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FIRST NATIONS HEALTH

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OVERVIEW

Supporting health equity for First Nations, Inuit and Métis peoples

Margo Greenwood[1,2,3]*, Donna Atkinson[1], Julie Sutherland[1]

Abstract

The National Collaborating Centre for Indigenous Health (NCCIH) is unique among the National Collaborating Centres as the only centre focused on the health of a population. In this fifth article of the *Canada Communicable Disease Report*'s series on the National Collaborating Centres and their contribution to Canada's public health response to the coronavirus disease 2019 (COVID-19) pandemic, we describe the work of the NCCIH. We begin with a brief overview of the NCCIH's mandate and priority areas, describing how it works, who it serves and how it has remained flexible and responsive to evolving Indigenous public health needs. Key knowledge translation and exchange activities undertaken by the NCCIH to address COVID-19 misinformation and to support the timely use of Indigenous-informed evidence and knowledge in public health decision-making during the pandemic are also discussed, with a focus on acting on lessons learned moving forward.

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Introduction

The National Collaborating Centres (NCCs) for Public Health (NCCPH) were established in 2005 as part of the federal government's commitment to renew and strengthen public health infrastructure in Canada following the 2003 severe acute respiratory syndrome epidemic (1). Funded by the Public Health Agency of Canada, the NCCs promote and support the timely use of scientific research and other knowledges in public health practice, programs and policies in Canada (2). The NCCs work to identify knowledge gaps and needs to stimulate research in public health priority areas, synthesize and disseminate new and existing research into user-friendly formats, and foster networks and collaborations among public health professionals, policy-makers and researchers. Hosted by academic or government organizations across Canada, each NCC focuses on a specific area of public health: Indigenous Health; Environmental Health; Infectious Diseases; Knowledge Translation Methods and Tools; Healthy Public Policy; and Determinants of Health (2). In this brief overview, we will present the mandate and priority areas of the National Collaborating Centre for Indigenous Health (NCCIH), along with descriptions of how NCCIH works, who it serves and how it adapted to evolving Indigenous public health needs during the coronavirus disease 2019 (COVID-19) pandemic.

National Collaborating Centre for Indigenous Health: Sharing knowledge, making a difference

Situated on the traditional territory of the Lheidli T'enneh First Nation in Prince George, British Columbia (BC), the NCCIH, formerly the NCC for Aboriginal Health, (3) is hosted at the University of Northern British Columbia—a small, research-intensive university serving rural, remote and northern populations. The NCCIH's mandate is to strengthen public health systems and support health equity for First Nations, Inuit and Métis peoples in Canada through knowledge translation and exchange. This work is guided by four overarching principles intended to 1) respect diversity and the unique interests of First Nations, Inuit and Métis peoples, 2) support the inclusion and participation of First Nations, Inuit and Métis peoples in the public health system, 3) incorporate Indigenous knowledge and holistic approaches and 4) encourage collaboration and capacity building. The NCCIH applies these principles to its work in several key priorities areas that reflect our understanding of, and approach to, transforming Indigenous public health in Canada.

Priority areas

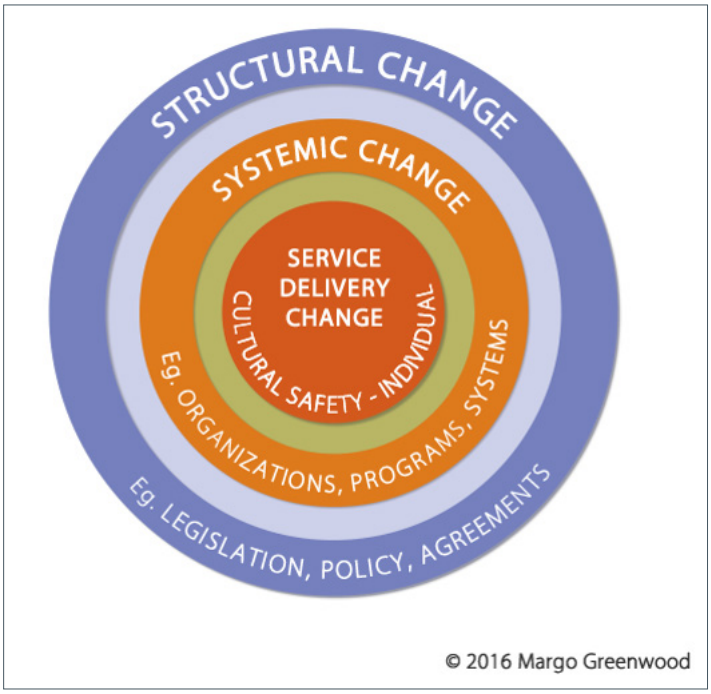
Key priority areas are informed by direct and ongoing engagement with public health stakeholders and community members through a variety of methods, including convening national gatherings, supporting and participating in networks and committees, conducting environmental scans and literature reviews, administering surveys and undertaking focus groups and key informant interviews (2). The NCCIH Advisory Committee, composed of First Nations, Inuit, Métis and non-Indigenous public health experts from across the country, provides strategic direction and advice to the NCCIH and offers ongoing feedback on strategic priorities to ensure the work's relevance to First Nations, Inuit and Métis peoples and communities. With the eight-year renewal of the NCC program in 2019, the NCCIH's priority areas remain committed to addressing emerging Indigenous public health issues.

