res 2010;200(1):198–215. DOI

14. Satterthwaite MA. Strategy-proofness and Arrow's conditions: existence and correspondence theorems for voting procedures and social welfare functions. J Econ Theory 1975;10(2):187–217. DOI

15. Fligner MA, Verducci JS. Distance based ranking models. J R Stat Soc B 1986;48(3):359–69. DOI

16. Brandl M, Selb R, Seidl-Pillmeier S, Marosevic D, Buchholz U, Rehmet S. Mass gathering events and undetected transmission of SARS-CoV-2 in vulnerable populations leading to an outbreak with high case fatality ratio in the district of Tirschenreuth, Germany. Epidemiol Infect 2020;148:e252. DOI PubMed

17. Dalton C, Katelaris A, Wilson N. Open with Care: Minimising COVID-19 Superspreading Settings in Australia. SSRN. June 22, 2020. DOI

18. European Centre for Disease Prevention and Control. COVID-19 clusters and outbreaks in occupational settings in the EU/EEA and the UK. Solna, Sweden. ECDC; (updated 2020-08-11). https://www.ecdc.europa.eu/en/publications-data/covid-19-clusters-and-outbreaks-occupational-settings-eueea-and-uk

19. Liu Y, Eggo RM, Kucharski AJ. Secondary attack rate and superspreading events for SARS-CoV-2. Lancet 2020;395(10227):e47. DOI PubMed

20. Nishiura H, Oshitani H, Kobayashi T, Saito T, Sunagawa T, Mutsui T, Wakita T, MHLW COVID-19 Response Team, Suzuki M. Closed environments facilitate secondary transmission of coronavirus disease 2019 (COVID-19). medRxiv 2020.02.28.20029272. DOI

21. Weed M, Foad A. Rapid scoping review of evidence of outdoor transmission of COVID-19. medRxiv. 2020.09.04.20188417. DOI

22. Public Health Agency of Canada. National Collaborating Centre for Methods and Tools. Evidence Brief of Size of Gatherings and Characteristics of High Risk Transmission Events 2020. Ottawa (ON): PHAC; 2020. https://www.nccmt.ca/covid-19/covid-19-evidence-reviews/194

23. Lednicky JA, Lauzardo M, Fan ZH, Jutla A, Tilly TB, Gangwar M, Usmani M, Shankar SN, Mohamed K, Eiguren-Fernandez A, Stephenson CJ, Alam MM, Elbadry MA, Loeb JC, Subramaniam K, Waltzek TB, Cherabuddi K, Morris JG Jr, Wu CY. Viable SARS-CoV-2 in the air of a hospital room with COVID-19 patients. Int J Infect Dis 2020;100:476–82. DOI PubMed

24. Leclerc QJ, Fuller NM, Knight LE, Funk S, Knight GM; CMMID COVID-19 Working Group. What settings have been linked to SARS-CoV-2 transmission clusters? Wellcome Open Res 2020;5:83. DOI PubMed

25. Lakha F, Rudge JW, Holt H. Rapid synthesis of evidence on settings which have been associated with SARS-CoV-2 transmission clusters. 2020 (accessed 2020-12-05). https://superspreadingdatabase.github.io/Evidence_on_clusters_final.pdf

26. Scott N, Palmer A, Delport D, Abeysuriya R, Stuart R, Kerr CC, Mistry D, Klein D, Sacks-Davis R, Heath K, Hainsworth S, Pedrana A, Stoove M, Wilson D, Hellard ME. Modelling the impact of reducing control measures on the COVID-19 pandemic in a low transmission setting. Med J Aust 2020;214(2):79–83. DOI PubMed

27. Sneppen K, Taylor RJ, Simonsen L. Impact of Superspreaders on dissemination and mitigation of COVID-19. medRxiv. 2020.05.17.20104745. DOI

28. Health Information and Quality Authority. Evidence summary on activities or settings associated with a higher risk of SARS-CoV-2 transmission. HIQA; 2020 (accessed 2021-03-15). https://www.hiqa.ie/sites/default/files/2020-11/Evidence-summary-activities-and-settings-at-higher-risk.pdf

29. Adam DC, Wu P, Wong JY, Lau EH, Tsang TK, Cauchemez S, Leung GM, Cowling BJ. Clustering and superspreading potential of SARS-CoV-2 infections in Hong Kong. Nat Med 2020;26(11):1714–9. DOI PubMed

30. Brauner JM, Mindermann S, Sharma M, Johnston D, Salvatier J, Gavenciak T, Stephenson AB, Leech G, Altman G, Mikulik V, Norman AJ, Monrad JT, Besiroglu T, Ge H, Hartwick MA, The YW, Chindelevitch L, Gal Y Kulveit J. The effectiveness of eight nonpharmaceutical interventions against COVID-19 in 41 countries. medRxiv. 2020.05.28.20116129. DOI

31. Esra RT, Jamesion L, Fox MP, Letswalo D, Ngcobo N, Mngadi S, Estill J, Meyer-Rath G, Keiser O. Evaluating the impact of non-pharmaceutical interventions for SARS-CoV-2 on a global scale. medRxiv. 2020.07.30.20164939. DOI

32. Morawska L, Tang JW, Bahnfleth W, Bluyssen PM, Boerstra A, Buonanno G, Cao J, Dancer S, Floto A, Franchimon F, Haworth C, Hogeling J, Isaxon C, Jimenez JL, Kurnitski J, Li Y, Loomans M, Marks G, Marr LC, Mazzarella L, Melikov AK, Miller S, Milton DK, Nazaroff W, Nielsen PV, Noakes C, Peccia J, Querol X, Sekhar C, Seppänen O, Tanabe SI, Tellier R, Tham KW, Wargocki P, Wierzbicka A, Yao M. How can airborne transmission of COVID-19 indoors be minimised? Environ Int 2020;142:105832. DOI PubMed

33. Walker A, Houwaart T, Wienemann T, Vasconcelos MK, Strelow D, Senff T, Hülse L, Adams O, Andree M, Hauka S, Feldt T, Jensen BE, Keitel V, Kindgen-Milles D, Timm J, Pfeffer K, Dilthey AT. Genetic structure of SARS-CoV-2 reflects clonal superspreading and multiple independent introduction events, North-Rhine Westphalia, Germany, February and March 2020. Euro Surveill 2020;25(22):2000746. DOI PubMed

34. Dyal JW, Grant MP, Broadwater K, Bjork A, Waltenburg MA, Gibbins JD, Hale C, Silver M, Fischer M, Steinberg J, Basler CA, Jacobs JR, Kennedy ED, Tomasi S, Trout D, Hornsby-Myers J, Oussayef NL, Delaney LJ, Patel K, Shetty V, Kline KE, Schroeder B, Herlihy RK, House J, Jervis R, Clayton JL, Ortbahn D, Austin C, Berl E, Moore Z, Buss BF, Stover D, Westergaard R, Pray I, DeBolt M, Person A, Gabel J, Kittle TS, Hendren P, Rhea C, Holsinger C, Dunn J, Turabelidze G, Ahmed FS, deFijter S, Pedati CS, Rattay K, Smith EE, Luna-Pinto C, Cooley LA, Saydah S, Preacely ND, Maddox RA, Lundeen E, Goodwin B, Karpathy SE, Griffing S, Jenkins MM, Lowry G, Schwarz RD, Yoder J, Peacock G, Walke HT, Rose DA, Honein MA. COVID-19 among workers in meat and poultry processing facilities—19 states, April 2020. MMWR Morb Mortal Wkly Rep 2020;69(18):557–61. DOI PubMed

35. Kucharski AJ, Klepac P, Conlan AJ, Kissler SM, Tang ML, Fry H, Gog JR, Edmunds WJ; CMMID COVID-19 working group. Effectiveness of isolation, testing, contact tracing, and physical distancing on reducing transmission of SARS-CoV-2 in different settings: a mathematical modelling study. Lancet Infect Dis 2020;20(10):1151–60. DOI PubMed

36. Kretzschmar ME, Rozhnova G, Bootsma MC, van Boven M, van de Wijgert JH, Bonten MJ. Impact of delays on effectiveness of contact tracing strategies for COVID-19: A modelling study. Lancet Public Health 2020;5(8):e452–9. DOI PubMed

37. Shaw AK, White LA, Michalska-Smith M, Borer ET, Craft ME, Seabloom EW, Snell-Rood EC, Travisano M. Lessons from movement ecology for the return to work: modeling contacts and the spread of COVID-19. PLoS One 2021;16(1):e0242955. DOI PubMed

38. Rafeemanesh E, Ahmadi F, Memarzadeh M. A review of the strategies and studies on the prevention and control of the new coronavirus in workplaces. Arch Bone Jt Surg 2020;8 (Suppl1):242–6. DOI PubMed

39. Charlotte N. High rate of SARS-CoV-2 transmission due to choir practice in France at the beginning of the COVID-19 pandemic. J Voice 2020;S0892-1997(20)30452-5. Epub ahead of print. DOI PubMed

40. Prakash MK. Eat, Pray, Work: A meta-analysis of COVID-19 Transmission Risk in Common Activities of Work and Leisure. medRxiv. 2020.05.22.20110726. DOI

41. Hamner L, Dubbel P, Capron I, Ross A, Jordan A, Lee J, Lynn J, Ball A, Narwal S, Russell S, Patrick D, Leibrand H. High SARS-CoV-2 attack rate following exposure at a choir practice—Skagit County, Washington, March 2020. MMWR Morb Mortal Wkly Rep 2020;69(19):606–10. DOI PubMed

42. Kohanski MA, Lo LJ, Waring MS. Review of indoor aerosol generation, transport, and control in the context of COVID-19. Int Forum Allergy Rhinol 2020;10(10):1173–9. DOI PubMed

43. Public Health Agency of Canada. National Collaborating Centre for Methods and Tools. Rapid Review on SARS-CoV-2 Aerosol Transmission, Update 2. Ottawa (ON): PHAC; 2021. https://www.nccmt.ca/covid-19/covid-19-evidence-reviews/418

44. Moritz S, Gottschick C, Horn J, Popp M, Langer S, Klee B, Purschke O, Gekle M, Ihling A, Mikolajczyk R. The risk of indoor sports and culture events for the transmission of COCID-19 (Restart-19). medRxiv. 2020.10.28.20221580. DOI

45. Miller SL, Nazaroff WW, Jimenez JL, Boerstra A, Buonanno G, Dancer SJ, Kurnitski J, Marr LC, Morawska L, Noakes C. Transmission of SARS-CoV-2 by inhalation of respiratory aerosol in the Skagit Valley Chorale superspreading event. Indoor Air 2021;31(2):314–23. DOI PubMed

46. Davies NG, Klepac P, Liu Y, Prem K, Jit M, Eggo RM; CMMID COVID-19 working group. Age-dependent effects in the transmission and control of COVID-19 epidemics. Nat Med 2020;26(8):1205–11. DOI PubMed

47. Levin AT, Hanage WP, Owusu-Boaitey N, Cochran KB, Walsh SP, Meyerowitz-Katz G. Assessing the age specificity of infection fatality rates for COVID-19: systematic review, meta-analysis, and public policy implications. Eur J Epidemiol 2020;35(12):1123–38. DOI PubMed

48. Kang SJ, Jung SI. Age-related morbidity and mortality among patients with COVID-19. Infect Chemother 2020;52(2):154–64. DOI PubMed

49. Kim L, Garg S, O'Halloran A, Whitaker M, Pham H, Anderson EJ, Armistead I, Bennett NM, Billing L, Como-Sabetti K, Hill M, Kim S, Monroe ML, Muse A, Reingold AL, Schaffner W, Sutton M, Talbot HK, Torres SM, Yousey-Hindes K, Holstein R, Cummings C, Brammer L, Hall AJ, Fry AM, Langley GE. Risk factors for intensive care unit admission and in-hospital mortality among hospitalized adults identified through the US coronavirus disease 2019 (COVID-19)-associated hospitalization surveillance network (COVID-NET). Clin Infect Dis 2021;72(9):e206–14. DOI PubMed

50. Liu X, Zhang S. COVID-19: face masks and human-to-human transmission. Influenza Other Respir Viruses 2020;14(4):472–3. DOI PubMed

51. Public Health Agency of Canada. National Collaborating Centre for Methods and Tools. Evidence Brief on the use of Face Masks to Prevent COVID-19 in Community Settings. Ottawa (ON): PHAC; 2020 (accessed 2020-12-05). https://www.nccmt.ca/covid-19/covid-19-evidence-reviews/246

52. van Doremalen N, Bushmaker T, Morris DH, Holbrook MG, Gamble A, Williamson BN, Tamin A, Harcourt JL, Thornburg NJ, Gerber SI, Lloyd-Smith JO, de Wit E, Munster VJ. Aerosol and surface stability of SARS-CoV-2 as compared with SARS-CoV-1. N Engl J Med 2020;382(16):1564–7. DOI PubMed

53. James A, Eagle L, Phillips C, Hedges DS, Bodenhamer C, Brown R, Wheeler JG, Kirking H. High COVID-19 attack rate among attendees at events at a church—Arkansas, March 2020. MMWR Morb Mortal Wkly Rep 2020;69(20):632–5. DOI PubMed

54. Ong SW, Tan YK, Chia PY, Lee TH, Ng OT, Wong MS, Marimuthu K. Air, surface environmental, and personal protective equipment contamination by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from a symptomatic patient. JAMA 2020;323(16):1610–2. DOI PubMed

55. Arrow KJ. A difficulty in the concept of social welfare. J Polit Econ 1950;58(4):328–46. DOI

56. Gibbard A. Manipulation of voting schemes: a general result. Econom Soc. 1973;41(4):587–601. https://www.jstor.org/stable/1914083

57. Mallows CL. Non-null ranking models. I. Biometrika 1957;44(1/2):114–30. DOI

Appendix

A1: Rank orderings and generalized Mallows models

Imagine that we have a set of N rankings over n choices. In our case, N represents the number of experts and n denotes the criteria (items). The problem is to find the consensus ranking among the experts, which best agrees with the N rankings offered by the experts.

Consensus ranking finds application in social welfare analysis. In 1950, Kenneth Arrow showed (55) that if a decision-making body consists of at least two members with at least three options to decide among, then it is impossible to design a social welfare function that simultaneously satisfies all the reasonable requirements of a fair system:

- If every voter prefers alternative X over alternative Y, then the group prefers X over Y
- If every voter's preference between X and Y remains unchanged, then the group's preference between X and Y will also remain unchanged (even if voters' preferences between other pairs like X and Z, Y and Z, or Z and W change)
- There is no dictator: no single voter possesses the power to always determine the group's preference

Arrow's impossibility theorem has several technical conditions in its formal statement (see section A3) which defines the "fair" system. While the theorem tells us that no deterministic preferential voting system exists which satisfies the technical fairness requirements, in practice all systems do not work poorly at all times. The impossibility theorem finds application in the study of voting systems and important results can be found in (14,56).

Rankings consist of bijections of the set of integers $\{1,2,3,...,n\}$ onto themselves. We will denote rankings with the symbols π and σ. For example, the ranking $\pi = \{2,4,1,3\}$ means that item 1 is ranked second, which we denote as $\pi(1) = 2$; item two is ranked fourth, $\pi(2) = 4$. Every ranking has an inverse π^{-1} which gives the items in terms of the ranks: $\pi \cdot \pi^{-1} = e = \{1,2,3,...,n\}$. Given a set of rankings, we would like to find the center or the consensus of the set over some distance measure between rankings. There are many distance metric for rankings, but in this article we will focus on two of the most popular: the Kendall distance and the Hamming distance. For any distance measure $d(\cdot,\cdot)$ we have $d(\sigma,\pi) = d(\sigma\pi^{-1}, e)$. When the reference ranking is the identity ranking e, we use the notion $d(\sigma,e) = d(\sigma)$.

The Kendall distance between two ranking π and σ is defined by,

Equation 1:

$$d_k(\pi, \sigma) = \sum_{\substack{l \prec j \\ \pi}} 1\left[j \precsim_{\sigma} l\right]$$

The notation $l \prec_{\pi} j$ means that item l precedes j in ranking π. The Kendall distance counts the number of pairwise discrepancies between rankings. With n items, the largest Kendall distance between any two rankings is $n(n-1)/2$. On the other hand, the Hamming distance $d_h(\pi, \sigma)$ counts the number of positions that disagree between two rankings,

Equation 2:

$$d_k(\pi, \sigma) = \sum_{j=1}^{n} 1\left[\pi(j) \neq \sigma(j)\right]$$

Thus, the Hamming distance takes values between 2 and n inclusively. The Kendall and Hamming distance measures have the important property that they can be decomposed as a sum over $n-1$ and n terms respectively,

Equation 3

$$d_k(\pi, \sigma) = \sum_{j=1}^{n-1} V_j(\pi\sigma^{-1}),$$

$$d_h(\pi, \sigma) = \sum_{j=1}^{n} H_j(\pi\sigma^{-1}),$$

where,

Equation 4:

$$V_j(\sigma) = \sum_{l>j} 1\left[l <_{\sigma} j\right],$$

Equation 5:

$$H_j(\sigma) = \begin{cases} 0, \text{ iff } \sigma(j) = j, \\ 1, \text{ otherwise.} \end{cases}$$

Given a metric for computing distances between rankings, we can build a probability measure over the space. Mallows model (14) is an exponential location probability model over the rankings defined by a central ranking, σ_0, and a dispersion parameter, θ, namely,

Equation 6:

$$P(\pi) = \frac{e^{-\theta\, d_{k,h}(\pi,\sigma_0)}}{\psi(\theta)},$$

where $\psi(\theta)$ is a normalization constant. In a sense, the Mallows model is the extension of the Gaussian distribution to rankings. When $\theta > 0$, the ranking σ_0 is the mode of the distribution—the consensus—and as θ increases the distribution becomes more sharply peaked around σ_0. If $\theta > 0$, σ_0 becomes the anti-mode.

We see that in the Mallows model, all rankings with the same distance from σ_0 are degenerate in probability. With distance measures that decomposed as a sum like those in equation 3, we can break the degeneracy by attaching θ_j to each component of the sum (57). For the Kendall and Hamming distance, the Mallows model generalizes using discrepancy measures

Equation 7:

$$d_k(\pi, \pi_0;\boldsymbol{\theta}) = \sum_{j=1}^{n-1} \theta_j V_j(\pi\pi_0^{-1}),$$

$$d_h(\pi, \pi_0;\boldsymbol{\theta}) = \sum_{j=1}^{n} \theta_j H_j(\pi\pi_0^{-1}),$$

such that

Equation 8:

$$P(\pi) = \frac{e^{d_{k,h}(\pi,\sigma_0;\boldsymbol{\theta})}}{\psi(\theta)},$$

where $\theta = (\theta_1,\theta_2,\cdots)$. The central ranking σ_0 and θ can be estimated by maximum likelihood or other approximate techniques.

The value of $V_j(\sigma)$ in equation 3 gives the number of items in $j+1{:}n$ which are ranked before j in σ. Therefore, the parameters θ_j reflect the strength of a ranking around the consensus $\sigma_0(j) = i$ in that the larger θ_j the larger the probability that $\pi(j) \leq i$. That is, large θ_j in the generalized Mallows model with the Kendall distance implies that item j is ranking in the first i positions with high probability across all the rankings. Similarly, $H_j(\sigma)$ of the Hamming distance counts the rank discrepancies. Thus, the parameter θ_j corresponds to the strength of consensus at rank j; large θ_j implies high agreement on the item at the j-th rank.

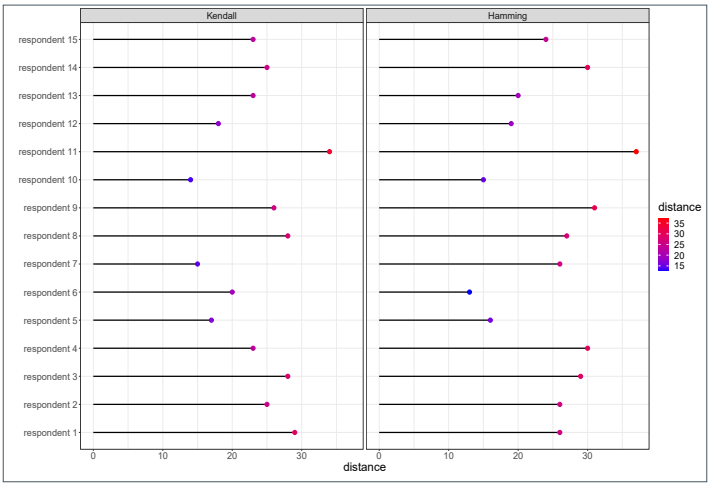
A2: Hamming parameters

To better see the strength of consensus in the rankings across items, the Hamming θ_j parameters against the cross-entropy of a criterion's rank is shown in Figure A1. The cross-entropy measures the amount of impurity in the ranks,

$$e_j = -\sum_{i=1}^{15} p_{ij} \log(p_{ij})$$

where j is the item label, i denotes the rank, and p_{ij} gives the probability of the i-th rank for item j. Criteria with large rank dispersion have high cross-entropy. The Hamming θ_j parameters also measure the strength of consensus at a given rank. Figure A1 shows criteria separating into three basic clusters with increasing consensus appearing towards the southeast corner of the plot. Under the Hamming model, the respondents have particularity strong agreement on the criteria at rank 1, 2 and 15.

Figure A1: Kendall and Hamming distances of each respondent's ranking from the generalized Mallows model rankings



A3: Formal conditions of Arrow's Impossibility Theorem

Suppose that we are asked to extract a preference order on a given set of options for society. Each individual provides a preference order on the set of outcomes. We desire a ranked voting electoral system, the preference aggregation rule or social welfare function, which transforms the set of preferences into a single global societal preference order. Arrow's theorem says that if there are at least two members in the society and at least three options to decide among, then it is impossible to design a preference aggregation rule that satisfies all of the conditions below at once (conditions assumed to define a "fair system"):

- **Non-dictatorship:** The social welfare function should account for the wishes of all voters

- **Unrestricted domain, or universality:** Each set of individual voter preferences should produce a unique and complete ranking of societal choices from the social welfare function. Thus:
  - It must result in a complete ranking of preferences for society
  - It must be deterministic; each time the preferences are presented in the same way, the welfare function generates the same societal preference order
- **Independence of irrelevant alternatives (IIA):** The social preference between two choices should depend only on the individual preferences between changes in rankings of irrelevant alternatives should have no impact on the societal ranking
- **Monotonicity, or positive association of social and individual values:** If any individual changes a preference order by promoting a choice, then the societal preference order should either promote that same choice in the new ranking or leave it at the same position. An individual should not be able to penalize a choice by increasing its preference
- **Non-imposition, or citizen sovereignty:** Every possible societal preference order should be achievable by some set of individual preferences

Multisystem inflammatory syndrome in children in Canada

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Abstract

This article provides a summary of the epidemiology of multisystem inflammatory syndrome in children (MIS-C) cases reported nationally in Canada by provincial and territorial health authorities. Multisystem inflammatory syndrome in children is a post-viral inflammatory syndrome that temporally follows coronavirus disease 2019 (COVID-19). Symptoms may include fever, abdominal pain, vomiting, diarrhea, skin rash and other signs of inflammation. In Canada, MIS-C is rare, with 269 cases reported to the Public Health Agency of Canada between March 11, 2020 and October 2, 2021. One hundred forty-two (53%) of these cases were lab-confirmed COVID-19 cases or epidemiologically-linked with COVID-19 cases. Cases have been reported in infants as young as one week to youth as old as 18 years, with a median age of six years. Cases were more likely to occur in males than females (58% vs 42%, respectively; p=0.006). Almost all MIS-C cases (99%) required hospitalization and 36% required intensive care unit admission. No deaths have been reported to date. The time trend of MIS-C aligns with the incidence rate time trend of COVID-19 reported in children, with a two to six-week lag.