The NCCIH has seven key priority areas. The first priority area is focused on the social determinants of health, or the conditions in which people are born, grow, live, work and age that influence health outcomes (4). As part of this work, NCCIH looks "beyond the social" to the determinants of health specific to First Nations, Inuit and Métis peoples, such as colonization, systemic racism and intergenerational trauma (5). Given that gender interacts with other determinants of health to influence health risks, outcomes, behaviours, opportunities and experiences across a person's lifespan, the NCCIH's activities and resources use gender-based analysis plus (GBA+) and other Indigenous-specific gender-based analysis tools and strategies to consider the unique experiences of Indigenous men, women, boys, girls and lesbian, gay, bisexual, transsexual, transgendered, intersexual, queer, questioning, two-spirited (LGBTTIQQ2S) in public health policies, programs and initiatives. Second, First Nations, Inuit, and Métis child, youth and family health is another important priority area because families and communities are not only an important source of strength and safety but also the place where health and wellness begins and thrives. Third, Indigenous people's relationships with and dependence on the land, waters, animals, plants and natural resources for their sustenance, livelihoods, cultures, identities, health and well-being are prioritized. Fourth, we work to address the disproportionate burden of chronic and infectious diseases on Indigenous populations by sharing knowledge and fostering dialogue on issues such as tuberculosis, sexually transmitted and bloodborne infections, and COVID-19 (6). Fifth, to support Indigenous perspectives and approaches to United Nation's 2030 Agenda for Sustainable Development (7) and Canada's Agenda National Strategy (8), NCCIH also focus on key aspects of the sustainable development goals such as reduced inequalities, climate action and poverty. Recognizing that Indigenous knowledges and perspectives are foundational to evidence-based decision-making, the NCCIH's sixth priority area is focused on the integration and application of diverse knowledge systems in public health. Finally, to address systemic anti-Indigenous racism in healthcare systems, the NCCIH prioritizes the development of knowledge products and activities on cultural safety and respectful relationships. The NCCIH website provides evidence-based, Indigenous-specific resources and tools in each of these priority areas. Demand for credible, user-friendly and culturally relevant information is reflected in the NCCIH's growing number of unique and returning visitors to the NCCIH's website, which increased by 47% and 51%, respectively, in the last fiscal year.

Conceptual change model

The NCCIH's approach to Indigenous public health transformation is grounded in a conceptual change model (**Figure 1**) (9) illustrated by three interconnected layers: structural change; systemic change; and service delivery change (9). The change model incorporates social determinants and Indigenous determinants of health approaches and a life course perspective, all of which are necessary for the multi-level, cross-disciplinary, concurrent implementation of policies, programs and practices to address health inequities of Indigenous peoples over the long term.

Figure 1: Conceptual change model of National Collaborating Centre for Indigenous Health's approach to Indigenous public health transformation



The outer layer of the model refers to the "big super structures" like high-level policies, legislation and/or formal agreements that are enablers of structural change. In Canada, examples of these big structural enablers include the Truth and Reconciliation Commission's (TRC) Calls to Action, the National Inquiry into Missing and Murdered Indigenous Women and Girls (MMIWG) Calls for Justice, and the United Nations

Declaration on the Rights of Indigenous Peoples (UNDRIP). The NCCIH has consistently identified, evolved and responded to these high-level policies, legislation and formal agreements by mobilizing knowledge to increase understanding and application of Indigenous-informed evidence at the policy level.

The second layer depicted in the change model refers to systemic change at the level of organizations and agencies responsible for operationalizing change, such as hospitals, schools, early childhood programs, child welfare agencies and mental health and addictions programs (9). Since its inception, NCCIH has mobilized knowledge to reduce inequities in Indigenous health at the program and organizational level by producing environmental scans, literature reviews, fact sheets, guidance documents and health promotion resources to inform evidence-based decision-making and adoption of best or promising practices. At the very centre of the model is service delivery change, where individuals interact with each other in providing or receiving healthcare or other services (9). The NCCIH has worked diligently over the last 16 years to develop resources and activities to deepen understanding, awareness, reflection and action at the individual or practice level, including the importance of cultural safety and respectful relationships.

National Collaborating Centre for Indigenous Health in the time of COVID-19

With the emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in late 2019, the NCCIH quickly mobilized to stop the spread of COVID-19 misinformation and to support the use of Indigenous-informed evidence and knowledge in public health decision-making. It began by establishing a COVID-19 quick links page on its website to provide reliable and timely information in response to the global explosion of research and information on COVID-19 (10). In collaboration with Indigenous Services Canada, it also created a COVID-19 resource library to provide easy access to over 370 First Nations, Inuit and Métis-specific resources and tools in English, French and multiple Indigenous languages. Published by both Indigenous and non-Indigenous researchers and organizations, the curated resource library covers a wide range of topics (e.g. barriers to care, harm reduction, infection prevention and control, emergency management) and formats (e.g. information sheets, posters, videos, protocols and guidelines, reports and journal articles). In addition to this preliminary work and to act on lessons learned, NCCIH conducted a survey of stakeholders in the spring of 2020 to identify ongoing and emerging knowledge needs and gaps related to First Nations, Inuit and Métis peoples and COVID-19. The survey aimed to inform the work moving forward for resource and tools development, as well to establish new partnerships and collaborations. The COVID-19 priority areas identified by survey respondents included mental health and wellness, stigma and discrimination, public health messaging, substance use, addictions and harm reduction, and housing and homelessness. With these priority areas in mind, NCCIH spent the subsequent months working with Indigenous health researchers, program managers, policy-makers, health professionals, government and national Indigenous organizations on a number of COVID-19 initiatives: webinars and podcasts; fact sheets; animated videos; reports; and a national survey on access to healthcare services during the pandemic.

Over a four-week period from January to February 2021, NCCIH delivered a series of webinars as part of its COVID-19 and First Nations, Inuit and Métis people's virtual gathering. Delivered in collaboration with Indigenous organizations and scholars from coast-to-coast-to-coast, the 2.5 hour webinars focused on key topic areas, including Indigenous Governance and Self-Determination in Planning and Responding to COVID-19 (11), Socio-Economic Impacts of COVID-19 on the Health and Well-Being on First Nations, Inuit and Métis Populations (12), Data Collection on COVID-19 Cases in First Nations, Inuit and Métis Populations and Communities (13), and Innovative Public Health Messaging on COVID-19 and Indigenous Peoples (14). Engagement in the webinar series was significant, with over 3,800 individuals registering from various sectors, including Indigenous organizations, local and regional public health units, health authorities, hospitals, universities or research centres, federal, provincial and territorial governments and non-profit organizations. Post-webinar survey data indicated that 94%–97% of respondents rated the webinars as excellent or very good and that the webinars enhanced their knowledge. Respondents also offered comments on the webinars, noting they were extremely informative, thought-provoking and a great mixture of academic, personal and experiential/artistic perspectives. In addition to the webinars, the Centre published a number of podcasts as part of our "Voices from the Field" series on topics such as grief, mourning and mental health (15), how to stay connected to traditions and ceremonies during a pandemic (16), respecting our Elders (17) and public health considerations for COVID-19 in evacuations of northern Indigenous communities (18).