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Keywords: inflammatory syndrome, COVID-19, children's health, surveillance, MIS-C

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Introduction

Since the emergence of the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) that causes coronavirus disease 2019 (COVID-19), data on children and youth aged 19 years and younger infected with SARS-CoV-2 indicate that they usually experience mild disease with less severe outcomes compared with adults. However, on April 26, 2020, clinicians in the United Kingdom reported an increase in accounts of previously healthy children presenting with a severe inflammatory syndrome with features similar to toxic shock syndrome and incomplete Kawasaki disease (1). These cases occurred in children who tested positive for recent or current infection with SARS-CoV-2 or who had an epidemiological link to a COVID-19 case (1). Since then, additional cases of children presenting with a severe inflammatory syndrome with evidence of COVID-19 infection have been reported worldwide. This illness has been labelled multisystem inflammatory syndrome in children (MIS-C) by the Centers for Disease Control and Prevention and the World Health Organization (WHO), and is defined by the WHO as follows (2):

Children and adolescents 0–19 years of age with fever for three or more days

AND

Two of the following:

- Rash or bilateral non-purulent conjunctivitis or mucocutaneous inflammation signs (oral, hands or feet)
- Hypotension or shock
- Features of myocardial dysfunction, pericarditis, valvulitis, or coronary abnormalities (including ECHO findings or elevated troponin/N-terminal pro-brain natriuretic peptide (NT-proBNP)
- Evidence of coagulopathy (by prothrombin time, partial thromboplastin time, elevated D-dimer)
- Acute gastrointestinal problems (diarrhea, vomiting or abdominal pain)

AND

Elevated markers of inflammation such as C-reactive protein, erythrocyte sedimentation rate or procalcitonin

AND

No other obvious microbial cause of inflammation, including bacterial sepsis, staphylococcal or streptococcal shock syndromes

AND

Evidence of COVID-19 (reverse transcription polymerase chain reaction; RT-PCR, antigen test or serology positive) or likely contact with patients with COVID-19.

Canada expanded this case definition to include cases that met the WHO criteria for MIS-C, with and without COVID-19 diagnosis. This was done to capture possible cases that may have had RT-PCR testing too late in their course of infection (false negatives), and those who, more commonly in the early stages of the pandemic, may not have had access to COVID-19 testing or serology testing (3).

The Public Health Agency of Canada began collecting data on June 30, 2020 on cases of MIS-C dating back to March 11, 2020, when the pandemic was first declared. This report presents cases with illness onset from March 11, 2020 to October 2, 2021 (epidemiological week 11 of 2020 to week 39 of 2021).

Current situation

A total of 269 cases of MIS-C were reported to the Public Health Agency of Canada during the surveillance period. Data from March 11, 2020 to May 31, 2021 were available from 12 of 13 provinces and territories (PTs), of which, 11 reported lab-confirmed, epi-linked and non-COVID-19-related cases and one reported lab-confirmed cases only. Data were available from 11 PTs for the rest of surveillance period. Of the 269 cases, 127 (47%) tested positive for COVID-19 via RT-PCR, antigen test or serology and an additional 15 (6%) were epidemiologically-linked to a lab-confirmed COVID-19 case. The remaining 127 (47%) either tested negative or were not tested for COVID-19. Details on the COVID-19 testing conducted for each case were not available. The proportion of MIS-C cases among confirmed COVID-19 cases in children aged 19 years and younger was 0.039% in Canada during the surveillance period.

The characteristics of MIS-C cases reported in Canada are summarized in **Table 1**. The median age was six years old (range one week to 18 years), with 58% of cases in children ages five years and older. When cases are restricted to those with a positive COVID-19 test or epidemiological link to a confirmed case of COVID-19, the median age is eight years old (range one week to 18 years), with 70% of cases aged five years or older. This differs from Kawasaki disease, which primarily affects children younger than five years of age (4). Multisystem inflammatory syndrome in children was more likely to occur in males than females (p=0.006), with over half (58%) of reported cases in males. Nearly all (99%) of MIS-C cases required hospitalization, with 36% requiring intensive care unit admission. Where outcome information was available, the majority of cases had recovered. The remaining cases were either convalescing or stable at the time of the most recent case report update. No deaths were reported to date.

To date, the number of cases of MIS-C reported in Canada were highest from December 2020 to early March 2021. This followed a peak in the incidence of COVID-19 reported in children and

Table 1: Characteristics of reported cases of multisystem inflammatory syndrome in children according to SARS-CoV-2[a] infection status, Canada, March 11, 2020 to October 2, 2021

Characteristic	Lab-confirmed only (n=127)		Lab-confirmed and/or epidemiological link (n=142)		No known evidence of SARS-CoV-2 infection or exposure (n=127)		All patients (n=269)	
	n	%[b]	n	%	n	%	n	%
Sex								
Male	82	65	92	65	65	51	157	58
Female	45	35	50	35	62	49	112	42
Age category (years)								
Younger than 1	1	1	1	1	15	12	16	6
1–4	36	28	41	29	55	43	96	36
5–9	46	36	51	36	30	24	81	30
10–14	30	24	34	24	15	12	49	18
15–19	14	11	15	11	12	9	27	10
Range								
Median age (range in years)	8 (0–18)		8 (0–18)		4 (0–17)		6 (0–18)	
Hospitalized[c]								
Yes	127	100	142	100	125	98	267	99
No	0	0	0	0	2	2	2	1

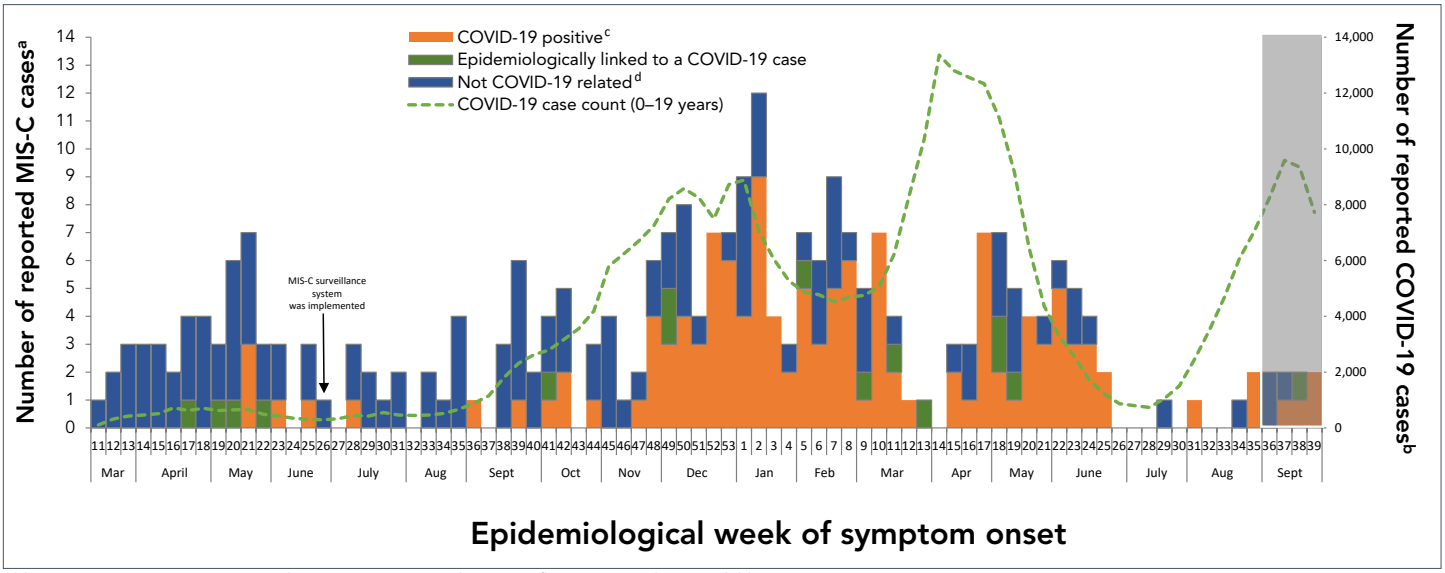
Table 1: Characteristics of reported cases of multisystem inflammatory syndrome in children according to SARS-CoV-2[a] infection status, Canada, March 11, 2020 to October 2, 2021 (*continued*)

Characteristic	Lab-confirmed only (n=127)		Lab-confirmed and/or epidemiological link (n=142)		No known evidence of SARS-CoV-2 infection or exposure (n=127)		All patients (n=269)	
	n	%[b]	n	%	n	%	n	%
ICU admission								
Yes	98	57	76	54	22	17	98	36
No	54	43	66	46	102	80	168	62
Unknown	0	0	0	0	3	2	3	1
Outcome[d]								
Recovered	72	57	82	58	102	80	184	68
Convalescing/ stable	53	42	58	41	22	17	80	30
Deteriorating	1	1	1	1	0	0	1	0
Unknown	1	1	1	1	3	2	4	1

Abbreviations: ICU, intensive care unit; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2
[a] Severe acute respiratory syndrome coronavirus 2
[b] Percentages are rounded to the nearest whole number. The sum of a category's percentages therefore may not add up to 100%
[c] One province or territory reported hospitalized cases only
[d] Patient outcomes were updated by provincial and territorial health authorities when possible. Data presented here were at the time of the most recent update

youth in December 2020 and early January 2021 (**Figure 1**). Although the incidence of COVID-19 declined from January 2021 to early March 2021, the number of MIS-C cases reported remained elevated for several reasons. First, MIS-C is a post-viral syndrome and literature reports suggest it typically manifests 2–6 weeks after SARS-CoV-2 infection (5–7). It is, therefore, expected that case numbers may remain high in the weeks following a high incidence of COVID-19. Second, COVID-19 case counts among children and youth in Canada were still high in the months of February and March 2021. As COVID-19 cases in children and youth have risen again in late March and April 2021, we can expect to see additional MIS-C cases reported following these periods.

Figure 1: Reported cases of multisystem inflammatory syndrome in children by epidemiological week of symptom onset compared with cases of COVID-19 in children and youth aged 0–19 years, Canada, March 11, 2020 to October 2, 2021(N=269)



Abbreviations: COVID-19, coronavirus disease 2019; MIS-C, multisystem inflammatory syndrome in children
[a] Data source: MIS-C National reporting from provinces and territories
[b] Data source: Coronavirus diseases 2019 national surveillance system
[c] COVID-19 positive via RT-PCR, antigen test or serology
[d] No known evidence of SARS-CoV-2 infection or exposure to a COVID-19 case
Note: The shaded area represents a period of time where it is expected that cases have occurred but have not yet been reported nationally

Strengths and limitations

The data in this report are subject to several limitations. First, data are incomplete as not all provinces and territories participated in the national surveillance of MIS-C and one province only reported cases that were lab-confirmed. Second, case reporting may also be delayed due to limited capacity at provincial and territorial health authorities. Case counts for the most recent couple of months in particular should be interpreted with caution. Third, it is difficult to discern whether cases were infected with COVID-19 or not due to several factors: RT-PCR testing may be negative if completed too late in the course of infection; serology testing may not be available; there are inherent challenges in interpreting serology results; and patients may not know that they have been in contact with a case of COVID-19. For this reason, cases with no known evidence of SARS-CoV-2 infection or exposure to a COVID-19 case were included in the analysis; however, these cases may not be COVID-19-related and, therefore, not true cases of MIS-C. Due to similarities between the symptoms of MIS-C and Kawasaki disease and the difficulties in diagnosing these diseases, there may be misclassification of cases, especially the cases without a known COVID-19 link. More detailed laboratory testing data is needed to further differentiate between cases related and unrelated to COVID-19.

Conclusion

Cases of MIS-C in Canada are rare; however, when illness does occur it is severe, with nearly all cases requiring hospitalization and one third requiring admission to the intensive care unit. All children in Canada with MIS-C have recovered or are recovering, with no deaths reported. The time trend of MIS-C aligns with the time trend of the incidence of COVID-19 in children, with a two- to six-week lag. This pattern has been reported in other publications, supporting 1) the temporal association of MIS-C with COVID-19 and 2) the current understanding that MIS-C results from a delayed immunologic response to SARS-CoV-2 infection (7). In Canada, MIS-C is more likely to occur in males then females.

Although MIS-C is rare, it is serious, and it is not yet known why some children develop this syndrome and others do not. Furthermore, the long-term effects of MIS-C remain largely unknown. The most effective way to prevent cases of serious illness in children is to follow public health measures that prevent the spread of COVID-19, including physical distancing, wearing masks, hand hygiene, staying home when sick and getting vaccinated against COVID-19 when eligible. The Public Health Agency of Canada will continue to work with provincial and territorial partners to monitor cases of serious inflammatory illness in children and keep the public informed of the risk to children and youth.

Authors' statement

ML — Methodology, software, formal analysis, investigation, data curation, writing–original draft, writing–review and editing, visualization
MS — Conceptualization, writing–original draft, writing–review and editing
SGS — Conceptualization, writing–original draft, writing–review and editing
MA — Writing–original draft, writing–review and editing
LE — Writing–original draft, writing–review and editing
SL — Writing–original draft, writing–review and editing
ADC — Writing–original draft, writing–review and editing
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None.

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References

1. Centers for Disease Control and Prevention. CDC Health Alert Network. Multisystem Inflammatory Syndrome in Children (MIS-C) Associated with Coronavirus Disease 2019 (COVID-19). Atlanta, GA: CDC; 2020. https://emergency.cdc.gov/han/2020/han00432.asp

2. Word Health Organization. Multisystem inflammatory syndrome in children and adolescents temporally related to COVID-19. Geneva, CH: WHO; 2020. https://www.who.int/news-room/commentaries/detail/multisystem-inflammatory-syndrome-in-children-and-adolescents-with-covid-19

3. Kucirka LM, Lauer SA, Laeyendecker O, Boon D, Lessler J. Variation in False-Negative Rate of Reverse Transcriptase Polymerase Chain Reaction-Based SARS-CoV-2 Tests by Time Since Exposure. Ann Intern Med 2020;173(4):262–7. DOI PubMed

4. Centers for Disease Control and Prevention. About Kawasaki Disease. Atlanta, GA: CDC; 2020 (accessed 2021-04-07). https://www.cdc.gov/kawasaki/about.html

5. Feldstein LR, Rose EB, Horwitz SM, Collins JP, Newhams MM, Son MB, Newburger JW, Kleinman LC, Heidemann SM, Martin AA, Singh AR, Li S, Tarquinio KM, Jaggi P, Oster ME, Zackai SP, Gillen J, Ratner AJ, Walsh RF, Fitzgerald JC, Keenaghan MA, Alharash H, Doymaz S, Clouser KN, Giuliano JS Jr, Gupta A, Parker RM, Maddux AB, Havalad V, Ramsingh S, Bukulmez H, Bradford TT, Smith LS, Tenforde MW, Carroll CL, Riggs BJ, Gertz SJ, Daube A, Lansell A, Coronado Munoz A, Hobbs CV, Marohn KL, Halasa NB, Patel MM, Randolph AG; Overcoming COVID-19 Investigators; CDC COVID-19 Response Team. Multisystem Inflammatory Syndrome in U.S. Children and Adolescents. N Engl J Med 2020;383(4):334–46. DOI PubMed

6. Dufort EM, Koumans EH, Chow EJ, Rosenthal EM, Muse A, Rowlands J, Barranco MA, Maxted AM, Rosenberg ES, Easton D, Udo T, Kumar J, Pulver W, Smith L, Hutton B, Blog D, Zucker H; New York State and Centers for Disease Control and Prevention Multisystem Inflammatory Syndrome in Children Investigation Team. Multisystem Inflammatory Syndrome in Children in New York State. N Engl J Med 2020;383(4):347–58. DOI PubMed

7. Belay ED, Abrams J, Oster ME, Giovanni J, Pierce T, Meng L, Prezzato E, Balachandran N, Openshaw JJ, Rosen HE, Kim M, Richardson G, Hand J, Tobin-D'Angelo M, Wilson S, Hartley A, Jones C, Kolsin J, Mohamed H, Colles Z, Hammett T, Patel P, Stierman B, Campbell AP, Godfred-Cato S. Trends in Geographic and Temporal Distribution of US Children With Multisystem Inflammatory Syndrome During the COVID-19 Pandemic. JAMA Pediatr 2021;175(8):837–45. DOI PubMed

RAPID COMMUNICATION

Rapid review of multisystem inflammatory syndrome in paediatrics: What we know one year later

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Abstract

Background: Multisystem inflammatory syndrome in children (MIS-C) associated with coronavirus disease 2019 (COVID-19) is an emerging condition that was first identified in paediatrics at the onset of the COVID-19 pandemic. The condition is also known as pediatric inflammatory multisystem syndrome temporally associated with severe acute respiratory syndrome coronavirus 2 (PIMS-TS or PIMS), and multiple definitions have been established for this condition that share overlapping features with Kawasaki Disease and toxic shock syndrome.

Methods: A review was conducted to identify literature describing the epidemiology of MIS-C, published up until March 9, 2021. A database established at the Public Health Agency of Canada with COVID-19 literature was searched for articles referencing MIS-C, PIMS or Kawasaki Disease in relation to COVID-19.

Results: A total of 195 out of 988 articles were included in the review. The median age of MIS-C patients was between seven and 10 years of age, although children of all ages (and adults) can be affected. Multisystem inflammatory syndrome in children disproportionately affected males (58% patients), and Black and Hispanic children seem to be at an elevated risk for developing MIS-C. Roughly 62% of MIS-C patients required admission to an intensive care unit, with one in five patients requiring mechanical ventilation. Between 0% and 2% of MIS-C patients died, depending on the population and available interventions.

Conclusion: Multisystem inflammatory syndrome in children can affect children of all ages. A significant proportion of patients required intensive care unit and mechanical ventilation and 0%–2% of cases resulted in fatalities. More evidence is needed on the role of race, ethnicity and comorbidities in the development of MIS-C.

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Keywords: multisystem inflammatory syndrome in children, pediatric multisystem inflammatory syndrome, COVID-19, MIS-C, PIMS, PIMS-TS

Introduction

On March 11th, 2020 the World Health Organization declared a global pandemic of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Soon after, in April 2020, multisystem inflammatory syndrome in children (MIS-C) associated with SARS-CoV-2 virus was identified in the United Kingdom (UK) (1). Multisystem inflammatory syndrome in children is an acute illness that is characterized by immune dysregulation with multisystem involvement and severe symptoms typically requiring hospitalization. The syndrome is thought to occur in children two to six weeks following infection with SARS-CoV-2 (2).

The syndrome is also known as pediatric inflammatory multisystem syndrome temporally associated with SARS-CoV-2 (PIMS-TS or PIMS). Multiple definitions have been established for this condition, including by the World Health Organization (3),

United States (US) Centers for Disease Control and Prevention (4), the Royal College of Paediatrics and Child Health in the UK (5) and the Canadian Paediatric Society (6,7). The definitions, which are similar but not identical, are provided in **Appendix A**.

There is no definitive diagnostic test for MIS-C and MIS-C is considered a separate but similar clinical syndrome to Kawasaki Disease (complete, incomplete, atypical or shock syndrome), toxic shock syndrome and macrophage activated syndrome (8).

Current situation

More than a year has elapsed since MIS-C was first identified during the ongoing coronavirus disease 2019 (COVID-19) pandemic and a large body of evidence is now available. This review aims to synthesize what is currently known and what is still unclear about the epidemiological characteristics of this emerging disease.

Methods

A database maintained by the Public Health Agency of Canada is populated daily with new COVID-19 literature and includes studies published since the start of the pandemic until March 9, 2021, in PubMed, Scopus, BioRxiv, MedRxiv, ArXiv, SSRN and Research Square. Articles were cross-referenced with the COVID-19 information centers centres run by Lancet, BMJ, Elsevier and Wiley. These COVID-19 studies were gathered in an Excel spreadsheet database and were searched to retrieve MIS-C literature.

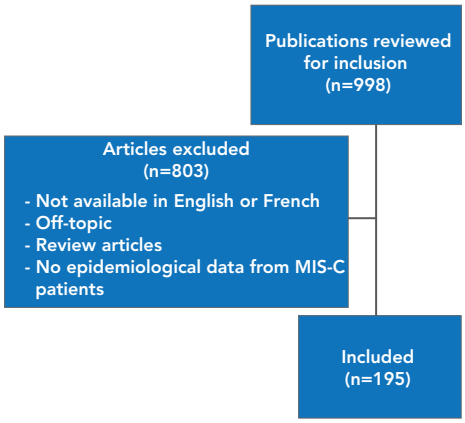
Articles (n=998) were screened for relevance and were included if epidemiological descriptions of MIS-C, PIMS, PIMS-TS or Kawasaki Disease related to COVID-19 were present. Articles (n=803) were excluded if they were not available in English or French, they were off-topic, they were review article or they did not contain epidemiological data from MIS-C patients. In total, 195 articles were deemed relevant and included in this review (**Figure 1**). Multiple articles could potentially refer to the same cases, and therefore double counting is a limitation of this review.

Results

A total of 195 articles were included in this review. The vast majority of articles were cohorts (prospective n=15, retrospective n=70 or ambi-directional n=4) and case reports (n=101), with a minority being case-controls (n=3) or natural experiments (n=2).

Most articles originated in the US (n=78) and the UK (n=23), with a smaller number from India (n=18) and European countries (France n=12, Italy n=10, Spain n=7). There were far fewer studies from Africa (South Africa n=2, Algeria n=1, Nigeria n=1, Egypt n=1) and Asia (South Korea n=2, Japan n=1, Indonesia n=1).

Figure 1: Article exclusion tree



Abbreviation: MIS-C, multisystem inflammatory syndrome in children

Case reports were summarized together (articles=101, MIS-C cases=207), as individual patient information was often available. The cohorts, case-controls and natural experiment articles were also summarized together and are referred to as cohorts in the results section (articles=94, MIS-C cases=4,630). Article summaries are available in **Supplemental material.**

Age and sex

In the cohort articles, 50 of 72 (70%) articles reported the median age of MIS-C patients as between seven and 10 years (**Figure 2**). In addition, the median age of 184 patients reported in case reports was 8.8 years, ranging from one month to 20 years (23 cases did not have individual age data). However, MIS-C has been reported in all paediatric age groups, with wide ranges in many articles (**Figure 3**).

Figure 2: Median age of multisystem inflammatory syndrome in children cases presented in cohort articles (n=72)

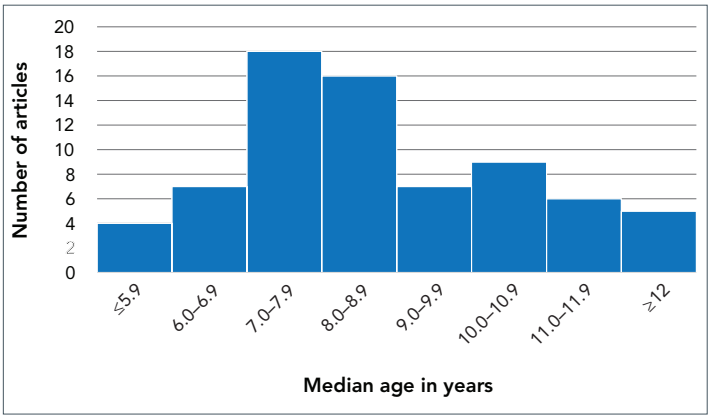
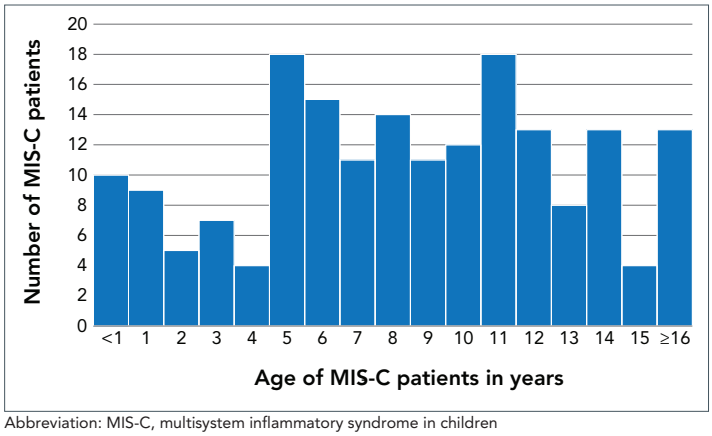


Figure 3: Age of multisystem inflammatory syndrome in children patients reported in case report articles (n=101, MIS-C cases=185)



Abbreviation: MIS-C, multisystem inflammatory syndrome in children

More male than female MIS-C cases were identified in this review. Cohort articles that report on sex gave an overall average of 58% male, with 64 of 89 (72%) reporting more male MIS-C cases than female. Additionally, there were 115 males out of 197 patients identified in case reports, for a total of 58% male (10 cases did not have sex data).

Race, ethnicity and comorbidities

The distribution of race, ethnicity and comorbidities in MIS-C cases is less clear than of age and sex. This is in part because of the varied general population of the geographies represented in the articles and in part due to issues with incomplete data collection. In addition, race and ethnicity are known to affect the likelihood of becoming infected with COVID-19 initially (9–13) and could also affect the likelihood of developing MIS-C subsequently (**Figure 4**). This is a complex relationship, which few articles have sought to disentangle.

Figure 4: Relationship[a] between general population, COVID-19 and MIS-C cases

Abbreviations: COVID-19, coronavirus disease 2019; MIS-C, multisystem inflammatory syndrome in children
[a] There is evidence that racial and ethnic minority groups are disproportionately affected by COVID-19 (arrow 1). The effect of race and ethnicity on arrow 2 is less clear

In the United States, the US Centers for Disease Control and Prevention states that, compared with White people, Black people are 1.1 times more likely to be infected and 2.8 times more likely to be hospitalized with COVID-19, while Hispanic people are 2.0 times more likely to be infected and 3.0 times more likely to be hospitalized with COVID-19 (10). Many factors have been identified as causes of these disparities. Racial and ethnic minorities face several issues, including discrimination, access to health care and income inequality. Black and Hispanic people are also more likely to live in crowded housing and have a higher likelihood of being frontline workers, leading to higher risk of COVID-19 infections (11). These disparities and the resulting high burden of COVID-19 cases may partially or wholly explain the disproportionately high rates of MIS-C sometimes reported among Black and Hispanic populations.

Three articles describing large cohorts took a closer look at the relationship between race, ethnicity and MIS-C cases (**Table 1**). Overall, one article found a disproportionately high incidence of MIS-C in Black and Hispanic children compared to White children (incidence rate ratio of 3.15 and 1.70 respectively) (14). If race and ethnicity play no role in the development of MIS-C after COVID-19 (arrow 2 in Figure 4), the expectation is that a proportionate number of children of every race and ethnicity will develop MIS-C after COVID-19. Three studies suggest that this is not the case, and that Black children are overrepresented among MIS-C cases when compared to those hospitalized with COVID-19 (14–16). Conversely, Hispanic children are

Table 1: Comparison of the racial and ethnic composition of the general population, hospitalized coronavirus disease 2019 cases and multisystem inflammatory syndrome in paediatric cases

Racial and ethnic composition		% Composition		
		Lee *et al.* (14) (US)[a] (n=182)	Feldstein *et al.* (15) (US)[b] (n=421)	Swann *et al.* (16) (UK) (n=651)
Black children	Percentage of Black children in the general paediatric population	22.2%	N/A	N/A
	Percentage of Black children among hospitalized paediatric COVID-19 cases	19.9%	21.5%	7.4%
	Percentage of Black children among MIS-C cases	34.4%	32.3%	17.3%
Hispanic children	Percentage of Hispanic children in the general paediatric population	35.6%	N/A	N/A
	Percentage of Hispanic children among hospitalized paediatric COVID-19 cases	40.0%	45.4%	N/A
	Percentage of Hispanic children among MIS-C cases	29.8%	35.8%	N/A
White children	Percentage of White children in the general paediatric population	26.1%	N/A	N/A
	Percentage of White children among hospitalized paediatric COVID-19 cases	13.8%	18.4%	51.2%
	Percentage of White children among MIS-C cases	12.8%	11.7%	30.8%

Abbreviations: COVID-19, coronavirus disease 2019; MIS-C, multisystem inflammatory syndrome in children; UK, United Kingdom; US, United States
[a] New York, New York
[b] 31 states across US

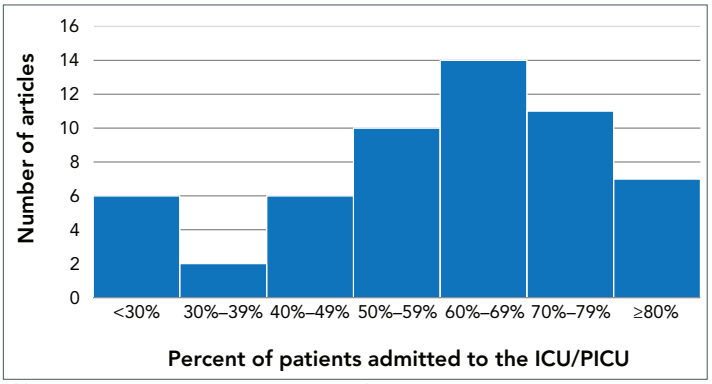
underrepresented among MIS-C cases when compared to those hospitalized with COVID-19 (14,15). There is also some evidence that White children are underrepresented among MIS-C cases when compared to those hospitalized with COVID-19 (15,16).

The most commonly reported comorbidities in the articles of children with MIS-C were asthma and obesity. However, one article found that MIS-C patients were more likely to have no comorbidities than acute COVID-19 patients (15), while a second found that MIS-C patients are slightly more likely to be obese than those in the general population (17). Overall, the evidence on comorbidities in MIS-C patients is relatively underdeveloped.

Outcomes

A large proportion of MIS-C patients (generally more than half) were admitted to an intensive care unit (ICU) or pediatric intensive care unit (PICU). In articles where ICU/PICU admission was not required as part of the study design, 56 cohort articles reported 62% of patients were admitted to ICU (**Figure 5**), while 80 case reports stated 78% of patients were admitted to ICU.

Figure 5: Percent of cases of multisystem inflammatory syndrome in paediatric patients admitted to ICU/PICU in cohort articles where ICU/PICU admission was not required by the study design (n=56)

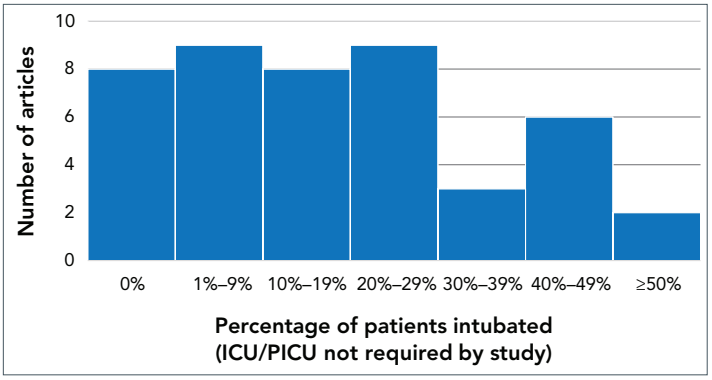


Abbreviations: ICU, intensive care unit; PICU, paediatric intensive care unit

In addition, approximately one in five MIS-C patients required intubation. In articles where ICU admission was not required as part of the study design, 45 cohort articles reported 22% of patients were intubated (**Figure 6**). In addition, in 14 cohort studies that did require ICU/PICU admission, 32% of patients were intubated. Finally, 76 case reports stated 34% of patients required intubation.

Generally, approximately 2% of MIS-C patients died. In 72 cohort articles that reported on outcomes, 2.0% of all patients died (n=78/3,977 cases), although 48 of 72 articles reported no deaths at all. In 88 case reports, 6.4% of all patients died. The case reports tend to highlight unique or more serious cases, which may explain why the overall mortality rate in these articles was much higher than in the cohort articles.

Figure 6: Percent of cases of multisystem inflammatory syndrome in paediatrics patients that were intubated in cohort articles where the study design did not require ICU/PICU admission (n=45)



Abbreviations: ICU, intensive care unit; PICU, paediatric intensive care unit

Discussion

There is a growing body of evidence outlining the epidemiological characteristics of MIS-C patients. It is clear that MIS-C affects children of all ages, with median age reported between seven and 10 years in 70% of articles. There seems to be proportionally fewer cases reported in children and young adults 16 years and older relative to rates of COVID-19 infection in these groups, but this may be due to many of the articles being based on work in paediatric hospitals. When compared with rates of COVID-19 cases, older teenagers and young adults in the US are more likely to be infected (or tested and identified as cases) than children, contrary to what has been reported about MIS-C rates so far (18).

The overrepresentation of male MIS-C cases is not seen in the rates of COVID-19 in children. In the US, male and female children are affected by COVID-19 roughly equally, with slightly higher rates in girls (18). However, the slight overrepresentation of male children is also seen in Kawasaki Disease, a closely related condition that has a better-developed body of evidence available. There is some suggestion that the male overrepresentation is due to genetic factors in Kawasaki Disease (19), which could be explored further to determine if this is also the case for MIS-C.

In regard to race and ethnicity, it is well established that racial and ethnic minority groups are disproportionately burdened by COVID-19 cases because of sociodemographic and other related factors (11–13). There is some evidence that Black and Hispanic children are disproportionately affected by MIS-C as well. The evidence presented here is from only two US and one UK study, and further studies are needed to verify these observations.

There is some evidence from studies on Kawasaki Disease that suggest genetic factors might play a role, with certain Asian groups being overrepresented amongst Kawasaki cases (20). Exploration of similar mechanisms in MIS-C would provide further insight.

In addition, comorbidities were inconsistently reported and are interrelated with other epidemiological factors, such as race and ethnicity. It is thus less clear how obesity, asthma and other comorbidities contribute to the development of MIS-C.

Finally, it is clear that MIS-C is a syndrome that causes serious symptoms that require hospitalization and often admission to an ICU or PICU. Access to adequate care, including intubation in severe cases, is critical in the treatment of MIS-C.

Conclusion

Multisystem inflammatory syndrome in children can affect children of all ages, with a median age most commonly reported between seven and 10 years. Males were more often affected (58% of cases). Many patients, often more than half, were admitted to the ICU or PICU, with a fifth requiring intubation. Between 0% and 2% of MIS-C patients died, depending on the context and available treatment. More evidence is needed on the role of race, ethnicity and comorbidities in the development of MIS-C. Future avenues of study include surveillance reports targeting incidence, along with studies on sequelae.

Authors' statement

MS — Methodology, investigation, writing–original draft
RE — Conceptualization, writing–review and editing, supervision
NB — Writing–review and editing
LW — Writing–review and editing
T-LB — Writing–review and editing
ET — Writing–review and editing
MEJ — Writing–review and editing
SB-A — Writing–review and editing

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Supplemental material

Summary of evidence on multisystem inflammatory syndrome in children (n=195)

References

1. European Centre for Disease Prevention and Control. Paediatric inflammatory multisystem syndrome and SARS-CoV-2 infection in children Paediatric inflammatory multisystem syndrome and SARS-CoV-2 infection in children ECDC; 2020 (accessed 2020-11-27). https://www.ecdc.europa.eu/sites/default/files/documents/covid-19-risk-assessment-paediatric-inflammatory-multisystem-syndrome-15-May-2020.pdf

2. Centers for Disease Control and Prevention. Reporting Multisystem Inflammatory Syndrome in Children (MIS-C). Atlanta, GA: CDC; 2020 (accessed 2021-04-26). https://www.cdc.gov/mis-c/pdfs/hcp/MIS-Children-Handout-FINAL.pdf

3. World Health Organization. Multisystem inflammatory syndrome in children and adolescents temporally related to COVID-19. Geneva, Switzerland: WHO; 2020 (accessed 2020-11-27). https://www.who.int/news-room/commentaries/detail/multisystem-inflammatory-syndrome-in-children-and-adolescents-with-covid-19

4. Centers for Disease Control and Prevention. Information for Healthcare Providers about Multisystem Inflammatory Syndrome in Children (MIS-C). Atlanta, GA; CDC: 2020 (accessed 2020-11-27). https://www.cdc.gov/mis-c/hcp/

5. Royal College of Paediactrics and Child Health. Paediatric multisystem inflammatory syndrome temporally associated with COVID-19 (PIMS) - guidance for clinicians. London, UK: RCPCH; 2020 (accessed 2020-11-27). https://www.rcpch.ac.uk/resources/paediatric-multisystem-inflammatory-syndrome-temporally-associated-covid-19-pims-guidance

6. Canadian Paediatric Society. Case definition for COVID-19 study. Ottawa (ON): CPSP; 2020 (accessed 2021-05-10). https://www.cpsp.cps.ca/uploads/studies/COVID-19-case-definition-rev-06-2020.pdf

7. Canadian Paediatric Society. Berard R, Scuccimarri R, Haddad E, Morin M, Chan K, Dahdah N, McCrindle BW, Price VE, Yeung RSM, Laxer RM, Acute Care Committee. Paediatric inflammatory multisystem syndrome temporally associated with COVID-19 (spring 2021 update). Ottawa (ON): CPS; 2020 (updated 2021-03-21). https://cps.ca/en/documents/position/pims

8. Nakra NA, Blumberg DA, Herrera-Guerra A, Lakshminrusimha S. Multi-System Inflammatory Syndrome in Children (MIS-C) Following SARS-CoV-2 Infection: Review of Clinical Presentation, Hypothetical Pathogenesis, and Proposed Management. Children (Basel) 2020;7(7):69. DOI PubMed

9. Public Health Ontario. Enhanced Epidemiological Summary. COVID-19 in Ontario – A Focus on Diversity. Toronto (ON): PHO; (updated 2020-05-14). https://www.publichealthontario.ca/-/media/documents/ncov/epi/2020/06/covid-19-epi-diversity.pdf?la=en

10. Information for Healthcare Providers about Multisystem Inflammatory Syndrome Risk for COVID-19 Infection, Hospitalization, and Death By Race/Ethnicity. Atlanta, GA, CDC; 2021 (accessed 2021-04-27). https://www.cdc.gov/coronavirus/2019-ncov/covid-data/investigations-discovery/hospitalization-death-by-race-ethnicity.html

11. Information for Healthcare Providers about Multisystem Inflammatory Syndrome. Health Equity Considerations and Racial and Ethnic Minority Groups. Atlanta, GA: CDC; 2021 (accessed 2021-05-07). https://www.cdc.gov/coronavirus/2019-ncov/community/health-equity/race-ethnicity.html

12. Escobar GJ, Adams AS, Liu VX, Soltesz L, Chen YI, Parodi SM, Ray GT, Myers LC, Ramaprasad CM, Dlott R, Lee C. Racial Disparities in COVID-19 Testing and Outcomes : Retrospective Cohort Study in an Integrated Health System. Ann Intern Med 2021;174(6):786–93. DOI PubMed

13. Toronto Public Health. COVID-19: Status of Cases in Toronto – City of Toronto. Toronto (ON): TPH; 2021 (accessed 2021-05-10). https://www.toronto.ca/home/covid-19/covid-19-latest-city-of-toronto-news/covid-19-status-of-cases-in-toronto/

14. Lee EH, Kepler KL, Geevarughese A, Paneth-Pollak R, Dorsinville MS, Ngai S, Reilly KH. Race/Ethnicity Among Children With COVID-19-Associated Multisystem Inflammatory Syndrome. JAMA Netw Open 2020;3(11):e2030280. DOI PubMed

15. Feldstein LR, Tenforde MW, Friedman KG, Newhams M, Rose EB, Dapul H, Soma VL, Maddux AB, Mourani PM, Bowens C, Maamari M, Hall MW, Riggs BJ, Giuliano JS Jr, Singh AR, Li S, Kong M, Schuster JE, McLaughlin GE, Schwartz SP, Walker TC, Loftis LL, Hobbs CV, Halasa NB, Doymaz S, Babbitt CJ, Hume JR, Gertz SJ, Irby K, Clouser KN, Cvijanovich NZ, Bradford TT, Smith LS, Heidemann SM, Zackai SP, Wellnitz K, Nofziger RA, Horwitz SM, Carroll RW, Rowan CM, Tarquinio KM, Mack EH, Fitzgerald JC, Coates BM, Jackson AM, Young CC, Son MBF, Patel MM, Newburger JW, Randolph AG; Overcoming COVID-19 Investigators. Characteristics and Outcomes of US Children and Adolescents with Multisystem Inflammatory Syndrome in Children (MIS-C) Compared with Severe Acute COVID-19. JAMA 2021;325(11):1074-87. DOI

16. Swann OV, Holden KA, Turtle L, Pollock L, Fairfield CJ, Drake TM, Seth S, Egan C, Hardwick HE, Halpin S, Girvan M, Donohue C, Pritchard M, Patel LB, Ladhani S, Sigfrid L, Sinha IP, Olliaro PL, Nguyen-Van-Tam JS, Horby PW, Merson L, Carson G, Dunning J, Openshaw PJ, Baillie JK, Harrison EM, Docherty AB, Semple MG; ISARIC4C Investigators. Clinical characteristics of children and young people admitted to hospital with covid-19 in United Kingdom: prospective multicentre observational cohort study. BMJ 2020;370:m3249. DOI PubMed

17. Godfred-Cato S, Bryant B, Leung J, Oster ME, Conklin L, Abrams J, Roguski K, Wallace B, Prezzato E, Koumans EH, Lee EH, Geevarughese A, Lash MK, Reilly KH, Pulver WP, Thomas D, Feder KA, Hsu KK, Plipat N, Richardson G, Reid H, Lim S, Schmitz A, Pierce T, Hrapcak S, Datta D, Morris SB, Clarke K, Belay E; California MIS-C Response Team. COVID-19-Associated Multisystem Inflammatory Syndrome in Children - United States, March-July 2020. MMWR Morb Mortal Wkly Rep 2020;69(32):1074–80. DOI PubMed

18. Leidman E, Duca LM, Omura JD, Proia K, Stephens JW, Sauber-Schatz EK. COVID-19 Trends Among Persons Aged 0-24 Years - United States, March 1-December 12, 2020. MMWR Morb Mortal Wkly Rep 2021;70(3):88–94. DOI PubMed

19. Kwon YC, Kim JJ, Yun SW, Yu JJ, Yoon KL, Lee KY, Kil HR, Kim GB, Han MK, Song MS, Lee HD, Ha KS, Sohn S, Ebata R, Hamada H, Suzuki H, Ito K, Onouchi Y, Hong YM, Jang GY, Lee JK; Korean Kawasaki Disease Genetics Consortium. Male-specific association of the FCGR2A His167Arg polymorphism with Kawasaki disease. PLoS One 2017;12(9):e0184248. DOI PubMed

20. Rowley AH. Kawasaki disease: novel insights into etiology and genetic susceptibility. Annu Rev Med 2011;62:69–77. DOI PubMed

Appendix A: Definitions of multisystem inflammatory syndrome in children

The definition of multisystem inflammatory syndrome (MIS-C) published by the World Health Organization (3) states:

- Children and adolescents 0–19 years of age with fever for more than three days

AND

- Two of the following:
  - Rash or bilateral non-purulent conjunctivitis or muco-cutaneous inflammation signs (oral, hands or feet)
  - Hypotension or shock
  - Features of myocardial dysfunction, pericarditis, valvulitis, or coronary abnormalities (including ECHO findings or elevated Troponin/NT-proBNP)
  - Evidence of coagulopathy (by PT, PTT, elevated d-Dimers)
  - Acute gastrointestinal problems (diarrhoea, vomiting, or abdominal pain)

AND

- Elevated markers of inflammation such as erythrocyte sedimentation rate (ESR), C-reactive protein (CRP), or procalcitonin

AND

- No other obvious microbial cause of inflammation, including bacterial sepsis, staphylococcal or streptococcal shock syndromes

AND

- Evidence of the coronavirus disease 2019 (COVID-19) (reverse transcription polymerase chain reaction (RT-PCR), antigen test or serology positive), or likely contact with patients with COVID-19

The case definition of MIS-C published by the United States Centers for Disease Control (4) states:

- An individual aged younger than 21 years presenting with fever (greater than 38.0°C for greater than or equal to 24 hours, or report of subjective fever lasting greater than or equal to 24 hours), laboratory evidence of inflammation, and evidence of clinically severe illness requiring hospitalization, with multisystem (more than two) organ involvement (cardiac, renal, respiratory, hematologic, gastrointestinal, dermatologic or neurological)

AND

- No alternative plausible diagnoses

AND

- Positive for current or recent severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection by RT-PCR, serology, or antigen test; or exposure to a suspected or confirmed COVID-19 case within the four weeks prior to the onset of symptoms

The definition of pediatric inflammatory multisystem syndrome (PIMS) released by the United Kingdome Royal College of Paediatrics and Child Health (RCPCH) (5) states:

- A child presenting with persistent fever, inflammation (neutrophilia, elevated CRP and lymphopenia) and evidence of single or multi-organ dysfunction (shock, cardiac, respiratory, renal, gastrointestinal or neurological disorder) with additional features. This may include children fulfilling full or partial criteria for Kawasaki disease

AND

- Exclusion of any other microbial cause, including bacterial sepsis, staphylococcal or streptococcal shock syndromes, infections associated with myocarditis such as enterovirus (waiting for results of these investigations should not delay seeking expert advice)

AND

- SARS-CoV-2 PCR testing may be positive or negative

The definition of PIMS released by the Canadian Paediatric Society (6,7) states:

- Persistent fever (higher than 38.0°C for three or more days) and elevated inflammatory markers (CRP, ESR, or ferritin)

AND one of both of the following:

- Features of Kawasaki disease (complete or incomplete)
- Toxic shock syndrome (typical or atypical)

AND

- No alternative etiology to explain the clinical presentation

AND

- Patients need not have positive SARS-CoV-2 status for consideration

The impact of vaccination status on importation of COVID-19 among international travellers

Paul Ronksley[1]*, Tayler Scory[2], Robert Weaver[2], Meaghan Lunney[1], Rachel Rodin[3], Marcello Tonelli[2]

Abstract

Governments worldwide are looking for ways to safely enable international travel while mitigating the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and the associated coronavirus disease 2019 (COVID-19). However, few data describe the impact of vaccination on importation of COVID-19. We took advantage of the sequential introduction of two government policies in Canada to evaluate the real-world evidence of vaccine effectiveness among 30,361 international travellers arriving by air in Alberta, Canada. The proportion of COVID-19-positive results for travellers who were either fully vaccinated or partially vaccinated was 0.02% (95% CI: 0.00–0.10) (i.e. one positive case among 5,817 travellers). In contrast, 1.42% (95% CI: 1.27–1.58) of unvaccinated travellers tested positive for SARS-CoV-2 (341 cases among 24,034 travellers). These findings suggest that COVID-19 vaccinations approved in Canada, substantially reduced the risk of travel-related importation of COVID-19 when combined with other public health measures. The low absolute rate of infection among fully vaccinated or partially vaccinated international travellers may inform quarantine requirements in this population.

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Keywords: COVID-19, vaccination, international travel, case importation

Introduction

Governments worldwide are looking for ways to safely enable international travel while mitigating the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and the associated coronavirus disease 2019 (COVID-19). Vaccination campaigns are well underway in many high-income countries, and accumulating evidence suggests that vaccinated people are less likely to become infected. Few data describe the impact of vaccination on importation of COVID-19, a potentially useful indicator to inform border policy. Using data from two government-sponsored border testing programs, we provide real-world evidence on vaccine effectiveness among 30,361 international travellers arriving by air at the Calgary International Airport.

Current situation

In March 2020, the Canadian federal government closed borders to everyone except people meeting certain criteria (1). Of those allowed to cross the border, one group was termed "exempt travellers", and included members of flight crews, those transporting goods across the Canada-United States border, and others providing certain essential services. The remainder of those allowed to cross the border were termed "non-exempt travellers", including Canadian citizens; permanent residents; the immediate families of citizens/permanent residents; and others with a specific reason for travel, such as family reunification. The Calgary International Airport was one of four airports that remained open to flights from outside of Canada, the United States and the Caribbean, along with airports in Montréal, Toronto and Vancouver.

Data from January 6, 2021 to February 21, 2021 were obtained from non-exempt travellers who were eligible to enter Canada, arrived by air, and participated in the voluntary Alberta Border Testing Pilot Program (ABTPP) (2). The ABTPP was suspended at 11:59 p.m. EST on February 21, 2021 and all international travellers arriving in Alberta by air thereafter were subject to a mandatory border entry procedure (3). We report here on travellers from both the ABTPP and the mandatory program from January 6, 2021 to May 23, 2021.These travellers are called thereafter the `participants`.

All travellers in the current report were required to present proof of a negative molecular test for SARS-CoV-2 (e.g. Polymerase chain reaction (PCR), Nucleic acid test (NAT), Reverse transcription loop-mediated isothermal amplification (RT-LAMP), etc.), done fewer than 72 hours before the scheduled

departure to Canada (4), and to undergo molecular testing again 7–8 days after arrival. Full-vaccination status was defined by self-reported receipt of two doses of a COVID-19 vaccine approved in Canada (5) at least 14 days prior to arrival date. Partial vaccination was defined by self-reported receipt of one Canadian-approved COVID-19 vaccine dose prior to arrival date or two Canadian-approved COVID-19 vaccine doses less than 14 days prior to arrival date. Recipients of a single-dose vaccine were considered partially vaccinated. Those with no self-reported vaccination status were linked, where possible, to the provincial vaccination registry to determine their status at time of arrival date. Most of the international travellers were Alberta residents returning from abroad and provided a provincial healthcare number.