In partnership with BC's Northern Health Authority's Indigenous Health branch, the NCCIH also developed resources to address COVID-19 and stigma, including the animated videos "Healing in Pandemic Times: Indigenous Peoples, Stigma and COVID-19" (19) and "There is no Vaccine for Stigma: A Rapid Evidence Review of Stigma Mitigation Strategies During Past Outbreaks Among Indigenous Populations Living in Rural, Remote and Northern Regions of Canada and What Can Be Learned for COVID-19" (20). To support the rollout of COVID-19 vaccines in Canada, NCCIH also worked with several organizations to share and exchange knowledge to better understand vaccine hesitancy and promote vaccine confidence generally among First Nations, Inuit and Metis peoples. Key activities done in partnership with the NCC for

Infectious Diseases included a webinar on vaccine hesitancy and potential implications during the COVID-19 pandemic, with over 900 attendees (21), an animated video on building vaccine confidence (22), and a series of fact sheets on vaccine confidence and vaccine preventable diseases for Indigenous peoples and healthcare professionals (23). Additionally, the NCCIH published two articles in partnership with the Royal Society of Canada: "Vaccine Mistrust: A Legacy of Colonialism" (24) and "Enhancing COVID-19 Acceptance in Canada" (25). Finally, in partnership with Public Health Agency of Canada, NCCIH and NCC for Infectious Diseases are leading the development of a national survey on access to healthcare services during the pandemic, with a focus on sexually transmitted and blood-borne illnesses and harm-reduction services.

Conclusion

Through knowledge sharing, partnerships and collaboration, community engagement and rapid response to emerging public health challenges such as COVID-19, NCCIH joined the other NCCs in renewing and strengthening public health infrastructure in Canada. In its unique position among the NCCs of focusing on a specific, though diverse, population, the NCCIH strives to confront determinants of health that affect First Nations, Inuit and Métis peoples. Its conceptual change model created a foundation from which to work to address inequities at service delivery, systemic and structural levels and build a just society for all Indigenous peoples in Canada.

Authors' statement

All authors are equal contributors to this paper.

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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Canadian blood suppliers: An expanding role in public health surveillance?

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Abstract

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic galvanized blood donor seroprevalence studies, which continue to inform public health policy. We propose that the two Canadian blood suppliers, Héma-Québec and Canadian Blood Services, expand their role in public health surveillance in the post-pandemic period. Together blood suppliers have near-national reach, collecting blood donations nearly every day in all larger cities and many smaller municipalities. Blood donors are a healthy subset of the general population. Demographic data, routine infectious disease testing and screening questionnaire data are collected for all donations. Close to one million blood samples per year could be made available for surveillance. With 90% repeat donors, longitudinal sampling is possible. Current blood donor surveillance includes monitoring infectious marker rates in low risk (e.g. HIV, hepatitis C virus) or asymptomatic (e.g. West Nile virus) populations, and ad hoc studies to monitor transfusion-transmissible infections. These include tick-borne infections such as *Babesia microti* and foodborne infections such as hepatitis E. Canadian Blood Services and Héma-Québec are actively seeking to engage with public health professionals to further develop a role in public health surveillance.

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Introduction

Two publicly funded blood services provide Canadians with fresh and fractionated blood products. Héma-Québec serves Québec, and Canadian Blood Services serves the other nine provinces and the three territories. Formed in 1998 in the aftermath of the Commission of Inquiry on the Blood System in Canada (Krever Commission) into transfusion-transmitted HIV, the blood providers operate at arms-length of government to ensure autonomy. The scope of activities of blood providers has further developed into stem cell registries, umbilical cord-blood banking, human milk banking, tissue banking and coordinating organ transplantation (roles vary by blood supplier). Applied research is a high priority and both organizations have independent epidemiology and surveillance departments as well as research and development/innovation departments that primarily focus on blood safety and informing blood service policy.

In this commentary, we discuss the role of the blood services in public health surveillance to date and propose that this role be expanded.

SARS-CoV-2 heralded a new role for blood services

In March 2020, the World Health Organization declared COVID-19 a pandemic. Both blood services initiated and continue to undertake severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) serosurveillance (1,2). Blood services around the world capitalized on their infrastructure to quickly start seroprevalence studies to inform public health policy. By June 2020, a short three months after the pandemic was declared, 32 of 48 (67%) countries surveyed had had SARS-CoV-2 seroprevalence studies initiated by blood operators (3,4). In

most cases, the blood service was the only entity able to rapidly collect and test large numbers of blood samples from healthy individuals. In many countries these studies have continued. In the United States, blood operators collaborate with the Centers for Disease Control and Prevention, providing test results routinely.

In Canada, there was early strong engagement of blood operators with public health, public health laboratory networks, mathematical modellers and university partners. The approach by the two blood providers differed somewhat. Over 18,600 donations were tested by Héma-Québec in collaboration with the *Ministère de la Santé et des Services sociaux du Québec*, and later, with the Government of Canada COVID-19 Immunity Task Force. They carried out three cross-sectional studies including donor-reported infection history and risk factors (2). Canadian Blood Services worked with the Government of Canada COVID-19 Immunity Task Force to test cross-sectional samples from nine provinces monthly (over 250,000 samples tested) (1).

Both blood operators also worked with clinical trials groups to provide anti-SARS-CoV-2 convalescent plasma products to their studies. Canadian Blood Services also led a smaller seroprevalence study, funded by the Canadian Institutes of Health Research, testing 1,500 donations per month. This linked Canadian Blood Services to collaborators in universities, industry research groups, public health organizations and provincial/national public health laboratories. The data generated, and lessons learned, informed public health policy and guided laboratory practices in provincial and clinical laboratories. In addition, the data and knowledge were shared broadly with other laboratorians and led to further academic collaborations. These linkages continue as serological testing monitors vaccine rollout and antibody concentrations. Both blood suppliers are providing SARS-CoV-2 seroprevalence data to the Secretariat of the Government of Canada COVID-19 Immunity Task Force, housed at McGill University, Montréal, Québec. These data are contributing to analyses to evaluate the seroprevalence of natural infection as well as the impact of vaccine rollout.

Post-pandemic, should blood services in Canada play a role in supporting public health surveillance? Similar questions are being asked in many countries. In Denmark a role for blood donors in public health surveillance was already being implemented pre-pandemic (5).

Blood donors are a healthy subset of the general population

Blood donors must be 17 years old (18 in Québec) to donate blood, and there are relatively few donors over the age of 72. Prospective donors must complete a detailed health history questionnaire (6). Those for whom donation is not in their best interests because of their health or who are at risk of infections such as HIV or hepatitis are not eligible. There are also some travel restrictions, including people at risk of tropical infections and those who spent time in the United Kingdom and other areas where they may be at risk for the variant Creutzfeldt-Jakob disease.

Blood collection sites are in all larger cities, most smaller cities and many towns—most of the more populated areas of Canada. The age, sex and geographic region of donors is comparable to the general population up to 65 years of age (see **Figure 1** and **Figure 2**). Largely excluded are northern regions as well as some rural areas and remote towns. There are also non-represented populations, including long-term care residents and those in detention centres, or people who are less likely to donate because of language barriers.

Figure 1: Percentage of the general population and donors by geographic region[a] and age group[b]