Of the 30,361 non-exempt travellers, the majority traveled on flights originating in the United States (53.20%) and Mexico (20.79%). Their median age was 45.0 years and 52.5% were male. 28,658 (94.39%) were at least 12 years of age, of whom 1,595 (5.57%) were partially vaccinated and 4,227 (14.75%) were fully vaccinated. The proportion of positive results for participants who were either fully vaccinated or partially vaccinated was 0.02% (95% CI: 0.00-0.10 [i.e. one positive case among 5,817 participants who were tested for COVID-19]) (**Table 1**). In contrast, 1.42% (95% CI: 1.27–1.58) of unvaccinated participants tested positive for SARS-CoV-2 (341 cases among 24,034 participants). This equates to a relative risk for a positive test among vaccinated or partially vaccinated participants of 0.01 (95% CI: 0.00–0.09) compared with participants who were unvaccinated.

The positive test among the vaccinated traveller was followed up with sequencing and was negative for a variant of concern. Another specimen was obtained from this traveller three days later and a repeat molecular test was negative for SARS-CoV-2—which raised the possibility of an initial false positive test.

Conclusion

These findings suggest that Canadian-approved COVID-19 vaccinations substantially reduce the risk of travel-related importation of COVID-19 when combined with other public health measures. The low absolute rate of infection among vaccinated or partially vaccinated non-exempt travellers may inform quarantine requirements in this population. However, recognizing the timeframe of this report, future work should investigate whether the effectiveness of vaccinations in mitigating case importation among international travellers has changed following the recent increase in variants of concern (particularly the Delta variant).

Authors' statement

PER — Contributions to conception and design, interpreted of data; wrote first draft
RGW — Contributions to conception and design, interpreted of data
ML — Contributions to conception and design, interpreted of data
RR — Contributions to conception and design, interpreted of data
MT — Contributions to conception and design, interpreted of data, wrote first draft
TDS — Data analysis

All authors were involved in revising it critically for important intellectual content. All authors provide final approval of the version to be published and agreed to be accountable for all aspects of the work.

Competing interests

None.

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Table 1: COVID-19 test results among non-exempt international travellers arriving in Alberta by air between January 6, 2021 and May 23, 2021

Test results	Vaccinated			Partially vaccinated			Unvaccinated			Missing/unknown			Total		
	n	%	95% CI	n	%	95% CI	n	%	95% CI	n	%	95% CI	n	%	95% CI
Positive[a]	1	0.02	0.00–0.13	0	0.00	0.00–0.23	341	1.42	1.27–1.58	0	0.00	0.00–7.11	342	1.14	1.03–1.27
Negative	4,224	99.98	–	1,592	100	–	23,693	98.58	–	50	100	–	29,559	98.85	–
No test	2	–	–	3	–	–	455	–	–	0	–	–	460	–	–
Total	4,227	13.92	–	1,595	5.25	–	24,489	80.66	–	50	0.16	–	30,361	100	–

Abbreviations: CI, confidence interval; –, not reported
[a] Proportion of positive results for participants who were either vaccinated or partially vaccinated was 0.02% (0.00%, 0.10%)

References

1. Public Health Agency of Canada. List of Acts and Regulations. Ottawa (ON): PHAC; 2021 (accessed 2021-06-07). https://www.canada.ca/en/public-health/corporate/mandate/about-agency/acts-regulations/list-acts-regulations.html

2. Government of Canada. Alberta COVID-19 Border Testing Pilot Program. Ottawa (ON): Government of Canada; 2021 (accessed 2021-06-07). https://www.canada.ca/en/public-health/services/diseases/2019-novel-coronavirus-infection/latest-travel-health-advice/alberta-covid-19-border-testing-pilot-program.html

3. Government of Canada. Government of Canada introduces further restrictions on international travel. Ottawa (ON): Government of Canada; 2021 (accessed 2021-06-07). https://www.canada.ca/en/transport-canada/news/2021/01/government-of-canada-introduces-further-restrictions-on-international-travel.html

4. Government of Canada. COVID-19 testing for travellers. Ottawa (ON): Government of Canada; 2021 (accessed 2021-06-07). https://travel.gc.ca/travel-covid/travel-restrictions/flying-canada-checklist/covid-19-testing-travellers-coming-into-canada

5. Government of Canada. Approved COVID-19 Vaccines. Ottawa (ON): Government of Canada; 2021 (accessed 2021-06-07). https://www.canada.ca/en/health-canada/services/drugs-health-products/covid19-industry/drugs-vaccines-treatments/vaccines.html

RAPID COMMUNICATION

Re-verifying the elimination of measles, rubella and congenital rubella syndrome in Canada, 2016–2020

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Keywords: measles, rubella, congenital rubella syndrome, elimination, surveillance, public health

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Introduction

Elimination, in the context of measles, rubella and congenital rubella syndrome (CRS), refers to the absence of endemic measles/rubella virus transmission in a region or other defined geographic area for at least 12 months, in the presence of a high-quality surveillance system that meets targets of key performance indicators. In 1994, Canada and other countries of the World Health Organization (WHO) region of the Americas committed to the objectives of measles elimination by 2000 and rubella and CRS by 2010. Canada met these targets: eliminating measles transmission in 1998; rubella transmission in 2005; and endemically-acquired CRS in 2000. The WHO region of Americas was declared free of endemic rubella/CRS in 2015 and endemic measles in 2016.

At the request of the Pan American Health Organization (PAHO), Canada's elimination status of measles, rubella and CRS was verified in 2012 and again in 2017. Prior to submission to PAHO, the verification reports were reviewed, approved and endorsed by Canada's National Certification Committee (NCC). The NCC is a group of experts who are not directly involved with the management of vaccine preventable diseases or immunization program implementation at the national level, but who have the expertise to assist in ensuring that Canada is meeting PAHO'S goals of elimination and eradication. Members are responsible for reviewing Canada's current mechanisms of surveillance and progress towards elimination of targeted vaccine preventable diseases in Canada. Members have expertise in the fields of public health, infectious diseases and/or laboratory sciences.

Current situation

In early January 2021, Canada received notification from PAHO requesting a country report presenting updated data analyses related to the sustainability of measles, rubella and CRS elimination for the 2016–2020 period. A template was provided by PAHO using a set of indicators and questions related to five main areas: epidemiology of the diseases; quality of surveillance; laboratory surveillance; analysis of cohort population including vaccine coverage; and sustainability.

In the scope of this request, the NCC was called upon to review the report entitled *Re-verification of the Elimination of Measles, Rubella and Congenital Rubella Syndrome (CRS) Elimination, 2016-2020* (1). Specifically, the NCC reviewed the evidence and determined whether the collation of the evidence answered the following questions:

1. Had Canada sustained the elimination of measles, rubella and CRS since the Region of the Americas was declared a region free of these diseases in 2016 and 2015, respectively?
2. Is Canada ready to apply for re-verification of the elimination of measles and/or rubella if it has established that there had been endemic transmission of any of these two diseases?

The report was prepared by the Centre for Immunization and Respiratory Infectious Diseases and the National Microbiology Laboratory, with contributions from the COVID-19 Immunization Readiness Centre (COVID-19; coronavirus disease 2019) and the Centre for COVID-19 Vaccine Surveillance within the Public Health Agency of Canada. The report and supporting documents were approved by the Minister of Health of Canada in early May and then endorsed by the NCC. Canada submitted the NCC-endorsed report, along with supporting documents, to PAHO on June 14, 2021 as requested.

Results

Between 2016 and 2020, 199 cases of measles, two cases of rubella and one case of CRS were reported in Canada (**Table 1**). The range in measles cases reported annually was one to 113, with only one case reported in 2020—prior to the start of the COVID-19 pandemic. Slightly more females than males were affected by measles (n=111/199). Among cases where vaccination status was available, 53% were unvaccinated compared with 46% of cases who were up-to-date on vaccination. Among the reported measles cases, 80 (40%) were imported. Nineteen measles outbreaks were reported. The median age of measles outbreak cases was 17 years old (range 0–58 years). The majority of index cases (n=17) reported travel outside of Canada during their incubation period. The other two index cases included one case who did not travel outside Canada but was potentially exposed to an international case at a Canadian port and one case who did not report any travel outside Canada or exposure to a traveller. Measles strains of genotypes B3 and D8 were detected in Canada between 2016 and 2020 with the genotype D8 named strain MVs/Gir Somnath. IND/42.16/ reported throughout 2019.

Table 1: Pan American Health Organization essential criteria for the verification of the elimination of measles

Criterion[a]	Indicator	Description
Verify the interruption of endemic measles cases for a period of at least three years from the last known endemic case, in the presence of high-quality surveillance	Zero cases of endemic transmission	A total of 199 cases of measles, two cases of rubella and one case of CRS were reported between 2016 and 2020. The following is a breakdown of measles cases by source of transmission: Outside Canada: n=80 Within Canada: n=94 Within Canada, linked to case/chain of unknown origin: n=11 Unknown source: n=14
Maintain high-quality surveillance sensitive enough to detect imported and import-related cases	More than two suspect cases per 100,000 population adequately	Canada does not investigate on suspected cases of measles, rubella or CRS. The criterion is met for laboratory-confirmed cases.
Verify the absence of endemic measles virus strains through viral surveillance	Measles genotype assessed in 80% of outbreaks	100% (n=20/20) of measles outbreaks had a genotype and lineage identified. No outbreaks of rubella occurred although two sporadic cases occurred with genotype information for one.

Table 1: Pan American Health Organization essential criteria for the verification of the elimination of measles (*continued*)

Criterion[a]	Indicator	Description
Verify adequate immunization in the population	95% of population cohorts aged 1–40 years have received a measles-containing vaccine	Canada currently measures (biennially) measles vaccination coverage rates at two and seven years of age, and therefore is unable to assess measles vaccination coverage for all ages 1–40 years. The 2019 childhood National Immunization Coverage Survey estimated first dose measles-containing vaccine coverage in two-year-olds to be 90%.

Abbreviation: CRS, congenital rubella syndrome
[a] Data from Pan American Health Organization (2)

Conclusion

The epidemiological and virological evidence presented in the report support that Canada has sustained the elimination of measles, rubella and CRS since the WHO region of the Americas was declared a region free of these diseases in 2016 and 2015, respectively. Despite eliminating measles, rubella and CRS, cases and outbreaks were reported in Canada in the last five years. This is expected to continue until circulation of these viruses is eliminated in all World Health Organization regions. Canadians travelling abroad should continue to ensure they are up-to date on their vaccinations for measles and rubella. Health professionals should remain alert to symptoms of measles and rubella, especially as international travel restrictions related to COVID-19 begin to ease. Canada remains committed to measles and rubella elimination; therefore, continued epidemiological surveillance, including laboratory testing on suspected cases of measles and rubella, is essential.

Authors' statement

MS — Conceptualization, methodology, software, formal analysis, investigation, data curation, writing–original draft, writing–review and editing, visualization
JH — Methodology, formal analysis, writing–original draft, writing–review and editing
SGS — Conceptualization, writing–review and editing
MG — Writing–review and editing
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AT — Writing–review and editing
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Competing interests

None.

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References

1. National Certification Committee (Canada). Re-verification of the Elimination of Measles, Rubella and Congenital Rubella Syndrome (CRS) Elimination, 2016-2020. (Unpublished)

2. Pan American Health Organization. Measles elimination in the Americas. https://www3.paho.org/hq/index.php?option=com_content&view=article&id=12526:measles-elimination-in-the-americas&Itemid=40721&lang=en

Descriptive analysis of a tuberculosis outbreak from a northern Saskatchewan First Nations community—December 2018 to May 2019

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Abstract

Background: The tuberculosis (TB) incidence rate for northern Saskatchewan First Nations on-reserve is 1.5 higher than the national average. In December 2018 a member of one of these communities was diagnosed with 4+ smear-positive TB, spurring an outbreak investigation.

Objectives: To describe the public health response to TB outbreak investigation and highlight the risk factors associated with TB transmission in northern Saskatchewan; and to highlight the relevance of social network contact investigation tool in outbreak management.

Methods: Descriptive analysis included active TB cases and latent TB infection (LTBI) cases linked by contact investigation to the index case. Data were collected from active TB case files. Statistical analyses were performed and social network analysis conducted using household locations as points of contact between cases.

Results: A total of eight active TB cases and 41 LTBI cases were identified as part of the outbreak between December 2018 and May 2019. Half of the cases (4/8) were 25 to 34 years old, and five were smear negative. One-third of the people with LTBI were 15 to 24 years old, and about a half tested positive to the new tuberculin skin test (TST). The commonly reported risk factors for TB and LTBI cases were alcohol use, cigarette use, marijuana use, previous TB infection and homelessness. Social network analysis indicated a relationship between increased node centrality and becoming an active case.

Conclusion: Real-time social network contact investigation used in active-case finding was very successful in identifying cases, and enhanced nursing support, mobile clinics and mobile X-ray worked well as a means of confirming cases and offering treatment. TB outbreaks in northern Saskatchewan First Nations on-reserve communities are facilitated by population-specific factors. Efforts to implement context-specific interventions are paramount in managing TB outbreaks and preventing future transmission.

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Keywords: tuberculosis, outbreak, investigation, First Nations, Indigenous community, Saskatchewan, reserve, social network analysis, case finding

Introduction

Worldwide, tuberculosis (TB) is a major health problem with approximately 10 million people diagnosed in 2017 alone (1). In response, the World Health Organization (WHO) has outlined a collaborative global effort to reduce TB incidence to less than 10 cases per 100,000 by 2035 (2). Incidence rates in Canada have remained relatively stable over the last decade, with 1,737 new cases of active TB reported in 2016 (3), equating to an incidence rate of 4.8 per 100,000. However, the national rate does not accurately represent certain subsets of the Canadian population (2,3).

TB incidence rates in Saskatchewan are continually above the national average, at 7.9 active TB cases per 100,000 in 2016 (4). The same year there were 91 active cases of TB in Saskatchewan;

39 (43%) were in northern Saskatchewan, despite that only 3.6% of the province's population lives in this region (4,5). Of the 39 cases in northern Saskatchewan, 31 were on-reserve First Nations; this equates to an incidence rate of 87.1 per 100,000 in this population (4,6).

In Saskatchewan, all cases of active TB are reported by the local health authority to TB Prevention and Control Saskatchewan (TBPCS). Following diagnosis of active TB, contact tracing investigations are initiated to identify anyone who has been exposed for assessment and follow-up. Most of the northern Saskatchewan First Nations on-reserve population are managed by the Northern Inter-Tribal Health Authority (NITHA), who works with TBPCS as well as with the First Nations and Inuit Health Branch, Indigenous Services Canada.

In December 2018, a member of a NITHA community was diagnosed with 4+ smear-positive TB after being admitted to the hospital with severe complications related to TB. This person had been symptomatic for approximately eight months. Upon further investigation, it was found that they had been diagnosed with latent TB infection (LTBI) during a prior TB outbreak but had not completed treatment. It was concluded that this was a case of reactivation, not ongoing transmission, and could be considered to be an index case. The NITHA TB nurses immediately initiated contact tracing and social network contact investigation to identify exposed people. As of June 2019, an additional seven active TB cases and 41 LTBI cases with links to the index case had been diagnosed, prompting an outbreak investigation.

The objective of this report is to describe the sociodemographic and clinical characteristics of the outbreak cases as well as their risk factors and social network. The report also intends to highlight the integral public health interventions that helped mitigate the magnitude of this outbreak in a northern Saskatchewan First Nations on-reserve community.

Methods

Case identification

Both active and latent TB cases were included in this analysis. Cases were considered active if TB was confirmed clinically or in a laboratory or if the person had been potentially exposed to someone else with active TB, as identified through contact investigations. Laboratory confirmation required a culture, from sputum, body fluid or tissue that contains *Mycobacterium tuberculosis* complex. Clinical diagnosis includes a chest radiograph showing pulmonary changes indicative of TB, or histopathologic evidence of active TB, or response to anti-TB treatment, or active non-respiratory TB symptoms.

LTBI cases met the following requirements: a tuberculin skin test (TST) that confirms the presence of *M. tuberculosis*; no evidence of clinically active disease; no radiographic changes suggestive of active disease; negative microbiologic tests (if performed); and potential exposure to an active TB case from the outbreak.

Data collection

We extracted data from case files completed by TB nurses during case and contact investigations and follow-up assessments. The information in the case files included data on sociodemographic variables, clinical characteristics, risk factors, social networks and public health interventions.

Sociodemographic variables included age and sex, while the clinical characteristics included site of infection, sputum smear status, TST status and treatment status. Risk factors included cigarette use, alcohol use, marijuana use, homelessness and comorbidities. Social network data comprised the connections between active TB cases, LTBI cases and exposed households. We assessed public health interventions using data on case detection methods, numbers of individuals assessed, cases started on treatment and healthcare access.

Data analysis

Descriptive analysis of the outbreak cases was performed using statistical package R version 3.4.3 (R Foundation for Statistical Computing, Vienna, Austria), and the epidemic curve was created in Excel version 2019 (Microsoft Corp., Redmond, Washington, United States). Active TB cases and LTBI cases were separated for the purposes of the analysis. The cases were described using proportions for each of the sociodemographic, clinical and risk factor variables assessed.

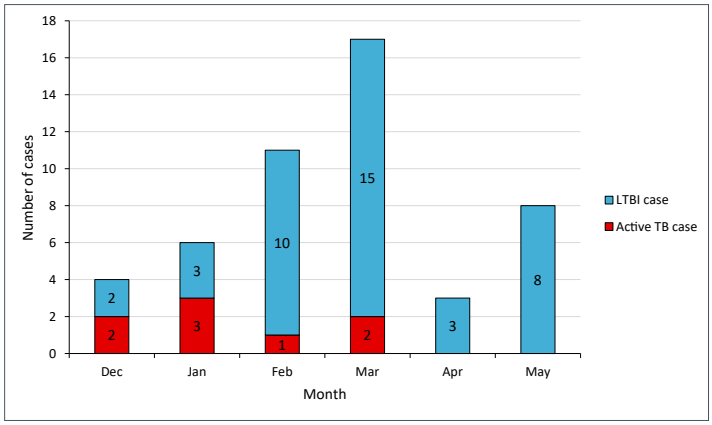
Social network analysis was conducted using the software program Gephi version 0.9.2 (Gephi Consortium, Compiegne, France). All people with active TB and LTBI were linked to the households they were known to visit, stay with or live with during the periods of infectivity. Averages on the number of edges for households and cases were also calculated.

Interventions were assessed using basic descriptive statistics of relevant indicators, which included both proportions and averages calculated in statistical package R.

Results

Eight active TB cases and 41 LTBI cases diagnosed between December 2018 and May 2019 met the inclusion criteria for the outbreak. The epidemic curve illustrates the amplification in cases following the diagnosis of the index case with a 4+ smear-positive TB infection on December 13, 2018 (**Figure 1**). All 8 active TB cases had been diagnosed by March 2019, while the number of LTBI cases diagnosed increased steadily to a peak of 15 cases in March and then declined noticeably.

Figure 1: Epidemic curve of a tuberculosis outbreak in a northern Saskatchewan First Nations on-reserve community, between December 2018 and May 2019



Abbreviations: LTBI, latent tuberculosis infection; TB, tuberculosis

Sociodemographic and clinical characteristics

Six of the eight people with active TB were male, and four were 25 to 34 years old (**Table 1**). Six were new TST positive test performed for the first time had a positive result, and only two were diagnosed with 4+ smear-positive TB. Six were diagnosed with pulmonary TB; two had TB lymphadenitis. All started the prescribed treatment.

Table 1: Sociodemographic and clinical characteristics of community members with active TB and LTBI in the December 2018 to May 2019 outbreak

Variables		Cases with active TB (n=8)		Cases with LTBI (n=41)	
		Number	%[a]	Number	%[a]
Sex	Male	6	75	20	49
	Female	2	25	21	51
Age group	<5	1	13	2	5
	5–14	1	13	5	12
	15–24	2	25	14	34
	25–34	4	50	8	20
	35–44	0	0	5	12
	45–54	0	0	4	10
	55–64	0	0	1	2
	65+	0	0	2	5
TST status[b]	New TST positive	6	75	23	56
	Past TST positive	2	25	18	44
Bacteriological status	Smear positive, culture positive	2	25	0	0
	Smear negative, culture positive	5	63	0	0
	Smear negative, culture negative	0	0	34	83
	No bacteriological confirmation	1	13	7	17
Site of infection	Pulmonary	6	75	N/A	N/A
	Lymphatic	2	25	N/A	N/A
Treatment	Yes	8	100	31	76
	No/declined	0	0	7	17

Abbreviations: LTBI, latent tuberculosis infection; N/A, not applicable; TB, tuberculosis; TST, tuberculin skin test
[a] Totals may not equal 100% due to rounding to the nearest whole number
[b] "New TST positive" refers to a person testing positive for a TST test for the first time; "past TST positive" refers to a person testing positive after previous positive TST tests

Equal portions of the people with LTBI were males (20/41; 49%) and females (21/41; 51%). The majority were 15 to 24 years old (14/41; 34%), and slightly over half were new TST positive (23/41; 56%). Only a few (7/41; 17%) declined treatment, on the recommendation of physicians, because of potential complications with other medications or pregnancy.

Risk factor analysis

People with active TB had a high prevalence of risk factors; five used cigarettes and alcohol and four used marijuana (**Table 2**). Two of those who did not use any substances were less than 15 years old. Two were experiencing homelessness; of note, one was the index case. Only two had had previous TB infection.

Table 2: Risk factors of community members with active TB and LTBI in the December 2018 to May 2019 outbreak

Variables		Cases with active TB (n=8)		Cases with LTBI (n=41)	
		Number[a]	%[b]	Number[a]	%[b]
Experiencing homelessness	Yes	2	25	4	10
	No	6	75	37	90
Comorbidity	Diabetes	0	0	1	2
	Previous TB infection	2	25	16	39
	Both	0	0	2	5
	None	6	75	21	51
Cigarette use	Yes	5	63	24	58
	No	3	38	16	39
Alcohol use	Yes	5	63	23	56
	No	3	38	17	41
Marijuana use	Yes	4	50	16	39
	No	4	50	24	59

Abbreviations: LTBI, latent tuberculosis infection; TB, tuberculosis
[a] Case counts may not add up to the total due to missing values
[b] May not add up to 100% due to rounding to the nearest whole number

People with LTBI had prevalence of risk factors similar to the active cases, with more than half (23/41) reporting using cigarettes and alcohol. Over one-third (16/41; 39%) reported using marijuana, and four were experiencing homelessness (10%). Two (5%) had had prior TB infection and diabetes; 16 (39%) had been previously diagnosed with a TB infection.

Social network analysis

Social network contact investigation successfully identified 39 (80%) of the 49 people with TB and LTBI (**Table 3**). The social network includes 62 nodes altogether: 13 exposed households (21%) and 49 cases (79%). There were an average of 9.4 edges per household and 2.5 edges per case.

Table 3: General characteristics of the social network of people with active TB and LTBI in the December 2018 to May 2019 outbreak

Variables		Case count	
		n	%
Method of detection of cases	Symptoms	1	2
	Traditional contact investigation	9	18
	Social network contact investigation	39	80
Nodes	Households	13	21
	Cases	49	79
Edges	Total	122	100

Abbreviations: LTBI, latent tuberculosis infection; TB, tuberculosis

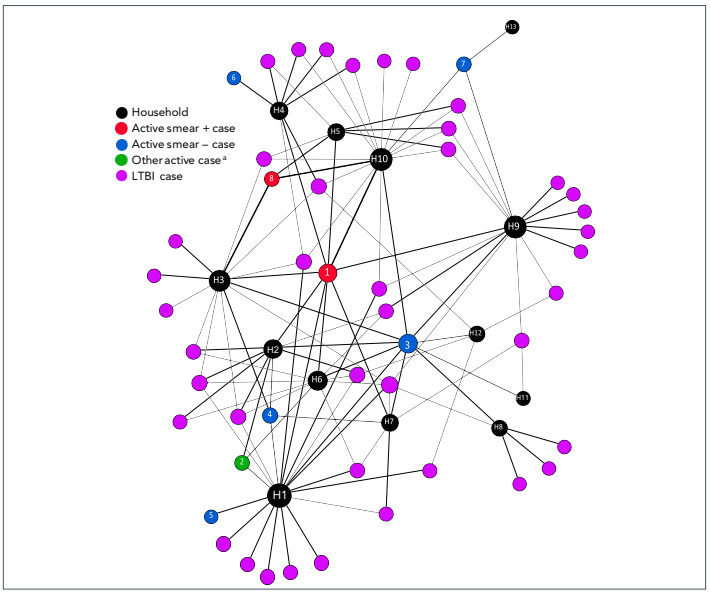
The social network map (**Figure 2**) illustrates the many potential TB transmission pathways. The person identified as the index case, who was experiencing homelessness, was highly transient and central to the network, exposing nine different households. Of note, active TB cases have higher connectivity in the network than LTBI cases, with an average of 4.3 edges per node compared to 2.1 edges per node for LTBI cases.

Certain network households appear to be key points of exposure and transmission from the index case, as Household 1 had connections to four secondary active TB cases and 14 LTBI cases; Household 1 was frequented by people experiencing homelessness and young families. In addition, Households 2, 3, 6, 9 and 10 are each connected to over 10 people within the network; together they have an average of 13.4 connected cases. These households are known to be key gathering points in the social network, serving as places for socialization, partying or card playing.

Public health interventions

Real-time social network contact investigation was used for the first time in a NITHA community to enhance case finding. In total, 136 individuals were involved in this outbreak investigation; 109 (80%) were identified through social network contact investigation while 26 (20%) were found during routine contact tracing interviews.

Figure 2: Social network analysis of a tuberculosis outbreak in a northern Saskatchewan First Nations on-reserve community



Abbreviations: H#, household number; #, case number in order of diagnosis; LTBI, latent tuberculosis infection
[a] Refers to an active case that has not been bacteriologically confirmed
Note: Node sizes reflect the centrality of the node; edge thickness reflects level of infectivity of a case

Integral to the management of the outbreak was follow-up, with TB nurses and TB physicians completing TSTs, symptom inquiries and clinical assessments. A total of 135 contacts were identified over a five-month period. In response to the influx of individuals, NITHA began sending two nurses per community visit, instead of one, until the community hired two part-time TB nurses to support management efforts. Mobile clinics were increased from every two months to monthly to decrease wait times for physician and mobile X-ray assessments.

Seven people (14%) declined treatment due to pregnancy or potential interactions with other medications. For the individuals who accepted treatment, the current practice in NITHA communities was to provide directly observed therapy (DOT) to improve medication adherence. As a result, it was decided to hire one additional full-time TB community worker and one part-time TB community worker to allow all of the new cases to begin treatment upon diagnosis.

In addition, TBPCS required that all children younger than five years old who were identified as potentially exposed be placed on window period prophylaxis (WPP) within two weeks of identification. In this outbreak 22 children in this age group were placed on WPP in this time-frame until final diagnosis.

Discussion

The findings from this outbreak highlighted the important factors related to TB transmission in a northern Saskatchewan First Nations on-reserve community. Of note, the outbreak cases were primarily young adults and most had a new TST positive result. Pulmonary infections were the most common manifestation of active TB, and the majority of cases were smear negative. Outbreak cases had a high prevalence of known risk factors, such as cigarette, alcohol and marijuana use. An important finding was the impact of homelessness on the outbreak, as six outbreak cases identified as being homeless, including the index case.

Social network analysis showed the complexity of the social networks and the importance of shared locations in a northern Saskatchewan First Nations on-reserve community. The high average number of households visited per case indicated the nature of transiency and pronounced socialization behaviour. In addition, there appeared to be a correlation between the level of connectivity to exposed households and having active TB or LTBI. Social network analysis also revealed the substantial amount of transmission between the index case and others.

The findings from this outbreak reflect current understanding of TB epidemiology in First Nations populations with regard to age, sex and location of disease (7); however, the rates of smear-positivity among active outbreak cases were much lower than expected. This low rate of smear-positivity likely reflects the enhanced case-finding, which facilitated earlier diagnosis.

The high prevalence of known risk factors among individuals identified as having active TB and LTBI in this outbreak may help explain its size and intensity. Substance use is known to suppress the immune system, increasing the likelihood of acquiring TB infection and progression to active TB disease (7–10). In addition, homelessness can be a critical factor in some TB outbreaks, as people experiencing housing insecurity are known to have multiple challenges, including access to health care and managing competing priorities that can hinder health-seeking behaviours (11–13). Investigations in this outbreak found that the index case had challenges accessing health care as a result of homelessness. The individual couch-surfed in several households, which lead to disease transmission or potential transmission to a number of people who lived or socialized there.

Despite the high rate of diabetes in First Nations populations and the associated increased risk of TB infection, its impact on the outbreak was minimal (7,14). Moreover, although prior TB infection is considered to reduce the likelihood of reacquiring TB (7,15), in the context of this outbreak, most past-positive individuals were considerably exposed and therefore required reassessment.

Results from the social network analysis echoed other findings, including the relationship between increased TB exposure and the likelihood of TB transmission and progression (7,13). Furthermore, the importance of location of households as it relates to transmission in an on-reserve setting was emphasized in this outbreak, providing further support to previous findings (13,16).

The implementation of social network contact investigation proved highly successful as it identified the majority of exposed individuals. Our results reflect the current understanding that social network contact investigation is a proven tool in settings where social stigma, high transiency, high degree of socialization and/or large numbers of exposed contacts exist (7,13,16). In contrast, traditional methods of contact investigation proved to be poor at identifying exposed individuals.

Despite the large influx of individuals, follow-up and treatment were major strengths during this outbreak. Understaffing and difficulty accessing health care is a common challenge on remote First Nations reserves (7,17); however, community capacity was increased following the start of the outbreak. Outbreak management efforts were also able to meet key management indicators outlined in the TB standards; these included all LTBI cases starting or being offered treatment and contact investigations being conducted within seven calendar days and contact follow-ups within 28 calendar days (7). Furthermore, all eligible LTBI cases accepted and were placed on treatment immediately following diagnosis, which is well above the current recommendation of 80% (7,18). Individuals in the community received DOT, a typical mode of treatment in challenging populations (7,19) The guideline on window prophylaxis, as outlined in the TB standards, was also followed exhaustively with all children younger than five years old (7).

Conclusion

TB outbreak interventions in unique populations, such as First Nations reserves, must consider context-specific challenges prior to their implementation, for example, population-specific demographics and risk factors of TB transmission. The high level of transiency between households in First Nations communities is an important factor to consider when conducting case findings, especially with people experiencing homelessness. Proactively tailoring management initiatives allows for greater outbreak management success and ultimately outbreak prevention in the future. Real-time social network contact investigation is an essential tool to enhance active case finding during outbreak investigation.

Authors' statement

BK — Conceptualization, data extraction and analysis, visualization, writing–original draft, writing–review & editing
SG — Conceptualization, writing–review & editing
GA — Conceptualization, writing–review & editing, supervision
SL — Writing–review & editing
LB — Investigation
SN — Investigation
NN — Conceptualization, investigation, writing–review & editing, supervision

The content and view expressed in this article are those of the authors and do not necessarily reflect those of the Government of Canada.

Competing interests

None.

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References

1. World Health Organization. Global tuberculosis report 2018. Geneva (CH): WHO; 2018. https://apps.who.int/iris/handle/10665/274453?locale-attribute=en&

2. World Health Organization. Towards TB elimination: an action framework for low-incidence countries. Geneva (CH): WHO; 2014. https://apps.who.int/iris/bitstream/handle/10665/132231/9789241507707_eng.pdf

3. Vachon J, Gallant V, Siu W. Tuberculosis in Canada, 2016. Can Commun Dis Rep 2018;44(3-4):75–81. DOI PubMed

4. TB Prevention and Control Saskatchewan. Tuberculosis in Saskatchewan and Canada [pre-release]. Saskatoon (SK): Saskatchewan Health Authority; 2018.

5. TB Partnership Working Group. Saskatchewan provincial tuberculosis strategy: 2013–2018. Government of Saskatchewan; 2013. https://www.saskatoonhealthregion.ca/locations_services/Services/TB-Prevention/Documents/Links/Saskatchewan%20Provincial%20Tuberculosis%20Strategy.pdf

6. Northern Inter-Tribal Health Authority. Unified Nations for a Healthier Tomorrow: 2016-2017 annual report. Prince Albert (SK): Northern Inter-Tribal Health Authority; 2017 (accessed 2021-06-02). https://www.nitha.com/wp-content/uploads/2018/03/Annual%20Report%2016-17%20Final.pdf

7. Menzies D. Canadian tuberculosis standards. 7th ed. Ottawa (ON): Canadian Thoracic Society, Canadian Lung Association, Public Health Association of Canada; 2014 (accessed 2021-09-11). https://www.canada.ca/en/public-health/services/infectious-diseases/canadian-tuberculosis-standards-7th-edition.html

8. Lin HH, Ezzati M, Murray M. Tobacco smoke, indoor air pollution and tuberculosis: a systematic review and meta-analysis. PLoS Med 2007;4(1):e20. DOI PubMed

9. Maurya V, Vijayan VK, Shah A. Smoking and tuberculosis: an association overlooked. Int J Tuberc Lung Dis 2002;6(11):942–51. PubMed

10. Rehm J, Samokhvalov AV, Neuman MG, Room R, Parry C, Lönnroth K, Patra J, Poznyak V, Popova S. The association between alcohol use, alcohol use disorders and tuberculosis (TB). A systematic review. BMC Public Health 2009;9:450. DOI PubMed

11. Gelberg L, Gallagher TC, Andersen RM, Koegel P. Competing priorities as a barrier to medical care among homeless adults in Los Angeles. Am J Public Health 1997;87(2):217–20. DOI PubMed

12. Tan de Bibiana J, Rossi C, Rivest P, Zwerling A, Thibert L, McIntosh F, Behr MA, Menzies D, Schwartzman K. Tuberculosis and homelessness in Montreal: a retrospective cohort study. BMC Public Health 2011;11(1):833. DOI PubMed

13. Cheng JM, Hiscoe L, Pollock SL, Hasselback P, Gardy JL, Parker R. A clonal outbreak of tuberculosis in a homeless population in the interior of British Columbia, Canada, 2008-2015. Epidemiol Infect 2015;143(15):3220–6. DOI PubMed

14. Jeon CY, Murray MB. Diabetes mellitus increases the risk of active tuberculosis: a systematic review of 13 observational studies. PLoS Med 2008;5(7):e152. DOI PubMed

15. Menzies D. Issues in the management of contacts of patients with active pulmonary tuberculosis. Can J Public Health 1997;88(3):197–201. DOI PubMed

16. Cook VJ, Shah L, Gardy J. Modern contact investigation methods for enhancing tuberculosis control in aboriginal communities. Int J Circumpolar Health 2012;71(1):18643. DOI PubMed

17. Aarluk Consulting Incorporated. Recruitment and retention of Inuit nurses in Nunavut. Iqaluit (NU): Nunavut Tunngavik Incorporated; 2009. https://www.tunngavik.com/files/2010/03/2010-02-nti-recruitment-retention-inuit-nurses-report_english.pdf

18. American Thoracic Society. Targeted tuberculin testing and treatment of latent tuberculosis infection. This official statement of the American Thoracic Society was adopted by the ATS Board of Directors, July 1999. This is a Joint Statement of the American Thoracic Society (ATS) and the Centers for Disease Control and Prevention (CDC). This statement was endorsed by the Council of the Infectious Diseases Society of America. (IDSA), September 1999, and the sections of this statement. Am J Respir Crit Care Med 2000;161(4 Pt 2):S221–47. DOI PubMed

19. Health Canada. Health Canada's strategy against tuberculosis for First Nations on-reserve. Ottawa (ON): Health Canada; 2012. https://www.canada.ca/en/public-health/services/publications/diseases-conditions/summary-health-canada-strategy-against-tuberculosis-first-nations-reserve.html

An outbreak of COVID-19 associated with a fitness centre in Saskatchewan: Lessons for prevention

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Abstract

Background: An outbreak of the coronavirus disease 2019 (COVID-19) occurred in Saskatchewan from September 12 to October 20, 2020. The index event, attendance at a local gym, seeded six additional clusters/outbreaks in multiple settings. These included a high school, a hospital, three workplaces (A, B and C) and several households. The overall cluster comprised 63 cases, 27 gym members and an additional 36 second, third and fourth generation cases.

Methods: All outbreak-related, laboratory-confirmed cases of COVID-19 were included in the analysis. Local public health authorities interviewed all cases and contacts and conducted environmental investigations of the fitness facility. We used descriptive epidemiological methods to understand transmission dynamics of the gym-associated cluster using case investigation, contact investigation and laboratory data, including whole genome sequencing.

Results: Sequencing data confirmed the unique lineage of cluster-related cases (n=32 sequenced; severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2] lineage B.1.1.72). In addition to gym attendance, infectious cases attended high school and were involved in other activities. Despite ongoing transmission in the fitness facility, no secondary cases were identified in the high school where four student belonging to the cluster attended class during their infectious period.

Conclusion: We describe an outbreak of COVID-19 where the index case(s) attended a fitness facility, and further spread occurred for 38 days despite active-case finding and isolation of positive cases over this period. Due to gym attendance over time, short-term closing and cleaning may not interrupt chains of transmission. Targeted, preventive public health action in fitness facilities may be warranted. Control measures worked to limit in-school acquisition.

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Keywords: COVID-19, SARS-CoV-2, gym, ventilation, physical distancing, cluster investigation, whole genome sequencing, active case finding, public health

Background

In September 2020, public health officials in Saskatchewan observed an increase in the number of laboratory-confirmed cases of the coronavirus disease 2019 (COVID-19) in city X. Five cases reported over a two-day period had a common link to a local gym. The date of onset of the index case was September 12, and an outbreak was declared on September 27. A total of 63 outbreak-related cases were identified with dates of onset from September 12 to October 20, 2020. Cases were confirmed to be related through whole genome sequencing. The majority (79.4%) of cluster-related cases were 18 to 64 years old, and 54.0% identified as male; all cases recovered. Secondary cases (n=23) were largely household contacts of gym goers.

Outbreaks of COVID-19 in fitness centres/gyms have occurred in many jurisdictions throughout the pandemic. Gyms are high-risk settings that facilitate the severe acute respiratory

syndrome coronavirus 2 (SARS-CoV-2) transmission. Researchers hypothesize that several risk factors contribute to viral transmission in fitness facilities:

- The length of time individuals typically spend in a gym (about 50 minutes)
- Increased respiration during physical activity
- Viral load of infectious person
- Facility size and ventilation
- Increased risk associated with group exercise classes, particularly where participants/instructors are in close proximity and/or speak loudly over music (1–6)

Of note, analytic studies examining the risk of community-acquired SARS-CoV-2 infection and gym attendance have not consistently pointed to an increase in disease acquisition among gym goers. For example, a study conducted in Oslo, Norway, randomly allocated individuals to either access to a fitness facility or no access to a fitness facility. Test positivity rates between the two groups after a 14-day period did not differ substantially (zero cases in the no access; one case not acquired in the fitness facility within the group with access) (7). Another recent case–control study found that, even after adjusting for potential confounding factors, attendance at a gym in the 14-day period prior to illness onset did not statistically significantly differ between symptomatic individuals who tested positive for SARS-CoV-2 infection and individuals who tested negative (8).

Public health conducts detailed work when investigating clusters of illness in order to mitigate the spread of disease and prevent future outbreaks. Particularly when the investigation involves a novel pathogen associated with a worldwide pandemic, thorough cluster investigations can serve to provide important data for understanding the spread and risk of acquisition. The objectives of our outbreak investigation were to identify and isolate all SARS-CoV-2 infectious cases to prevent further transmission and to understand the underlying conditions that may have contributed to viral transmission at the fitness facility, providing data for preventive action.

Methods

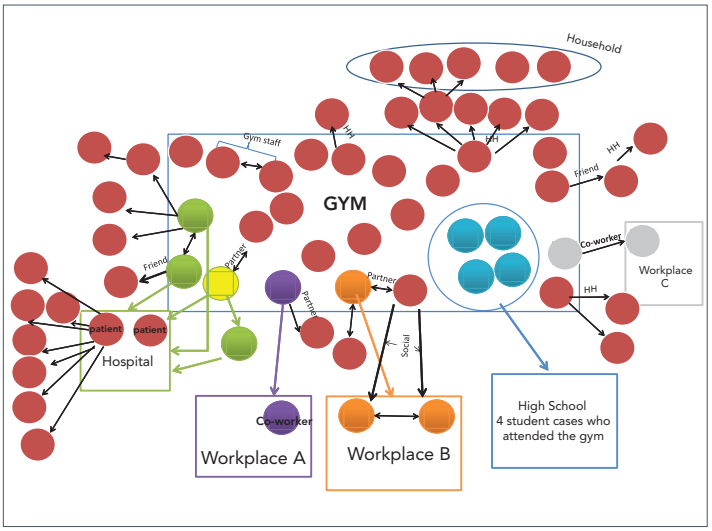
The Roy Romanow Provincial Laboratory (RRPL) uses reverse transcription polymerase chain reaction (RT-PCR) tests to identify the presence of SARS-CoV-2 in all submitted nasopharyngeal specimens. Under the provincial *Public Health Act, 1994*, all laboratory-confirmed cases of SARS-CoV-2 infection must be reported to local public health authorities. Through individual case interviews, using a standardized data collection worksheet, local authorities collect information on case demographics, date of symptom onset and all activities undertaken by the case during the infectious period.

In this investigation, trained public health nurses undertook contact-tracing interviews for all close contacts named by cases. Cases were required to self-isolate for 14-days from date of last contact with a confirmed case in order to break subsequent chains of transmission. In addition, all close contacts were offered testing. A case was defined as a lab-confirmed case of COVID-19 with symptom onset of September 12, 2020, or later, epidemiologically linked to the fitness centre. Epi-linked cases either attended the gym in person or identified as part of a transmission chain linked to a gym attendee.

We extracted laboratory data from the provincial laboratory information system, a repository of all laboratory results. Canada's National Microbiology Laboratory supplied whole genome sequencing data for all outbreak-related specimens.

We used descriptive epidemiology (counts, rates, proportions, epidemic curve) to understand the burden and timing of disease in the index and associated clusters and to characterize the cases and their outcomes. We used both detailed case and cluster investigation data to create a visual of the index cluster and transmission to other clusters (**Figure 1**). Whole genome sequencing data served to verify whether the cluster-associated cases were related. Additional qualitative contextual information provided by public health investigators, including public health nurses and public health inspectors, were included in the descriptive analysis.

Figure 1: Visualization of the index cluster and the spread to other clusters



Abbreviation: HH, household

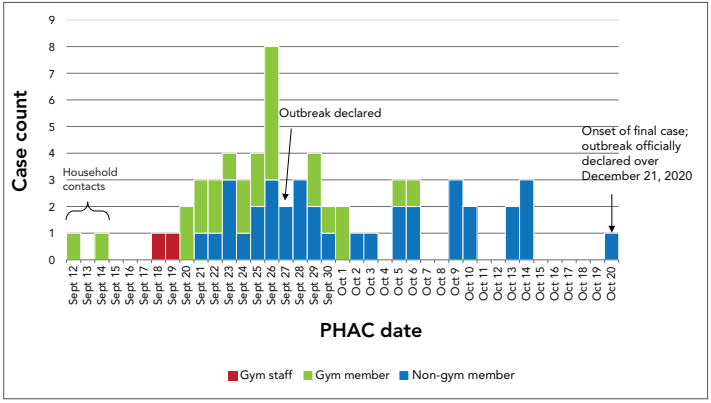
Results

The majority (79.4%) of the 63 cluster-related cases were 18 to 64 years old, and 54.0% were male. Just over half (57.1%) were not fitness centre members. Secondary cases were largely household contacts. No cases were hospitalized or died (see **Table 1** for a description of outbreak-associated cases; see **Figure 2** for an epidemic curve showing case data by date of symptom onset).

Table 1: Descriptive epidemiology of COVID-19 cases arising from attendance at a gym as the index exposure, City X, Saskatchewan, September 12 to October 20, 2020 (n=63)

Variable	Category	n	%
Age	Children (<18 years)	8	12.6
	Adults (18–64 years)	50	79.4
	Seniors (65+ years)	5	7.9
Sex	Male	34	54.0
	Female	29	46.0
Gym member	Yes	27	42.9
	No	36	57.1
Associated cluster settings	High school	4	6.3
	Hospital	13	20.6
	Workplace A	2	3.2
	Workplace B	3	4.8
	Workplace C	2	3.2
Case type	Secondary	23	36.5
	Tertiary	11	17.5
	Quaternary	2	3.2
Outcome	Hospitalized	0	0
	Not hospitalized, recovered	57	100.0
	Died	0	0
Gym attack rate	Cases/all gym-members who attended the gym in the first few weeks of investigation (September 20–27 and October 1–3)	27/251	10.8

Figure 2: Epidemic curve of COVID-19 outbreak associated with gym attendance, September 12 to October 20, 2020, by date of symptom onset or collection date (where asymptomatic) and cluster affiliation, city X, Saskatchewan (n=63)



Abbreviation: PHAC, Public Health Agency of Canada

The index case date of symptom onset was September 12. Two days later, a gym attendee and household contact of the index case became ill. Four days after that another gym attendee became ill; transmission within the facility continued for several more weeks.

The index case reported engaging in individual physical activity (not group exercise) while at the gym and reported adherence to the recommended public health interventions. Mask wearing in fitness facilities was not mandated through a provincial health order until November 6, 2020.

Following declaration of the outbreak on September 27, information was gathered from the gym on attendance over the week prior and following the outbreak declaration (September 20 to October 3). The gym reported that 251 people attended over this time period for an overall attack rate of approximately 11% among gym goers (27/251; 10.8%).

Cases directly linked to the gym continued to occur until October 20 (total n=27 individuals). Two staff members were infected over the time period and reported mainly individual workouts (bodybuilding and cardio).

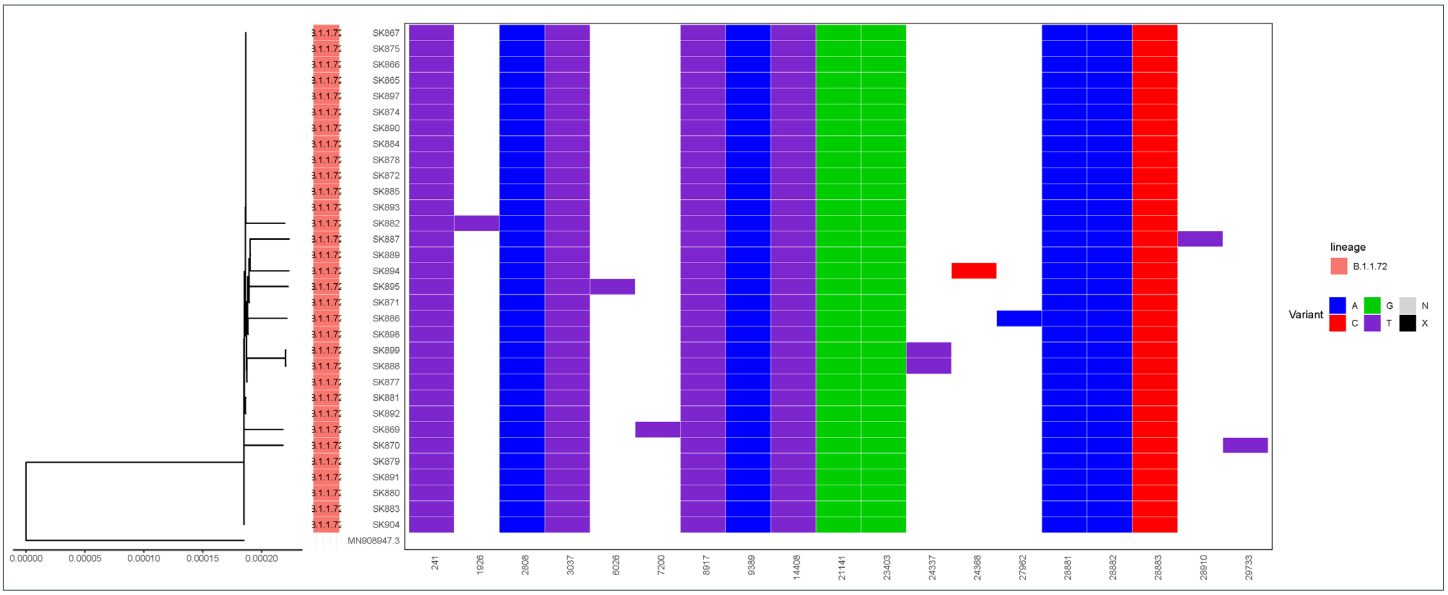
Four cases who attended the gym multiple times between September 16 and 24 also attended a large regional high school (n=590) while infectious. In spite of active-case finding, including testing of approximately 100 students at the high school, there was no evidence of secondary transmission in the school. These cases also took part in other high-risk activities while infectious at the school, including participating in football and hockey and attending at least four different class cohorts. Despite this, there was no evidence of additional cases at the school.