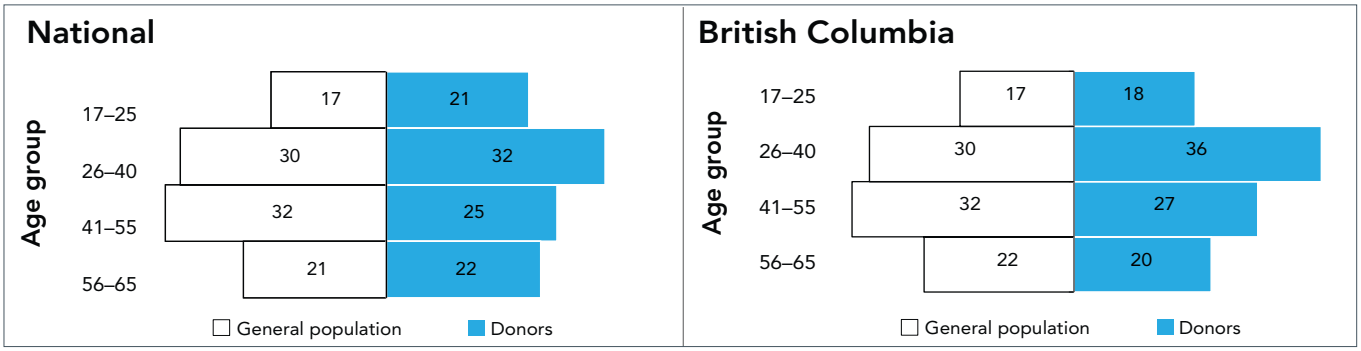
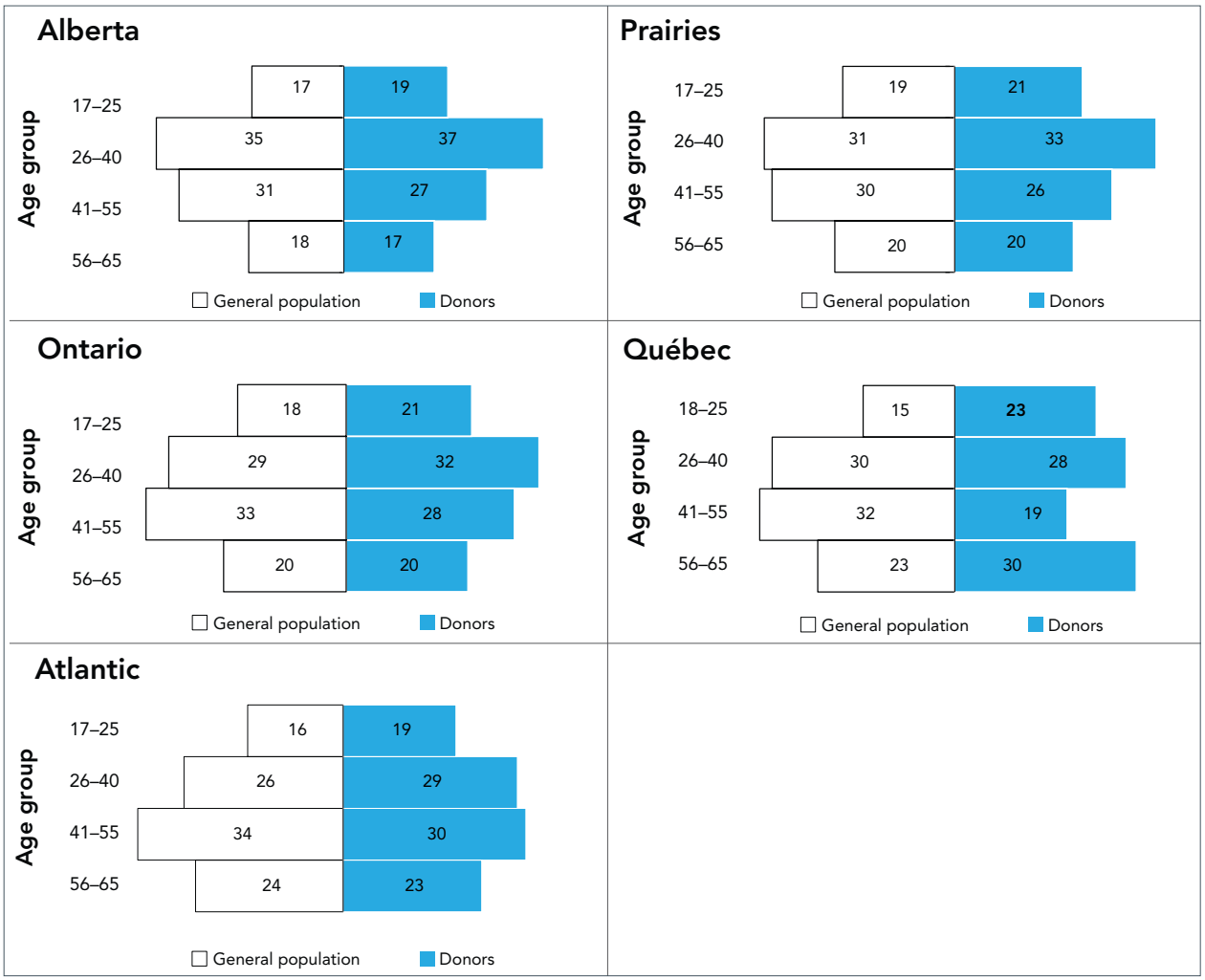
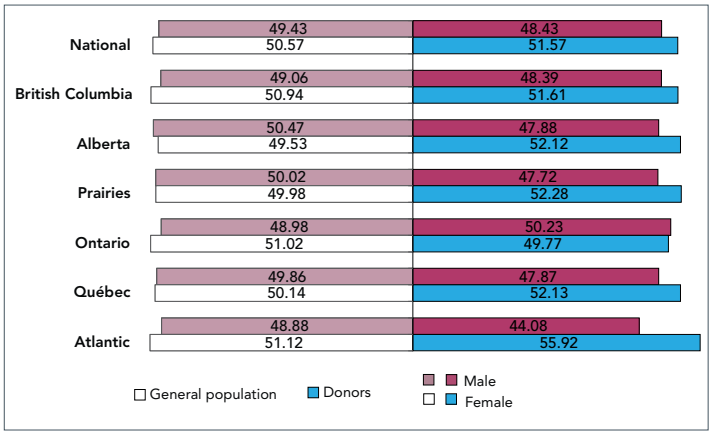