Public health measures to reduce SARS-CoV-2 transmission at the school were numerous. They included the following: mandatory masking in the classroom for Grades 4 and higher, including in the gymnasium; a "five block" schedule where students were placed in small learning groups; in-class lunch eating only; and staggered breaks throughout the day. After the four infectious cases were discovered, the school moved to online learning for approximately two weeks.

Laboratory investigations

Whole genome sequencing data for 32 of the cluster-related cases is shown in **Figure 3**. Sequence data analysis assigned all 32 specimens to pangolin lineage using Pangolin v2.1.7 and PangoLEARN data release January 16, 2021 (Centre for Genomic Pathogen Surveillance, United Kingdom), with nine unique single nucleotide variant profiles. SARS-CoV-2 in lineage B.1.1 has been identified worldwide and has been frequently found in sequences elsewhere in Saskatchewan. To date, the provincial laboratory has not identified SARS-CoV-2 lineage B.1.1 with the same unique nucleotide variant profile elsewhere in Saskatchewan, but this does not preclude its presence (9,10).

Figure 3: Whole genome sequencing data



Environmental investigation

With the collaboration of the gym owner, public health inspectors worked to investigate, respond and mitigate viral spread at the gym. Public health closed the gym on September 26 at 22:00 hours and permitted it to reopen on September 30 at 23:59 hours. Public health inspectors provided recommendations to the owner (physical distancing of patrons/equipment, cleaning product ingredient recommendations, frequency of cleaning) and, in accordance with government guidelines (11), permitted the gym to reopen following a deep clean of the facility.

The owner, in discussions with the local public health inspector, reported that gym members had adhered to physical distancing recommendations, but may not have adhered to the masking guidelines (provincial mask mandates were not in effect at the time). The inspector noted that not all gym equipment was spaced two metres apart; some cardio equipment was moved in order to comply with distancing regulations. Disinfection of the gym by electrostatic sprayer reportedly occurred; however, it was not clear how systematically or how frequently this took place.

Inspection of the air ventilation system found two main parts: the system in the main gym area was installed in 2013, while the system in the second, smaller area was installed in 2019. The inspection noted the air handling system was adequate for proper ventilation; however, actual airflow and air-exchange measurements were not measured. The gym owner reported changing the air filters every two weeks. Of note, the public health inspector indicated that the ventilation in the gym may have played a role in the outbreak: this particular gym is located in a low-ceiling basement setting.

Discussion

An outbreak of COVID-19 was associated with attendance at a gym in a Canadian city. A total of 63 outbreak-related cases, confirmed through whole genome sequencing, were identified with onset dates from September 12 to October 20, 2020; all cases recovered. Although outbreak-related cases attended school while infectious and in spite of active-case finding, including testing of approximately 100 students at the high school, there was no evidence of secondary transmission within the school. In this outbreak, gym attendance did not result in a one-time superspreading event. As a common cohort attends gyms over time, we hypothesize that short-term closing and cleaning may not be sufficient to interrupt chains of transmission in fitness facilities.

Public health investigations, including thorough case investigation and active-case finding by trained public health nurses, contact tracing, isolation of exposed individuals, inspection, education, surveillance and testing, all combined to control the spread of COVID-19. Despite that cases from the gym also attended high school classes and took part in sports activities while infectious, no viral transmission occurred within the school.

At the time the infectious cases attended school, the school had implemented numerous public health measures intended to reduce viral transmission. It is hypothesized that these measures reduced in-school spread; combined with growing evidence of children being less efficient viral transmitters when infected with wild type virus (12,13), though this rationale may be less applicable to older teenagers.

In this propagated outbreak investigation, we found gym attendance did not result in a one-time superspreading event. Dates of symptom onset for gym attendees were spread out over time (Figure 2), indicative of a cohort of gym goers intermingling at different times. Due to the nature of ongoing gym attendance over time, short-term closing and cleaning, as recommended in government guidelines for gym and fitness centres (11), will not necessarily interrupt chains of transmission.

Gyms/fitness facilities have been identified as high-risk settings for SARS-CoV-2 transmission in previous outbreak reports (1,3,4). Outside of outbreak reports, however, studies attempting to quantify the community-associated risk of infection in gyms have not uniformly demonstrated an increased risk. In the absence of an infectious case linked to a facility, as was the case in the Helsingen *et al*. study (7), it is not surprising test positivity rates among the gym goers and the non-gym goers remained low. A case-control study conducted by the Centers for Disease Control and Prevention (CDC) included only symptomatic individuals, that is, those who tested negative were controls and those who tested positive were cases (8). Given that study authors recruited only symptomatic positive individuals at the time of testing, it is possible a systematic selection bias occurred. Asymptomatic, infectious individuals (not sampled in the study) may have been more likely to visit a fitness facility prior to testing than symptomatic individuals (population under study) at the time of testing who may have been less likely to visit a fitness centre prior to testing if they were feeling unwell. This bias may have artificially decreased the risk associated with this setting type among study participants.

Cluster investigations are important for understanding the transmission dynamics of pathogens. Public health investigations have repeatedly demonstrated that there is a risk for infection with SARS-CoV-2 in fitness facilities. In the cluster described in this article, we hypothesize that the following factors likely contributed to viral transmission in the facility: non-adherence to some recommended public health measures; outbreak occurring prior to provincial mask mandate in fitness facilities; and low ceilings/basement setting with potentially inadequate ventilation.

Our study has limitations. We were not able to test all close contacts (investigators estimate we tested approximately 70%). A complete list of gym members was not available, and not all named contacts accepted a test or were receptive to public health follow-up. In addition, a fitness-facility-specific questionnaire was not administered to all cluster-involved cases because of public health workload. This limits our ability to quantify the impact of other variables that may be of importance, such as the amount of time spent at the gym and the number of visits to the facility during the period of interest.

It is likely that the increased risk of SARS-CoV-2 infection associated with fitness facility attendance is multifactorial. Gym attendance, by its very nature, occurs not just at one point in time and space (generating superspreading events); rather, risk of infection is associated with ongoing exposure among gym members. In this instance, public health measures of closing and cleaning fitness facilities may not have been sufficient. Targeting fitness facilities could be useful in reducing transmission, for example, proactive inspection of ventilation systems; client manifests (list of all gym attendees) required to be reported to public health; use of technology, such as QR codes, to track clients; restricted activities in gyms known to be higher risk (spin class, group fitness); and implementing active-case finding/rapid point-of-care testing, particularly among staff and instructors have a demonstrated higher risk of transmission than attendees (3).

Conclusion

Indoor fitness facilities are high-risk settings for SARS-CoV-2 viral transmission. Active-case finding using rapid point-of-care test kits at fitness facilities or routine testing of all gym members when community transmission rates are high may be effective strategies to consider in high-risk settings. As immunization against SARS-CoV-2 infection becomes routinely available at the population level, immunization status may be a useful piece of information to collect in such high-risk settings. It is likely immunized individuals will shed less virus; however, adherence to public health measures (such as deep cleaning, disinfection of equipment, physical distancing, reduction in group fitness activities and capacity limits) and mask use where ventilation is poor will continue to be important. This recommendation may extend to other settings such as places of worship and other congregate settings.

Authors' statement

EH, AL, RM and MT — Conducted data collection
MT, AC, JM, RM and MA — Prepared the materials and performed the analysis
MA — Wrote the manuscript

All authors contributed to the study conception and design, the interpretation, commented on drafts and contributed wording, read and approved the final manuscript.

The content and view expressed in this article are those of the authors and do not necessarily reflect those of the Government of Canada.

Competing interests

The authors declare that they have no conflict of interest.

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References

1. Bae S, Kim H, Jung TY, Lim JA, Jo DH, Kang GS, Jeong SH, Choi DK, Kim HJ, Cheon YH, Chun MK, Kim M, Choi S, Chun C, Shin SH, Kim HK, Park YJ, Park O, Kwon HJ. Epidemiological characteristics of COVID-19 outbreak at fitness centers in Cheonan, Korea. J Korean Med Sci 2020;35(31):e288. DOI PubMed

2. Pung R, Chiew CJ, Young BE, Chin S, Chen MI, Clapham HE, Cook AR, Maurer-Stroh S, Toh MP, Poh C, Low M, Lum J, Koh VT, Mak TM, Cui L, Lin RV, Heng D, Leo YS, Lye DC, Lee VJ; Singapore 2019 Novel Coronavirus Outbreak Research Team. Investigation of three clusters of COVID-19 in Singapore: implications for surveillance and response measures. Lancet 2020;395(10229):1039–46. DOI PubMed

3. Jang S, Han SH, Rhee JY. Cluster of coronavirus disease associated with fitness dance classes, South Korea. Emerg Infect Dis 2020;26(8):1917–20. DOI PubMed

4. National Collaborating Centre for Methods and Tools. Rapid review: What is known about the risk of COVID-19 transmission across different indoor settings in the community such as restaurants and gyms? Hamilton (ON): NCCMT; 2020. https://www.nccmt.ca/covid-19/covid-19-rapid-evidence-service/30

5. Furuse Y, Sando E, Tsuchiya N, Miyahara R, Yasuda I, Ko YK, Saito M, Morimoto K, Imamura T, Shobugawa Y, Nagata S, Jindai K, Imamura T, Sunagawa T, Suzuki M, Nishiura H, Oshitani H. Clusters of coronavirus disease in communities, Japan, January–April 2020. Emerg Infect Dis 2020;26(9):2176–9. DOI PubMed

6. Buonanno G, Morawska L, Stabile L. Quantitative assessment of the risk of airborne transmission of SARS-CoV-2 infection: prospective and retrospective applications. Environ Int 2020;145:106112. DOI PubMed

7. Helsingen LM, Løberg M, Refsum E, Gjøstein DK, Paulina Wieszczy P, Olsvik Ø, Juul FE, Barua I, Jodal HC, Herfindal M, Mori Y, Jore S, Lund-Johansen F, Fretheim A, Bretthauer M, Kalager M; The TRAiN study group. A Randomised Trial of Covid-19 Transmission in Training Facilities. medRxiv 2020.06.24.20138768 [Preprint]. Posted 2020-11-17 (accessed 2020-11-24). DOI

8. Fisher KA, Tenforde MW, Feldstein LR, Lindsell CJ, Shapiro NI, Files DC, Gibbs KW, Erickson HL, Prekker ME, Steingrub JS, Exline MC, Henning DJ, Wilson JG, Brown SM, Peltan ID, Rice TW, Hager DN, Ginde AA, Talbot HK, Casey JD, Grijalva CG, Flannery B, Patel MM, Self WH; IVY Network Investigators; CDC COVID-19 Response Team. CDC COVID-19 Response Team. Community and close contact exposures associated with COVID-19 among symptomatic adults ≥18 years in 11 outpatient health care facilities— united States, July 2020. MMWR Morb Mortal Wkly Rep 2020 Sep;69(36):1258–64. DOI PubMed

9. GISAID. Lineage B.1.1.72 [Internet]. Hixton (UK): Centre for Genomic Pathogen Surveillance; 2020 (accessed 2020-11-24). https://cov-lineages.org/lineages/lineage_B.1.1.72.html

10. GISAID. cov-lineages/pangolin [Internet]. Hixton (UK): Centre for Genomic Pathogen Surveillance; 2021 (accessed 2021-02-17). https://github.com/cov-lineages/pangolin

11. Government of Saskatchewan. Gyms and fitness facilities guidelines. Guidelines for the re-open Saskatchewan plan [Internet]. Regina (SK): Government of Saskatchewan; 2020 (accessed 2020-11-15). https://www.saskatchewan.ca/government/health-care-administration-and-provider-resources/treatment-procedures-and-guidelines/emerging-public-health-issues/2019-novel-coronavirus/re-open-saskatchewan-plan/guidelines/gyms-and-fitness-facilities-guidelines

12. Isaacs D, Britton P, Howard-Jones A, Kesson A, Khatami A, Marais B, Nayda C, Outhred A. To what extent do children transmit SARS-CoV-2 virus? J Paediatr Child Health 2020;56(6):978–9. DOI PubMed

13. Riediker M, Morawska L. Low exhaled breath droplet formation may explain why children are poor SARS-CoV-2 transmitters. Aerosol Air Qual Res 2020;20(7):1513–5. DOI

Invasive bacterial diseases in northern Canada, 1999 to 2018

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Abstract

Background: The International Circumpolar Surveillance (ICS) program conducts surveillance on five invasive bacterial diseases: pneumococcal disease (IPD), group A streptococcus (iGAS), *Haemophilus influenzae* (Hi), meningococcal disease (IMD) and group B streptococcus (GBS). Invasive bacterial diseases have a higher burden of disease in northern populations than the rest of Canada.

Methods: To describe the epidemiology of invasive bacterial diseases in northern Canada from 1999 to 2018, data for IPD, iGAS, Hi, IMD and GBS were extracted from the ICS program and the Canadian Notifiable Diseases Surveillance System (CNDSS) and analyzed.

Results: The annualized incidence rates for IPD, iGAS, Hi, GBS and IMD were 23.3, 10.5, 8.9, 1.9 and 1.1 per 100,000 population, respectively. The incidence of IPD, iGAS and Hi serotype b were 2.8, 3.2 and 8.8 times higher, respectively, in northern Canada than in the rest of Canada. Rates of disease decreased statistically significantly for IPD (β=−0.02) and increased statistically for iGAS (β=0.08) and Hi serotype a (β=0.04) during the study period. In Northern Canada, the annualized incidence rates for IPD, iGAS and Hi were statistically higher for Indigenous residents than for non-Indigenous residents. The highest incidence rates were among the very young and older age groups.

Conclusion: Invasive bacterial diseases represent a high burden of disease in Canada's northern populations. Indigenous peoples, children and seniors are particularly at risk.

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Keywords: Indigenous health, surveillance, *Haemophilus influenzae*, streptococcus, meningococcal disease, pneumococcal disease, vaccine, epidemiology

Introduction

The International Circumpolar Surveillance (ICS) program is a population-based invasive bacterial disease surveillance network of countries with circumpolar regions (1). The ICS program conducts surveillance on invasive bacterial diseases caused by *Streptococcus pneumoniae* (invasive pneumococcal disease, IPD), *Haemophilus influenzae* (invasive *Haemophilus influenzae*, Hi), *Streptococcus pyogenes* (invasive group A streptococcus, iGAS), *Neisseria meningitidis* (invasive meningococcal disease, IMD) and *Streptococcus agalactiae* (invasive group B streptococcus, GBS). Disease rates caused by these pathogens are elevated among the Indigenous peoples in countries with Arctic regions (2–7).

The ICS program started monitoring IPD in Canada in 1999 and expanded to monitoring the other four diseases in 2000. Six Canadian regions participate in the ICS program: Nunavut, the Northwest Territories, Yukon, northern Labrador and two northern Québec regions, Nunavik and Cree Territory. The ICS program also includes two reference laboratories, the National Microbiology Laboratory (NML) and the Laboratoire de santé publique du Québec (LSPQ), and a network of regional laboratories located across Canada that serves the northern regions. Up until 2009, the National Centre for Streptococcus (NCS) participated in the ICS program as a reference laboratory.

In 2018, the Canadian ICS population was estimated to be 168,090, accounting for 0.45% of the total national intercensal population of 37 million. While Indigenous people account for 4.9% of the total Canadian population, they represent approximately 60% of the northern Canadian population (8).

The National Advisory Committee on Immunization (NACI) provides national vaccine recommendations for IPD, HI and IMD; however, adoption of these recommendations are the responsibility of the provincial and territorial jurisdictions. The *H. influenzae* serotype b (Hib) *vaccine, the* meningococcal C conjugate (MenC) vaccine for infants and the Men-C-ACYW vaccine for early adolescents have been part of routine childhood immunization programs since 1997, 2007 and 2011, respectively (9). As part of the routine childhood immunization schedule, all six northern regions implemented the 7-valent pneumococcal conjugate vaccine (PCV7) for children younger than two years of age between 2002 and 2007, replacing PCV7 with the 10-valent pneumococcal conjugate vaccine (PCV10) by 2010 (10) and subsequently with the 13-valent pneumococcal conjugate vaccine (PCV13) by 2011 (according to a survey sent to ICS invasive bacterial diseases working group members). In mid-2018, Cree Territory and Nunavik switched to a four-dose PCV10 and PCV13 (3+1) vaccination schedule (*personal communication, ICS invasive bacterial diseases working group members, 2019*). NACI recommends that the 23-valent pneumococcal polysaccharide vaccine (PPV23) be given to those aged two years or older with high risk of IPD, and adults 65 years and older (11). High-risk children and adults include those with certain chronic diseases, immunocompromising conditions or functional or anatomic asplenia (11). The Canadian Immunization Guide recommendations for PPV23 have been implemented in all six regions, with minor differences in the age of vaccine administration in some regions (11–17).

The objective of this report is to describe the epidemiology of invasive bacterial diseases in northern Canada over the first 20 years of the ICS program (1999–2018) and compare their incidence rates to the rest of Canada. This report includes ICS data that have been previously published (1999–2013) (5,7). These data were included in this paper to provide a comprehensive analysis of invasive bacterial diseases over the first 20 years of the ICS program.

Methods

Epidemiological data

Data were extracted from the ICS program (1999–2018) and the Canadian Notifiable Diseases Surveillance System (CNDSS, 2000–2018). CNDSS data from before 2000 were not available. CNDSS data for invasive Hi non-serotype b were not included as only certain provinces and territories have reported these for certain years. CNDSS data for GBS were also not included because only GBS of newborns are nationally reported whereas ICS conducts surveillance on all GBS cases. Cases meeting the national case definition were included (18). Because there is no national case definition for general population GBS, the ICS case definition extends the national case definition for GBS of the newborn to individuals of all ages in northern Canada. Data include non-nominal demographic information, clinical information, severity, outcomes, underlying conditions and immunization history.

Laboratory data

S. pneumoniae isolates were serotyped using the Quellung reaction with pool, group, type and factor commercial antisera (Statens Serum Institut, Copenhagen, Denmark) (19). *S. pyogenes* isolates were identified using β-hemolysis on sheep blood agar, bacitracin susceptibility and pyrrolidonyl arylamidase test. M serotyping of invasive *S. pyogenes* isolates from 1999 to September 2006 was performed using a serological typing protocol described by Tyrrell *et al.* (20). From October 2006 to 2018, molecular *emm* typing of invasive *S. pyogenes* isolates was performed using polymerase chain reaction (PCR) tests and DNA sequencing according to the Centers for Disease Control and Prevention (CDC) protocol; the CDC invasive *S. pyogenes emm* sequence database was searched for designation of *emm* type using the basic local alignment search tool (BLAST) (21,22). *S. agalactiae* isolates were serotyped by latex agglutination (SSI Diagnostica; Statens Serum Institute, Copenhagen, Denmark) as described by Slotved *et al*. (23). *H. influenzae* was identified using Gram stain morphology and standard biochemical tests (24). The bacterial slide agglutination test, using commercial antisera (Difco, Becton Dickinson, Mississauga, Ontario), was used for serotyping, with results confirmed using PCR (25). *N. meningitidis* was identified by standard biochemical tests with serogrouping determined by a bacterial agglutination tests using in-house-produced antisera against the 12 different serogroups (26).

Phenotypic antimicrobial susceptibilities for the Canadian isolates were determined using Sensititre STP6F micro-broth dilution panels (Thermo Fisher, United States). Resistant, intermediate or susceptible interpretations of minimum inhibitory concentration for erythromycin, clindamycin, penicillin, cefepime, cefotaxime, ceftriaxone, meropenem, trimethoprim/sulfamethoxazole and tetracycline were determined using Clinical Laboratory Standards Institute guidelines (27).

Population data

Population estimates were based on the final postcensal estimates for July 1, 2016 (8). The Indigenous populations for northern Canada were estimated using the 1996, 2001, 2006, 2011 and 2016 Census (8,28–31). The proportion of the Indigenous population for a given census year was used to estimate the Indigenous population for the years until the next census.

Analysis

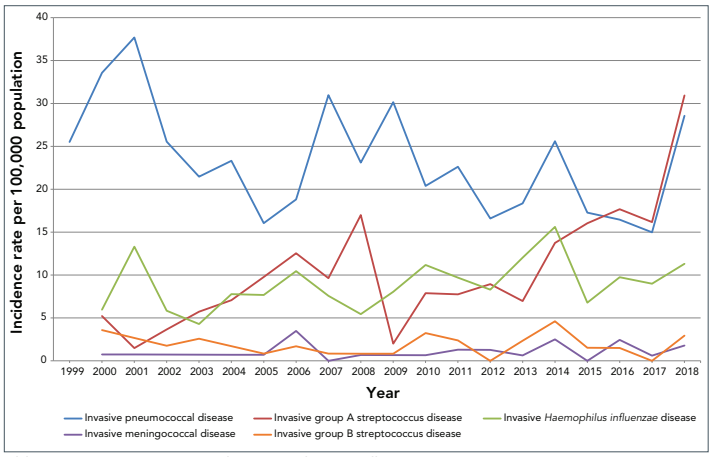
The direct method was used to calculate age-standardized rates by multiplying the age-specific rates by the 2011 general

Canadian population weights (32). Confidence intervals (95% CIs) of age-standardized rates were calculated using the method based on the gamma distribution (33). Two-tailed Fisher's exact and chi-square tests were used to compare proportions. Poisson and negative binomial regression were used to estimate disease trends. The exact Poisson test was used to compare rates. Statistical significance was set at $p<0.05$.

Analyses were conducted using Excel 2016 (Microsoft Corp., Redmond, Washington, United States), SAS Enterprise Guide 7.1 (SAS Institute Inc., Cary, North Carolina, United States) and R version 3.6.2 (R Foundation for Statistical Computing, Vienna, Austria).

Incidence rates for neonatal GBS cases were not calculated because annual live birth estimates for the northern regions were not available for this report. Age-standardized rates by sex for IMD and GBS were not calculated due to small numbers. GBS is not reportable in the province of Québec, and therefore Cree Territory and Nunavik are not included in the analyses.

Figure 1: Overall crude incidence rates of invasive bacterial diseases in the ICS regions by disease and year, 1999–2018



Abbreviation: ICS, International Circumpolar Surveillance

Results

Overview

From 1999 to 2018, a total of 692 cases of IPD were reported in northern Canada. From 2000 to 2018, a total of 311 cases of iGAS, 258 cases of Hi, 44 cases of GBS and 31 cases of IMD were reported in the same region. Demographic information for each disease is presented in **Table 1**, and the overall incidence for each disease from 1999 to 2018 is presented in **Figure 1**.

Invasive pneumococcal disease

The regression analyses found a significant overall downward trend in IPD incidence rate (per 100,000 population) over time (β=−0.02; $p=0.01$), but there was a sharp 92% increase in the number of cases reported from 2017 to 2018. The age-standardized incidence rates for males (28.26; CI: 25.30–31.53) and females (23.86; CI: 20.77–27.36) did not differ significantly. The incidence rate (per 100,000 population) was highest among infants younger than one year old (146.78; CI: 117.59–183.23), children one to four years old (49.80; CI: 41.13–60.29) and adults 60 years and older (51.07; CI: 43.22–60.32). The difference in the average annual incidence rates between those of Indigenous and non-Indigenous origin was significant in northern regions (Table 1). The age-standardized incidence rate of IPD in northern regions was 2.8 times higher than the rest of Canada (**Table 2**).

PCV7 serotypes (β=−0.19; $p<0.0001$) and PCV10-specific serotypes (β=−0.01; $p<0.0001$) have decreased significantly from 1999 to 2018 (**Figure 2**). PPV23-specific serotypes (β=0.06; $p<0.0001$) and non-vaccine serotypes have increased significantly from 1999 to 2018 (β=0.04; $p<0.05$). There were no statistically significant changes to the PCV13-specific serotypes from 1999 to 2018. Of the cases with available serotype data collected between 1999 and 2010, the most common were serotype 1 (18%), 8 (11%) and 14 (7%). After 2010, the most common serotypes were 7F (12%), 22F (9%), 10A (9%) and 9N (8%).

Table 1: Characterization of disease in northern Canada by crude incidence rate, demographics, fatality and hospitalization, 1999/2000–2018

Disease	N	Crude incidence rate per 100,000 population	Median age, years	Age range	Annualized incidence rate per 100,000 population by ethnicity			Hospitalization				Fatality[a]			
					Indigenous ethnicity	Non-Indigenous ethnicity	Difference between ethnicities, *p*-value	Cases		Incicence rate ratio		Death		Fatality rate ratio	
								N	%	Male:female	*p*-value	N	%	Male:female	*p*-value
IPD	692	23.3	37	0–98	31.3	7.0	<0.0001[b]	585	84.5	1.3	0.006[b]	59	8.5	1.3	0.3
iGAS	311	10.5	50	0–98	14.8	2.7	<0.0001[b]	273	87.8	1.3	0.03[b]	30	9.6	1.2	0.6
Hi	258	8.9	1	0–93	13.1	0.9	<0.0001[b]	222	86.0	1.1	0.5	19	7.4	1.6	0.3
GBS	44	1.9	32.5	0–88	1.8	1.3	0.3	41	93.2	0.9	0.7	0	0		–[c]
IMD	31	1.1	1	0–56	1.4	0.6	0.06	28	90.3	0.7	0.4	4	12.9	All male	0.06

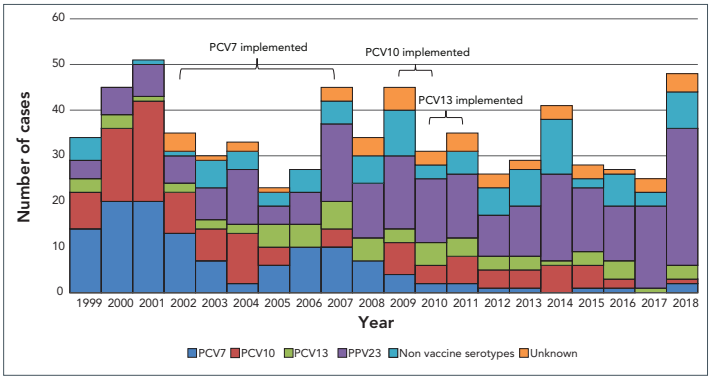
Abbreviations: GBS, group B streptococcus; Hi, invasive *Haemophilus influenzae*; iGAS, invasive group A streptococcus; IMD, invasive meningococcal disease; IPD, invasive pneumococcal disease
[a] Fatality is defined as death during the individual's illness
[b] Statistically significant
[c] No deaths were reported for either males or females

Table 2: Age-standardized incidence rates (per 100,000 population) of invasive bacterial diseases in Canada, by disease, region and year, 2000/2001–2018[a]

Disease	Age-standardized incidence rates			
	Northern regions		Rest of Canada	
	95%	CI	95%	CI
IPD[b]	25.68	23.45–28.09[c]	9.13	9.05–9.21[c]
iGAS	14.16	12.31–15.86[c]	4.45	4.40–4.50[c]
Hib[d]	0.70	0.45–1.13[c]	0.08	0.08–0.09[c]
IMD	0.75	0.51–1.17	0.52	0.51–0.54

Abbreviations: CI, confidence interval; Hib, *Haemophilus influenzae* serotype b; ICS, International Circumpolar Surveillance; iGAS, invasive group A streptococcus; IMD, invasive meningococcal disease; IPD, invasive pneumococcal disease
[a] One case of IPD and one case of iGAS with missing age were excluded from the ICS incidence rate calculation
[b] Age-standardized incidence rates for IPD do not include data for 1999–2000, when data were either not available or not reported by all provinces
[c] As the CIs are not overlapped, the age-standardized incidence rates for IPD, iGAS and Hib are significantly different between northern regions and the rest of Canada
[d] Comparisons of age-standardized incidence rates for *Haemophilus influenzae* serotype non-b (a–f and non-typeable serotypes) between northern Canada and the rest of Canada were not performed as these data are not available for all provinces

Figure 2: Distribution of invasive pneumococcal disease serotypes in northern Canada, by year and by vaccine serotype[a], 1999–2018



Abbreviations: PCV7, 7-valent pneumococcal conjugate vaccine; PCV10, 10-valent pneumococcal conjugate vaccine; PCV13, 13-valent pneumococcal conjugate vaccine; PPV23, 23-valent pneumococcal polysaccharide vaccine
[a] For the purposes of this graph, PCV7 includes all serotypes covered by the PCV7 vaccine, PCV10 includes the three additional serotypes not covered by the PCV7 vaccine, PCV13 includes the three additional serotypes not covered by the PCV10 vaccine, and PPV23 includes all serotypes not covered by any of the conjugate vaccines

All ICS regions had implemented the PCV13 vaccine schedule by January 1, 2011. Thirty-four cases that occurred after PCV13 implementation were age-appropriately vaccinated with at least one dose and serotyped. Individuals were age-appropriately vaccinated based on the minimum three-dose national recommendation. Of these 34 cases, three cases (9%) had vaccine-breakthrough disease. Breakthrough disease occurs if the serotype of the case is any of the serotypes covered by the vaccine administered. Two of these cases were serotype 19A and one was serotype 3. Of the 55 PPV23-vaccinated and serotyped cases, 46 cases (84%) had vaccine-breakthrough disease.

Of the 670 cases with information on clinical manifestation, bacteremia (n=577; 86.1%) and pneumonia (n=442; 66.0%) were the most commonly reported manifestations. Of the 692 IPD cases, 585 (85%) were hospitalized.

Of the 649 cases with information on fatality, 59 were fatal (9.1%).The majority of the fatal cases were 60 years and older (n=24; 41%), followed by those aged 40 to 59 years (n=20; 34%). Individuals in these two age groups had significantly higher risk of fatality than those in younger age groups (case fatality ratio [CFR] =14.2% vs. 4.4%; $p<0.0001$). The CFR did not vary between Indigenous and non-Indigenous people (9.5% vs. 6.1%; $p=0.31$). Of the 53 fatal cases with serotype information, 45% were PPV23-specific serotypes not covered by PCV13. The top six reported serotypes were 20, 10A, 15C, 22F, 15A and 3.

When fatality and hospitalization rates were compared for males and females, hospitalization was significantly higher for males (Table 1).

Antimicrobial susceptibility was examined for the IPD isolates with available data (**Table 3**).

Table 3: Proportion of antibiotic-susceptible IPD and iGAS isolates, 1999/2000–2018[a]

Antibiotic	Proportion of susceptible IPD isolates, %	Proportion of susceptible iGAS isolates, %
Ampicillin	100	100
Cefotaxime	100	100
Ceftriaxone	98.3	100
Cefuroxime	100	N/A
Chloramphenicol	99.8	98.1
Clindamycin	97.3	90.0
Erythromycin	92.4	81.4
Levofloxacin	99.8	98.9
Ofloxacin	99.4	100
Oxacillin	97.6	100
Penicillin	96.1	100
Rifampin	100	100
Tetracycline	93.3	100
Sulfamethoxazole/ Trimethoprim	92.9	76.2
Vancomycin	100	100

Abbreviations: iGAS, invasive group A streptococcus; IPD, invasive pneumococcal disease
[a] The proportion of antimicrobial susceptible isolates for invasive *Haemophilus influenzae* (Hi), invasive meningococcal disease (IMD) and group B streptococcus (GBS) were not included in the analyses due to the small case counts for a number of the antibiotics tested

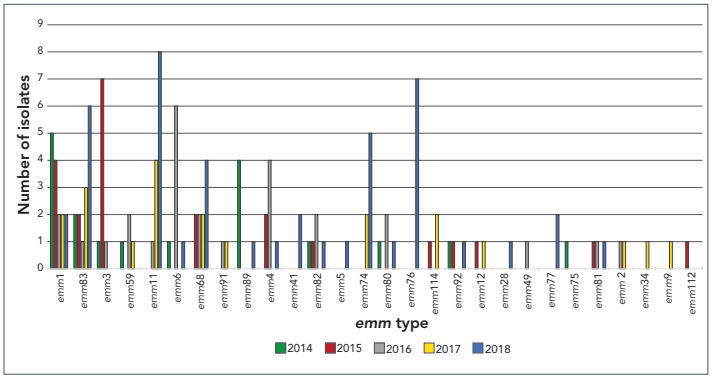
Invasive group A streptococcal disease

The incidence rate (β=0.08; $p<0.0001$) of iGAS (per 100,000 population) increased significantly from 2000 to 2018. The age-standardized incidence rates for males (16.07; CI: 13.65–18.84) and females (11.83; CI: 9.58–14.52) did not differ significantly. The incidence rate (per 100,000 population) was highest for infants younger than one year old (51.25; CI: 34.90–75.27) and adults 60 years and older (36.64; CI: 30.00–44.75). The difference in the average annual incidence rates between those of Indigenous and non-Indigenous

origin was significant in northern regions (Table 1). The age-standardized incidence rate of iGAS in northern regions was 3.2 times higher than the rest of Canada (Table 2).

Of the 311 iGAS cases, 249 were serotyped. The most common *emm* types were *emm*1 with 28 cases (11.2%), *emm*83 with 17 cases (6.8%), *emm*3 with 15 cases (6.0%) and *emm*11 and *emm*59 with 14 cases each (5.6%) **(Figure 3**). The predominant *emm* type varied across the years, and while *emm*1 was circulating most years, it was not always the most common strain in a given year. The most common strain in 2017 and 2018 was *emm*11.

Figure 3: Distribution of iGAS cases by *emm* type in northern Canada, 2014–2018



Abbreviation: iGAS, invasive group A streptococcus

Of the 307 cases with information on clinical manifestation, bacteremia (n=196; 63.8%) and cellulitis (n=96; 31.3%) were the most commonly reported manifestations, and 273 (88.9%) cases were hospitalized. Of the 296 cases with outcome information, 30 deaths (CFR: 10%) were reported. When fatality and hospitalization rates were compared for males and females, hospitalization was significantly higher for males (Table 1). The *emm* types with the highest fatality ratios were *emm*87 (50.0%) and *emm*2 (50.0%), followed by *emm*3 (33.3%) and *emm*75 (33.3%).

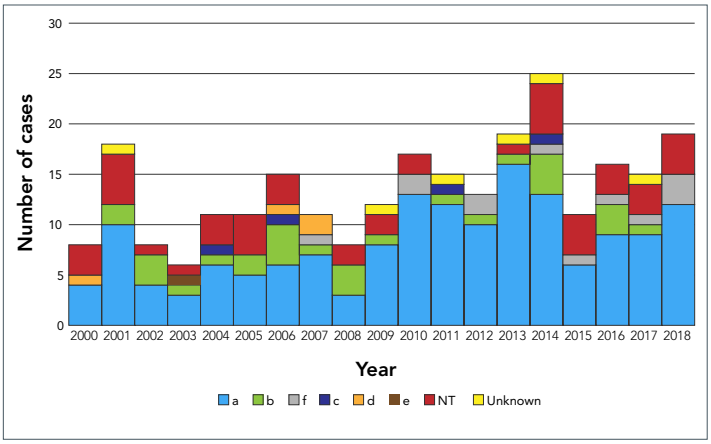
Antimicrobial susceptibility was examined for the iGAS isolates with available data (Table 3).

Invasive *Haemophilus influenzae* disease

There was no significant change in the (β=0.02; *p*=0.06) incidence rate of Hi (per 100,000 population) from 2000 to 2018. The age-standardized incidence rates for males (7.84; CI: 6.44–9.54) and females (6.85; CI: 5.44–8.63) did not differ significantly. The incidence rate (per 100,000 population) was highest among infants younger than one year old (195.15; CI: 160.29–237.59), children one to four years old (39.90; CI: 23.05–49.67) and adults 60 years and older (9.54; CI: 6.45–14.12). The difference in the average annual incidence rates between those of Indigenous and non-Indigenous origin was significant in northern regions (Table 1).

Hi serotype a (Hia) accounted for 60.5% of cases (n=156), non-typeable strains accounted for 17.8% (n=46), Hib accounted for 11.2% (n=29), serotype f accounted for 4.7% (n=12), serotype c and d accounted for 1.6% each (n=4), serotype e accounted for 0.4% (n=1) and 2.7% (n=6) had unknown serotype (**Figure 4**). Rates of Hia increased significantly from 2000 to 2018 (β=0.04; *p*=0.01), and 69.2% (n=108) of Hia cases were in children up to two years old. The age-standardized incidence rate of Hib in northern regions was 8.8 times higher than the rest of Canada (Table 2).

Figure 4: Distribution of invasive *Haemophilus influenzae* serotypes in northern Canada by year, 2000–2018



Abbreviations: a, invasive *Haemophilus influenzae* serotype a; b, invasive *Haemophilus influenzae* serotype b; c, invasive *Haemophilus influenzae* serotype c; d, invasive *Haemophilus influenzae* serotype d; f, invasive *Haemophilus influenzae* serotype f; NT, non-typeable strains

There were no significant changes in Hib rates from 2000 to 2018 (β=−0.01; *p*=0.7). Of the 29 Hib cases, three were adults and 26 children aged three years and younger. Of the 29 Hib cases, 14 (48%) were age-appropriately vaccinated, 10 (35%) were either unvaccinated or not up-to-date with their vaccinations, three (10%) were age ineligible for vaccination and two (7%) had unknown vaccine history.

Of the 246 cases with information on clinical manifestation, bacteremia (n=201; 81.7%) and pneumonia (n=87; 35.4%) were the most commonly reported manifestations. Of the 258 cases of Hi, 222 (86.0%) were hospitalized. Of the 226 cases with outcome information, 19 deaths (8.4%) were reported. Of these 19 cases, 11 were serotype a, five were non-typeable, two were serotype f and one was serotype b.

No significant difference was observed in the hospitalization and fatality rates of males and females (Table 1).

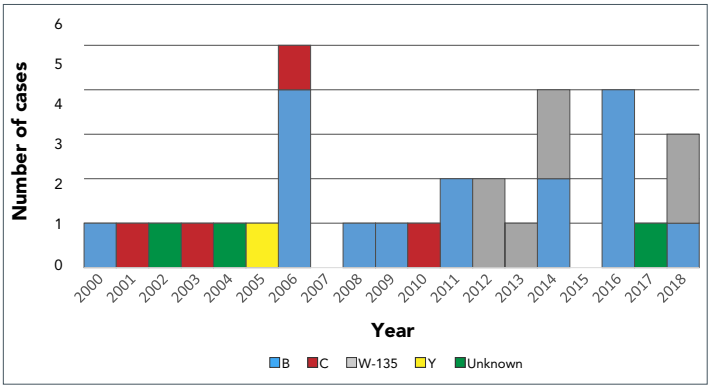
Invasive meningococcal disease

There was no significant change in the incidence rate of IMD (per 100,000 population) from 2000 to 2018 (β=0.03; *p*=0.3). The incidence rate (per 100,000 population) was the highest for

infants younger than one year old (29.57; CI: 17.83–49.04) and children one to four years old (3.99; CI: 2.00–7.98).

Of the 31 cases of IMD, 16 cases (52%) were serogroup B, seven (23%) were serogroup W, four (13%) were serogroup C, one (3%) was serogroup Y and three (10%) were of unknown serogroup (**Figure 5**). The seven serogroup W cases all occurred between 2012 to 2018, constituting 47% of all IMD cases during that period. No serogroup W cases were reported prior to 2012.

Figure 5: Distribution of invasive meningococcal disease cases, by year and serogroup, northern Canada, 2000–2018



Abbreviations: B, invasive meningococcal disease serotype B; C, invasive meningococcal disease serotype C; W, invasive meningococcal disease serotype W; Y, invasive meningococcal disease serotype Y

The median age of the serogroup B cases was younger than one year, with a range of 0–30 years; the median age of the serogroup W cases was younger than one year, with a range of 0–28 years; and the median age of the serogroup C cases was 29.5 years, with a range of 0–56 years.

The difference in the average annual incidence rates between those of Indigenous and non-Indigenous origin was not significant (Table 1). Of the 30 cases with information on clinical manifestation, meningitis (n=21; 70%) and bacteremia (n=13; 43%) were most commonly reported and 90% were hospitalized. Of the 30 cases with fatality information, four deaths (CFR: 13%) were reported.

No significant difference was observed in the hospitalization and fatality rates of males and females (Table 1).

Invasive group B streptococcal disease

There was no significant change in the incidence rate of GBS from 2000 to 2018 (β=−0.01; p=0.6). The incidence rate (per 100,000 population) was highest for infants younger than one year (46.16; CI: 29.09–73.26) and adults 60 years and older (3.97; CI: 2.07–7.64). The difference in the average annual incidence rates between those of Indigenous and non-Indigenous origin was not significant (Table 1).

Of the 44 GBS cases, 16 cases (36%) were neonatal and 28 cases (64%) were non-neonatal. Of the 16 neonatal cases, 10 were early onset disease, five were late onset disease and one was unknown. Of the seven neonatal cases with serotype information, four cases were serotype III and the remaining three were serotype Ia, Ib and V. Of the 15 neonatal cases with information on clinical manifestation, bacteremia (n=10) and meningitis (n=6) were most commonly reported.

Of the 28 non-neonatal cases, the median age was 55.5 years (range 0–88 years). Of the 25 non-neonatal cases with serotype information, 6 (24%) were serotypes III and V each, three (12%) were serotypes Ia, Ib and VI each, two (8%) were serotype IV, and one was serotype II and one serotype VI (4% each). Of the 27 non-neonatal cases with information on clinical manifestation, bacteremia (n=21; 78%), septic arthritis (n=6, 22%) and cellulitis (n=5, 19%) were most commonly reported. Of all the non-neonatal cases, 93% were hospitalized; no deaths were reported.

No significant difference was observed in the hospitalization and fatality rates between males and females (Table 1).

Discussion

In this report, we describe the epidemiology of invasive bacterial diseases in northern Canada from 1999 to 2018 and compared the incidence rates there to those in the rest of Canada. The rates of most of the invasive disease remained stable over time with the exception of IPD, which trended down, and iGAS, which trended up over time. The incidence of IPD, iGAS and Hib were 2.8, 3.2 and 8.8 times higher, respectively, in northern Canada than in the rest of the country. The average annual incidence rates for IPD, iGAS and Hi in northern Canada were significantly higher for those who identified as Indigenous than those of non-Indigenous origin. The highest incidence rates were among the very young and older people.

Similar to the Alaskan ICS population (*personal communication, T. Zulz, Jan 19, 2021*), in northern Canada, IPD presented the highest burden of disease and accounted for over half of the total reported cases during the study period. The incidence of iGAS in northern regions has been increasing, a trend that has also been observed nationally, where the incidence rate has increased three-fold from 2000 to 2018 (34), with outbreaks in the community, military bases and in shelters (35–38). Hia accounted for over 60% of cases and has been increasing significantly over the years. There is also a high prevalence of Hia in the Alaskan population (*personal communication, T. Zulz, Jan 19, 2021*). According to data collected from the US Active Bacterial Core surveillance sites, between 2002–2008 and 2009–2015, the prevalence of Hia disease increased by 13% annually with an overall increase of 148% (39).

The burden of disease for IMD and GBS is much lower than the other three diseases, and IMD and GBS rates did not significantly change during the study period. The results also indicate that there was no statistical difference between the age-standardized incidence rates of IMD for the rest of Canada and northern Canada.

The rates of IPD have significantly decreased over the years due to a significant decrease in PCV7 and PCV10-specific vaccine serotypes, indicating that the conjugate vaccine programs have been successful at reducing the circulation of the serotypes these vaccines protect against. There were no significant decreases of PCV13-specific serotypes over the years. Further study is required to monitor the impact of the PCV13 vaccine versus the PCV10 vaccine, especially following the recent switch from the PCV13 vaccine schedule to a mixed PCV10 and PCV13 vaccine schedule in the Québec regions.

Non-vaccine serotypes have significantly increased following the introduction of the conjugate vaccine programs. PPV23-specific serotypes have also increased and the high percentage of breakthrough disease indicates that the PPV23 vaccine is not as effective at preventing disease in the 65-year-and-older ICS population compared to the conjugate vaccines in the younger ICS population.

Rates of Hib have not significantly changed in northern Canada during this study period. No IMD serogroup C cases have been reported since 2010 and this may be due to the implementation of the Men-C-C vaccine in routine childhood vaccine programs by the mid-2000s (40). Within the last seven years, serogroup B and W have been reported exclusively and the highest burden has been in infants younger than one year.

Strengths and limitations

The ICS program is an important source of epidemiological and laboratory-linked information. It is the only enhanced invasive bacterial disease surveillance system that provides information on ethnicity in Canada, which means that it can be used to monitor the epidemiology of invasive bacterial diseases among the Indigenous peoples of northern Canada.

ICS is a passive surveillance system and some cases may be missed. In some communities, antibiotics may have been started prior to the collection of cultures. Results are unstable due to the small number of cases and small population sizes; therefore, caution should be used when interpreting the results. Because of incomplete reporting of clinical manifestation, vaccine history and underlying conditions and risk factors, these results may be under or overestimated. In addition, not all cases had further serotyping done.

Conclusion

The burden of invasive bacterial diseases is higher in the northern ICS population than the rest of Canada, especially in the Indigenous population. We have limited health information for the large Indigenous population in northern Canada, but existing health disparities need to be monitored and addressed. Ongoing surveillance is needed to continue monitoring disease trends, support prevention and control strategies, and inform immunization recommendations.

Authors' statement

GH — Methodology, software, formal analysis, investigation, data curation, writing–original draft, writing–review and editing, visualization
IM — Methodology, formal analysis, writing–original draft, writing–review and editing
RST — Methodology, formal analysis, writing–original draft, writing–review and editing
WHD — Methodology, formal analysis, writing–original draft, writing–review and editing
GJT — Methodology, formal analysis, writing–original draft, writing–review and editing
YAL — Methodology, formal analysis, writing–review, editing and project administration
CD — Conceptualization, writing–review and editing
FR-D — Methodology and writing–review and editing
SGS — Conceptualization, methodology, writing–review and editing, project administration

Competing interests

None.

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References

1. Parkinson AJ, Bruce MG, Zulz T, Parkinson A; International Circumpolar Surveillance Steering Committee. International Circumpolar Surveillance, an Arctic network for the surveillance of infectious diseases. Emerg Infect Dis 2008;14(1):18–24. DOI PubMed

2. Vaudry W, Talling D. Invasive pneumococcal infection in first nations children in northern Alberta. Can Commun Dis Rep 2002;28(20):165–72. PubMed

3. Christiansen J, Paulsen P, Ladefoged K. Invasive pneumococcal disease in Greenland. Int J Circumpolar Health 2004;63 Suppl 2:214–8. DOI PubMed

4. Singleton R, Hammitt L, Hennessy T, Bulkow L, DeByle C, Parkinson A, Cottle TE, Peters H, Butler JC. The Alaska Haemophilus influenzae type b experience: lessons in controlling a vaccine-preventable disease. Pediatrics 2006;118(2):e421–9. DOI PubMed

5. Degani N, Navarro C, Deeks SL, Lovgren M. Invasive bacterial diseases in northern Canada. Emerg Infect Dis 2008;14(1):34–40. DOI PubMed

6. Bruce MG, Deeks SL, Zulz T, Navarro C, Palacios C, Case C, Hemsley C, Hennessy T, Corriveau A, Larke B, Sobel I, Lovgren M, Debyle C, Tsang R, Parkinson AJ. Epidemiology of Haemophilus influenzae serotype a, North American Arctic, 2000-2005. Emerg Infect Dis 2008;14(1):48–55. DOI PubMed

7. Li YA, Martin I, Tsang R, Squires SG, Demczuk W, Desai S. Invasive bacterial diseases in northern Canada, 2006–2013. Can Commun Dis Rep 2016;42(4):74–80. DOI PubMed

8. Statistics Canada. Data tables, 2016 Census. Catalogue no. 98-400-X2016156. Ottawa (ON): Statistics Canada; (accessed 2020-01-31). https://www12.statcan.gc.ca/census-recensement/2016/dp-pd/dt-td/Rp-eng.cfm?TABID=2&Lang=E&APATH=3&DETAIL=0&DIM=0&FL=A&FREE=0&GC=0&GID=1257309&GK=0&GRP=1&PID=110511&PRID=10&PTYPE=109445&S=0&SHOWALL=0&SUB=0&Temporal=2017&THEME=122&VID=0&VNAMEE=&VNAMEF=&D1=0&D2=0&D3=0&D4=0&D5=0&D6=0

9. Public Health Agency of Canada. Canadian immunization guide [Internet]. Ottawa (ON): PHAC; 2020 (accessed 2020-06-30). https://www.canada.ca/en/public-health/services/canadian-immunization-guide/introduction.html

10. National Advisory Committee on Immunization (NACI). Update on pediatric invasive pneumococcal disease and recommended use of conjugate pneumococcal vaccines. Can Commun Dis Rep 2010;36(ACS-3):1-30. https://www.canada.ca/content/dam/phac-aspc/migration/phac-aspc/publicat/ccdr-rmtc/10pdf/36-acs-3.pdf

11. Papadatou I, Spoulou V. Pneumococcal vaccination in high-risk individuals: are we doing it right? Clin Vaccine Immunol 2016;23(5):388–95. DOI PubMed

12. Government of Newfoundland and Labrador. Newfoundland and Labrador immunization manual: section 2: routine immunization schedules. St John's (NL): Government of Newfoundland and Labrador; 2019.