Figure 1: Percentage of the general population and donors by geographic region[a] and age group[b] (*continued*)



[a] Geographic regions include National (Canada excluding territories), British Columbia, Alberta, Prairies (Manitoba and Saskatchewan), Ontario, Québec and Atlantic (New Brunswick, Nova Scotia, Newfoundland and Labrador, and Prince Edward Island)
[b] General population and donor age range of 17–65 years used for all provinces except for Québec where the age range is 18–65 years
Source: Statistics Canada (7)

Figure 2: Percentage of general population and donors by geographic region[a] and sex[b]



[a] Geographic regions include National (Canada excluding territories), British Columbia, Alberta, Prairies (Manitoba and Saskatchewan), Ontario, Québec and Atlantic (New Brunswick, Nova Scotia, Newfoundland and Labrador, and Prince Edward Island)
[b] Male or female
Source: Statistics Canada (7)

While it is true that blood donors consider themselves healthy and self-select to donate, this may also be true of apparently healthy volunteers recruited to participate in studies. SARS-CoV-2 seroprevalence appears to be similar in both the healthy general population and the blood donor population (8,9). Further studies comparing blood donors with the general population are needed to better characterize which segment(s) of the general population donors best represent.

Blood service capacity for surveillance

There are some important strengths of blood services in public health surveillance. Between Canadian Blood Services and Héma-Québec, there is near-national reach in terms of daily blood collection. From each of the annual 1.2 million donations, an extra ethylenediaminetetraacetic acid (EDTA; an anticoagulant) tube of blood is collected. About 20% of these

donations are used for testing, which is essential to be able to release the blood product, but this leaves about 950,000 samples that could be made available for surveillance. An important advantage of using blood donations for surveillance is that about 90% of donors donate repeatedly. These donors can form a cohort for on-going monitoring. Donors return according to their own preference and the interval between donation may vary unlike research cohort participants.

Hemoglobin levels are measured before each donation. Data including demographic variables (e.g. age, sex, postal code, and ethnicity), current medications, recent vaccinations and recent travel history are collected via the routine donor history questionnaire (6). Currently, it is not possible to add more research questions to the donor history questionnaire, but electronic surveys could be sent within days of collecting samples. A recent survey of donor HIV risk factors to assess compliance with screening questions achieved a response rate of about 33% from the 40,000 donors invited to participate. Both blood operators also have the infrastructure, staffing and protocols to safely collect large volumes of plasma (>250 mL) from donors in a safe and controlled manner.

Examples of blood service surveillance relevant to public health

All blood donations are tested for HIV, hepatitis C virus, and hepatitis B virus using a nucleic acid test (NAT) and serology and human T-lymphotropic virus and syphilis using serology. West Nile virus (WNV) is tested seasonally using NAT, and *Trypanosoma cruzi* is tested in at-risk donors using serology (see **Table 1**). Repeat reactive specimens also undergo confirmatory testing where available. Depending on the positive assay target, specimens may also be sent to the National Microbiology Laboratory for nucleic acid sequencing and strain analysis. Positive results are reported to public health authorities where required by law.

Table 1: Infections routinely tested for in all blood donations, Canada

Infection	Markers
HIV	Antibody
	Nucleic acid
Hepatitis B virus	Hepatitis B surface antigen
	Antibody to hepatitis B core antigen
	Nucleic acid
Hepatitis C virus	Antibody
	Nucleic acid
West Nile virus	Nucleic acid
Human T-lymphotropic virus	Antibody
Trypanosoma cruzi (Chagas disease, at-risk donors only)	Antibody
Treponema pallidum	Antibody

Blood donors are a population who believe that they are not at risk and have replied in the negative to a battery of risk questions. Nevertheless, about 40 people per year test positive for hepatitis C virus and hepatitis B virus (10,11). These responses can provide insight into infected individuals with no apparent self-declared risk and may be useful in determining the potential benefit of screening low-risk populations. Testing for human T-lymphotropic virus and *T. cruzi* provides insight into these rare, non-reportable infections. Given the rise in diseases of despair blood donor screening may also shed light on sexual and high-risk behavioural networks that are not readily apparent to public health investigators (12,13).