13. Government of Newfoundland and Labrador. Newfoundland and Labrador immunization manual: section 5: immunization programs for high risk groups. St John's (NL): Government of Newfoundland and Labrador; 2019.

14. Government of Yukon. Yukon immunization program: section 8 - biological products. Whitehorse (YU): Government of Yukon; 2019.

15. Government of Northwest Territories. NWT immunization schedule: publicly funded vaccines for infants and children. Yellowknife (NT): Government of Northwest Territories; 2018.

16. Chief Public Health Office. Routine immunization schedule 2010: adults previously immunized. Iqaluit (NU): Government of Nunavut; 2010.

17. Government of Quebec. Pneumococcal polysaccharide vaccine. Québec (QC): Government of Quebec; 2017 (accessed 2020-05-31). https://www.quebec.ca/en/health/advice-and-prevention/vaccination/pneumococcal-polysaccharide-vaccine

18. Public Health Agency of Canada. Case definitions for diseases under national surveillance. Can Commun Dis Rep 2009;35 Suppl 2:1–123. https://www.canada.ca/content/dam/phac-aspc/migration/phac-aspc/publicat/ccdr-rmtc/09pdf/35s2-eng.pdf

19. Austrian R. The quellung reaction, a neglected microbiologic technique. Mt Sinai J Med 1976;43(6):699–709. PubMed

20. Tyrrell GJ, Lovgren M, Kress B, Grimsrud K. Invasive group A streptococcal disease in Alberta, Canada (2000 to 2002). J Clin Microbiol 2005;43(4):1678–83. DOI PubMed

21. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol 1990;215(3):403–10. DOI PubMed

22. Centers for Disease Control and Prevention. Streptococcus Laboratory. Protocol for emm typing. Atlanta (GA): CDC; 2018 (accessed 2020-03-31). https://www.cdc.gov/streplab/groupa-strep/emm-typing-protocol.html

23. Slotved HC, Elliott J, Thompson T, Konradsen HB. Latex assay for serotyping of group B Streptococcus isolates. J Clin Microbiol 2003;41(9):4445–7. DOI PubMed

24. Ledeboer NA, Doern GV. Haemophilus. In: Versalovic J, Carroll KC, Jorgensen JH, Funke G, Landry ML, Warnock DW, editors. Manual of clinical microbiology. 10th ed. Washington (DC): ASM Press; 2011. p. 585–602.

25. Falla TJ, Crook DW, Brophy LN, Maskell D, Kroll JS, Moxon ER. PCR for capsular typing of Haemophilus influenzae. J Clin Microbiol 1994;32(10):2382–6. DOI PubMed

26. Riou JY, Guibourdenche M. Laboratory methods: Neisseria and Branhamella. Paris (FR): Institut Pasteur; 1992.

27. Clinical Laboratory Standards Institute. CLSI M100-S26: Performance standards for antimicrobial susceptibility testing, 26th ed. Wayne (PA): CLSI; 2016.

28. Statistics Canada. Aboriginal peoples of Canada: highlight tables, 2001 Census. Tables: 97F0024X2001007. Ottawa (ON): Statistics Canada; (accessed 2020-01-31). https://www150.statcan.gc.ca/n1/en/catalogue/97F0024X2001007

29. Statistics Canada. 2011 National Household Survey: data tables. Catalogue number: 99-011-X2011034. Ottawa (ON): Statistics Canada; (updated 2016-01-07; accessed 2020-01-31). https://www12.statcan.gc.ca/nhs-enm/2011/dp-pd/dt-td/Ap-eng.cfm?LANG=E&APATH=3&DETAIL=0&DIM=0&FL=A&FREE=0&GC=0&GID=0&GK=0&GRP=0&PID=107504&PRID=0&PTYPE=105277&S=0&SHOWALL=0&SUB=0&Temporal=2013&THEME=94&VID=0&VNAMEE=&VNAMEF=

30. Statistics Canada. 2006 Census area profiles of population. Profile of Aboriginal Peoples for Canada, Provinces, Territories, Census Divisions and Census Subdivisions, 2006 Census. 2006 Census of Population, Statistics Canada Catalogue no. 94-578-XCB2006001. Ottawa (ON): Statistics Canada; (updated 2015-02-09; accessed 2020-01-31). https://www12.statcan.gc.ca/datasets/Index-eng.cfm?Temporal=2006&Theme=73&VNAMEE=&GA=-1&S=0

31. Statistics Canada. Data tables, 1996 Census. Catalogue no. 95F0251XDB96001. Ottawa (ON): Statistics Canada; (updated 2019-06-04; accessed 2020-01-31). https://www12.statcan.gc.ca/English/census96/data/tables/Rp-eng.cfm?LANG=E&APATH=3&DETAIL=1&DIM=0&FL=A&FREE=1&GC=0&GID=0&GK=0&GRP=1&PID=15504&PRID=0&PTYPE=89103&S=0&SHOWALL=No&SUB=0&Temporal=2006&THEME=7&VID=0&VNAMEE=&VNAMEF=

32. Centre for Population Health Data. 2011 Population Weights. Ottawa (ON): Statistics Canada; 2020.

33. Fay MP, Feuer EJ. Confidence intervals for directly standardized rates: a method based on the gamma distribution. Stat Med 1997;16(7):791–801. PubMed

34. Public Health Agency of Canada. Notifiable disease pre-built charts. Ottawa (ON): PHAC; 2021 (accessed 2021-02-28). https://diseases.canada.ca/notifiable/charts-pre-built

35. Loewen K, Bocking N, Matsumoto CL, Kirlew M, Kelly L. Epidemiologic features of invasive group A Streptococcus infection in a rural hospital: 6-year retrospective report and literature review. Can J Rural Med 2017;22(4):131–8. PubMed

36. Athey TB, Teatero S, Sieswerda LE, Gubbay JB, Marchand-Austin A, Li A, Wasserscheid J, Dewar K, McGeer A, Williams D, Fittipaldi N. High incidence of invasive group A Streptococcus disease caused by strains of uncommon emm types in Thunder Bay, Ontario, Canada. J Clin Microbiol 2016;54(1):83–92. DOI PubMed

37. Hammond-Collins K, Strauss B, Barnes K, Demczuk W, Domingo MC, Lamontagne MC, Lu D, Martin I, Tepper M. Group A Streptococcus Outbreak in a Canadian Armed Forces Training Facility. Mil Med 2019;184(3-4):e197–204. DOI PubMed

38. Dickson C. 2021 International Circumpolar Surveillance Invasive Bacterial Disease Working Group meeting. Updating public health guidelines for invasive group A streptococcus. Forthcoming, 2021.

39. Soeters HM, Blain A, Pondo T, Doman B, Farley MM, Harrison LH, Lynfield R, Miller L, Petit S, Reingold A, Schaffner W, Thomas A, Zansky SM, Wang X, Briere EC. Current epidemiology and trends in invasive Haemophilus influenzae disease-United States, 2009-2015. Clin Infect Dis 2018;67(6):881–9. DOI PubMed

40. National Advisory Committee on Immunization (NACI). Meningococcal C conjugate vaccination recommendations for infants. An Advisory Committee Statement (ACS). Can Commun Dis Rep 2007;33(ACS-11):1–12. https://www.canada.ca/en/public-health/services/reports-publications/canada-communicable-disease-report-ccdr/monthly-issue/2007-33/preamble.html

A commentary on a flawed public health investigation

John Hardie*

Abstract

The possibility of hepatitis C being transmitted between dental patients was the genesis of an extensive and expensive look-back investigation conducted by an Ontario Public Health Unit. This investigation was performed with a minimal knowledge of nosocomial infections of dental origin, an enthusiastic reliance on untested checklist indicators and an absence of any of the criteria justifying such an investigation. As a consequence, the entire exercise was based on the false premise that an infection control lapse had occurred. This commentary will address these flaws, and other aspects of the Public Health Unit's response that detracted from its credibility. The provision of a realistic assessment of disease transmission in dentistry should result in Public Health Units conducting informed and mutually beneficial inspections of dental practices.

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Keywords: public health, dentistry, nosocomial infections, IPAC lapse

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Introduction

The article, "A public health response to a newly diagnosed case of hepatitis C associated with lapse in Infection Prevention and Control Practices in a dental setting in Ontario, Canada" by Johnston *et al*. was published in the July/August 2021 edition of the *Canada Communicable Disease Report* (1). The article was written from a public health perspective with a minimal appreciation of dental procedures and dental infection control. As a consequence, the article provides a biased impression of hepatitis C transmission in dentistry.

In 2019, a survey was published in the *Canada Communicable Disease Report* demonstrating that the staff of Ontario Public Health Units lacks the knowledge, training and expertise to appropriately investigate alleged infection prevention and control lapses (IPAC) occurring in health settings such as dental practices (2). Despite these damning conclusions, such inspections continue unabated with findings that are unsatisfactory for all concerned.

Major reasons for this include misinformation on disease transmission in dentistry, failure to appreciate the vulnerability of blood-borne viruses and an over reliance on checklist audits. By addressing these and related topics this commentary will illustrate the faults in the above article while offering a realistic assessment of hepatitis C transmission in dental practice.

Disease transmission in dentistry

The following is a brief summation of the reality of disease transmission in dentistry.

- A 1993 conclusion that, "The lack of epidemiological evidence of transmission of infectious diseases on dental instruments and handpieces must be remembered, particularly when assessing a laboratory study." (3).
- There are no confirmed cases of human immunodeficiency virus (HIV), hepatitis B virus (HBV) or hepatitis C virus (HCV) being transmitted in Canadian dental practices (4).
- A 44 year investigation (1946–1990) of health care facilities (before the present era of infection control recommendations) failed to find a single case of cross contamination from dental instruments (5).
- A 2010 extensive review in the United Kingdom found no evidence of dental services causing the transmission of infections (6).
- A 2013 report on the transmission of HCV in an oral surgery practice was, as admitted by the investigators, based on pure speculation (7).
- A 2016 United States investigation covering a 12-year period found not a single case of HIV transmission linked to a dental practice and failed to clinically substantiate that presumptive transmissions of HBV and HCV were due to failures in dental infection control (8).

- In 2018, the suspected transmission of bacterial endocarditis in an oral surgery practice was likely related to the inadequate preparation, storage and use of intravenous medications rather than to alleged IPAC lapses involving instruments (9).

From the 1940s to the present there have been billions of dental treatments performed—most without the current infection control protocols. As shown above, historical and current investigations have failed to reveal that dental instruments were vectors for the transmission of infections. In their haste to conduct the alleged IPAC lapse investigation the authors of the article did not perform a thorough review of the pertinent literature.

Vulnerability of bloodborne viruses

According to the Ontario Agency for Health Protection and Promotion (OAHPP), "Low–level disinfection eliminates vegetative (live) bacteria, some fungi and enveloped viruses." (10). Hepatitis C virus is a lipid-enveloped virus that is readily destroyed by the common disinfectants that have been used by generations of dentists. Do the article's authors believe that the HCV would survive physical cleaning, immersion in a low level disinfectant and the harsh environment of a steam sterilizer—even if it was operating at less than 100% efficiency?

HIV and HBV are also lipid-enveloped viruses. This fact, combined with the low pathogenicity of oral microorganisms, is the reason why there is an absence of clinically-substantiated evidence that dental instruments transmit infections. It is unfortunate that public health officials continue to ignore these data.

Reliance on checklist audits

Public Health Ontario checklists were used to determine if IPAC lapses had occurred. These lists contain approximately 100 indicators whose adoption is supposed to prevent and/or control dentally acquired infections. OAHPP demands that such indicators are, "…based on validated evidence that has been demonstrated to improve outcomes" (9). In other words, there must be clinical evidence of disease transmission prior to the use of the indicator that was prevented or controlled following the indicator's adoption.

The article cites 14 deficient indicators to justify the presence of IPAC lapses. Among these were the inconsistent use of chemical indicators, the incomplete record keeping and the improper cleaning of dental handpieces. However, there are no clinical studies that demonstrate that these and the other checklist failures cause nosocomial infections of dental origin that were avoided by complying with the indicators. The reality is that the checklists have not been validated. This should not be surprising as Nicolle noted in the *Canadian Journal of Infectious Diseases* that, "Infection control interventions have yet to be validated in health care settings outside of acute care." (11).

Without the validation that OAHPP requires, IPAC lapses cannot be identified; and without such identification, it is inappropriate and disingenuous to suggest in the article's title that one exists.

Related topics

The following issues further detract from the article's credibility.

- **Uniqueness of hepatitis C-genotype 2:** The reported rate for hepatitis C in Ontario is 36.5 per 100,000 with 10%–15% of those being genotype 2 (12). With a population of 15 million there will be approximately 550 to 800 cases of hepatitis genotype 2. This detracts from the authors' frequent assertions that the rarity of genotype 2 imparts a uniqueness to their article.
- **Risk categories:** The socioeconomic status of the involved patients is not known. However, they were treated at community dental clinics, which would question their reliability as historians of their health, sexual and recreational activities necessitating a thorough investigation of their risk factors for hepatitis C. This is not mentioned in the article, instead there is a passing reference to the fact that the index patient had no, "…reported current or past risk factors related to HCV infection" (1).
- **Look-back investigation:** The article describes a look-back investigation. Dr. Danila and his team categorized these as expensive and limited in their ability to demonstrate transmission because of the relatively small number of patients studied and a low risk of transmission (13). This investigation consumed 1,187.5 hours, which could translate into a bountiful supply of taxpayer money. The authors admit that there is "…minimal scientific evidence of transmission of HCV in dental practice". This admission alone should have cast doubts on the success of the investigation. Three criteria justify look-back investigations (13): 1), definite evidence of disease transmission to a patient; 2), egregious violations of infection control; and 3), as part of a collaborative study. This investigation satisfies none of these qualifiers.
- **Editing errors:** In the Case definition section, the days before and after the procedure are classified as "business" days. However, in the Discussion section "business" is absent. In the Results section the source case is described as, "the probable source case". In the Discussion section—without any rational justification—this has morphed into being the definitive, "source case".

- **Impossible hypothesis:** In the Introduction, the HCV outbreak is downgraded to a "potential" outbreak and the exposures to HCV are deemed "potential" exposures. This means that the authors' hypothesis should read, "… a **potential** HCV transmission may have occurred at Facility B **potentially** between the **probable** source case and the index case". The bolded corrections are such that it would be impossible to test the hypothesis making it invalid.

Dentistry and hepatitis C

Endoscopes are heavily contaminated during use and their complicated design results in reprocessing errors. Dental instruments are simpler in design, not subjected to the same bioburden and are often used for non-invasive procedures. Investigations on the risk of improperly reprocessed ear nose and throat endoscopes transmitting bloodborne infections serve as worst case scenarios for IPAC lapses during the decontamination of dental instruments. Such studies have shown that the risk of transmitting HIV is seven in 10 trillion, for HBV it is 2.4 in a billion and for HCV it is between that for HIV and HBV (13). These findings prove that there is an infinitesimal risk of contracting blood borne infections, including hepatitis C, from dental instruments. The authors appear to be unaware of these risk assessments.

Conclusion

The public health response was an administrative exercise as it was not based on an actual HCV outbreak but a potential one. While it involved over a thousand staff hours, it was flawed in that it relied on non-validated checklists, it had no clinical justification for conducting the look back investigation, it exaggerated the uniqueness of the case and it was based on a hypothesis that cannot be tested. The authors' peers will judge the value of the response to an unproven IPAC lapse.

As explained above, there are historical and factual reasons why there are a dearth of clinically-substantiated disease transmissions from dental instruments. Perhaps, public health officials will use these reasons to consider the reality of disease transmission in dentistry—allowing them to conduct more informed investigations of dental practices in the future.

References

1. Johnston C, Sunil V, Ser D, Holt AM, Garber G, Macdonald L, Kristjanson E, Mazzulli T, Olsha R, Ryding D, Noseworthy AL. A public health response to a newly diagnosed case of hepatitis C associated with lapse in Infection Prevention and Control practices in a dental setting in Ontario, Canada. Can Commun Dis Rep 2021;47(7-8):347–52. DOI PubMed
2. Cadieux G, Brown C, Sachdeva H. Public health investigation of infection prevention and control complaints in Ontario, 2015–2018. Can Commun Dis Rep 2019;45(11):289–95. DOI PubMed
3. Epstein JB, Rea G, Sibau L, Sherlock CH. Rotary dental instruments and the potential risk of transmission of infection: herpes simplex virus. J Am Dent Assoc 1993;124(12):55–9. DOI PubMed
4. Hardie J. The Surprising Absence of Disease Transmission from Infection Control Disasters. Oral Health 2015;14–8. https://www.oralhealthgroup.com/features/the-surprising-absence-of-disease-transmission-from-infection-control-disasters/
5. Goodman RA, Solomon SL. Transmission of infectious diseases in outpatient health care settings. JAMA 1991;265(18):2377–81. DOI PubMed
6. Fox C. Evidence summary: what 'cost of illness' evidence is there about cross-infection related infections in dental practice? Br Dent J 2010;209(2):87–8. DOI PubMed
7. Weaver JM. Confirmed transmission of hepatitis C in an oral surgery office. Anesth Prog 2014;61(3):93–4. DOI PubMed
8. Cleveland JL, Gray SK, Harte JA, Robison VA, Moorman AC, Gooch BF. Transmission of blood-borne pathogens in US dental health care settings: 2016 update. J Am Dent Assoc 2016;147(9):729–38. DOI PubMed
9. Ross KM, Mehr JS, Greeley RD, Montoya LA, Kulkarni PA, Frontin S, Weigle TJ, Giles H, Montana BE. Outbreak of bacterial endocarditis associated with an oral surgery practice: new Jersey public health surveillance, 2013 to 2014. J Am Dent Assoc 2018;149(3):191–201. DOI PubMed
10. Public Health Ontario. Provincial Infectious Diseases Advisory Committee (PIDAC). Best Practices for Infection Prevention and Control Programs in Ontario. In All health Care Settings, 3rd edition. Toronto, ON: PHO; (updated 2012-05). https://www.publichealthontario.ca/-/media/documents/B/2012/bp-ipac-hc-settings.pdf
11. Nicolle LE. Infection control in acute care facilities: evidence-based patient safety. Can J Infect Dis 2001;12(3):131–2. DOI PubMed
12. Public Health Ontario. Hepatitis C in Ontario, 2018: Surveillance summary one year after a case definition update. Toronto (ON): PHO; 2020 (accessed 2020-09-30). https://www.publichealthontario.ca/-/media/documents/r/2020/report-hepc-surveillance-2018.pdf?la=en
13. Danila RN, MacDonald KL, Rhame FS, Moen ME, Reier DO, LeTourneau JC, Sheehan MK, Armstrong J, Bender ME, Osterholm MT. A look-back investigation of patients of an HIV-infected physician. Public health implications. N Engl J Med 1991;325(20):1406–11. DOI PubMed
14. Holodniy M, Oda G, Schirmer PL, Lucero CA, Khudyakov YE, Xia G, Lin Y, Valdiserri R, Duncan WE, Davey VJ, Cross GM. Results from a large-scale epidemiologic look-back investigation of improperly reprocessed endoscopy equipment. Infect Control Hosp Epidemiol 2012;33(7):649–56. DOI PubMed

What is the evidence on the Delta variant among children?

Source: Emerging Sciences Group of the Public Health Agency of Canada. Emerging Evidence on COVID-19: Evidence on the Virulence, Transmission and Impact of the Delta variant (B.1.617.2) among Children. October 2021. Full report available from: ocsoevidence-bcscdonneesprobantes@phac-aspc.gc.ca

Background: Evidence is beginning to emerge on the effects of the Delta variant on children. To further inform public health strategies to protect children, this evidence brief summarizes what is known on the virulence and transmissibility of the Delta variant among children aged 0–18 years and the impact of public health interventions including vaccines.

Methods: Twenty databases and key websites were searched for relevant reviews, peer-reviewed publications and preprints up to October 8, 2020. Data from studies were extracted into evidence tables and the key findings were summarized.

Results: Twenty-three studies were included, with 17 studies published in the last month. This included one cluster-randomized trial, four surveillance studies, one ecologic study, seven outbreak investigations, six predictive models on the impact of public health measures and four predictive models on the impact of different vaccination coverages in children.

Virulence (n=4)

Current evidence suggests that Delta is not more virulent in children than the original variant or Alpha.

- Two surveillance studies in the United States (US) and one in the United Kingdom (UK) reported that although the incidence and hospitalization rates have increased, the proportion of the coronavirus disease 2019 (COVID-19) cases with severe outcomes (e.g. intensive care unit admission, invasive mechanical ventilation and mortality) had not changed among children during June–August 2021 surge of the Delta variant compared to pre-Delta rates.

Transmissibility (n=8)

Without public health measures, such as vaccines, physical distancing, cohorting and masking, Delta has high transmissibility in children.

- This has been documented in seven outbreak studies in both school and community settings. Clusters with teachers or instructors as the source case were typically larger and showed higher reproduction numbers compared to students. In one modelling study, Delta was estimated to result in nearly 10 times the cases attributable to being in school compared to Alpha.
- One randomized control trial (RCT) and three predictive models suggested that cases in schools closely followed those of the community.
- Children can have a high viral load. One US study reported high viral load (Ct<20) in 18.3% of COVID positive children and of those, 70% were asymptomatic.

Impact of Public Health Measures (n=12)

Vaccination

There is new evidence that vaccine prevents severe disease in children.

- A single empirical study from the US identified that at the start of the Delta surge (June–July 2021) vaccinated adolescents had 10.1 times lower hospitalization rates compared to unvaccinated adolescents. Specifically, compared to the states with the highest vaccination coverage, states with the lowest vaccination coverage had 3.4 times higher adolescent emergency department visits and 3.7 times higher hospitalizations rates.
- Four models from the UK, US, Australia and China analyzed the impact of vaccination coverage in different age groups among children on cases, hospitalizations and deaths following rising infection rates and school re-opening in the fall 2021. Predictions suggested up to 90% reduction in COVID-19 cases could be achieved with extending vaccine coverage to include most paediatric age groups.
- Most models suggest that very high vaccine coverage is needed (>80%) to nullify the additional benefit of other public health measures (e.g. mask policies, quarantine policies, social distancing, cohorting in schools) both in the community and in schools.

Other public health measures

There is new evidence that a layered approach of vaccines in the eligible population (≥12 years) along with other public health measures are effective in decreasing the spread of COVID-19 in schools.

- A modelling study from the UK showed that whole class quarantine for 10 days following discovery of a case can have a significant impact on stopping onward transmission and was shown to have similar impact to a high stringency public health measure scenario with masking, cohorting and increased ventilation in schools.

- A US ecological study estimated that paediatric case rates in counties with school mask requirements experienced 18.53 fewer cases per 100,000 per day compared to counties without school mask requirements. Modelling studies have shown a protective impact of mask requirements in elementary, middle and high schools on school transmissions and community infection rates.
- Predictive models suggested that increasing the number of public health measures employed and higher vaccination coverage in the school and community populations were always more protective than fewer public health measures.
- The most effective public health measures varied across five modelling studies, but typically included mask requirements and either cohorting or testing strategies. It appears the combination of public health measures and vaccination coverage required to minimise risk of transmission in a school setting depends on the local epidemiology of COVID-19, and the feasibility of implementing different public health measures in a particular setting (e.g. schools) or for an activity (e.g. sports).

Conclusion: Based on preliminary evidence, the Delta variant in children does not appear to be more virulent than the original variant or Alpha. Without vaccines and other public health measures, however, Delta has high transmissibility in children. Current evidence indicates that vaccines and additional public health measures are effective in decreasing transmission of COVID-19 in schools. Empirical studies are needed to confirm, refute or qualify these findings.

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CANADA COMMUNICABLE DISEASE REPORT

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