Historically, both blood establishments have played important roles in monitoring emerging infectious diseases. By 2003, in response to the emergence of WNV in Canada, both blood services were testing blood donations and monitoring incidence with the West Nile Virus Task Force. Public health surveillance of WNV identifies symptomatic individuals who seek medical assistance, whereas blood donors will be initially screened with a WNV NAT either early stage or asymptomatic, unlike in public health laboratories. Blood operators may also send early WNV NAT-positive samples to the National Microbiology Laboratory or the *Laboratoire de santé publique du Québec* for molecular characterization.

As a result of these unique screening and testing approaches, in some years the first WNV infection of the season is identified in a blood donor. In Québec, the 2012 WNV data were used to estimate the underreported rate of neurologic WNV at between 26% and 37.5% (14). This was used to inform physician education materials, which subsequently shown (or demonstrated) to have improved case identification. Additional studies utilizing WNV-positive donor samples may involve the identification and characterization of viral genetic variants and the possible incursion of new lineages into the country (15,16). Finally, it is important to note that the WNV NAT is actually a broadly reactive assay for the Japanese encephalitis serocomplex and adds an additional level of surveillance for Japanese encephalitis, Kunjin virus, Murray Valley encephalitic virus, Saint Louis encephalitis virus and Usutu virus (17).

In the case of emerging tick-borne pathogens, in 2013 the first *Babesia microti*-positive public health case was reported in Manitoba, but no *B. microti* NAT or antibody-positive donations were identified from about 14,000 donations tested (18–20). In 2018, of 50,000 donations Canada-wide, there was one NAT-positive donation in Manitoba, and in a subset of 14,000 donations from the geographic region spanning Manitoba to Nova Scotia, four antibody-positive donations were identified, all in southwestern Ontario (21). In 2019, a donor who felt unwell after donating was found to be *B. microti*-positive. An investigation that involved Canadian Blood Services, the National Microbiology Laboratory, an additional reference laboratory and two provincial public health laboratories found

that transfusion-transmitted babesiosis had not occurred (20). Thus, two of the three known endemic NAT-positive cases were found in blood donors, suggesting that *B. microti* has gained a foothold in Canada. Blood donor studies can potentially evaluate infections and document exposures from other emerging tick-borne and arthropod-borne infections such as *Borrelia burgdorferi*, *Anaplasma phagocytophilum*, Powassan virus and Eastern equine encephalitis virus. This type of surveillance is important in the context of climate change and expanding vector habitats.

Hepatitis E was evaluated in two national studies (22,23). In the first study of 14,000 donors tested, no hepatitis E virus NAT-positive donations were identified, but 5.6% were antibody positive. In the second study of about 50,000 donations tested with a more sensitive NAT assay, 1 in 4,615 tested positive for hepatitis E viral RNA. This was one of the largest hepatitis E virus studies carried out in Canada.

Strengths and limitations of blood donors for public health surveillance

The near-national reach of blood services' daily collections and laboratory capacity can be leveraged to rapidly survey pathogens at a relatively low cost. Importantly, blood services cross jurisdictional boundaries and have streamlined decision-making processes. For national surveillance activities, there are substantial advantages over other sources of healthy individuals, for example, patient testing and pregnancy screening programs, which are generally local rather than national.

Both blood services conduct and enable research with the oversight of external research ethics committees that follow the guidance outlined in the *Tri-Council Policy Statement: Ethical Conduct for Research Involving Humans* (24). Blood services also undertake unique lookback processes (investigating recipients of a test-/disease-positive donor) and traceback processes (investigating donations and donors from a disease-/test-positive recipient) for blood recipients or donors with a suspected blood-borne infection (20,25). These processes could be leveraged to support further active surveillance.

The potential disadvantages of using blood donors as a data source are that some segments of the population are underrepresented, such as those living in rural areas, older adults, people with serious illnesses and those with risk factors for transfusion-transmissible diseases. Furthermore, children are not eligible to donate blood, and anthropometric measurements and biologic samples such as urine are not currently available.

Future directions

More research is needed to understand how the donor population differs from the general population. Increased collaboration between blood services and provincial and federal public health departments will help initiate new research projects. A potential role of blood services in the surveillance of vaccine-preventable infections is being explored, and an expanded role in vector-borne infection surveillance would be a natural extension of blood service surveillance. Héma-Québec has established a biobank specifically for COVID-19 projects, and Canadian Blood Services has stored samples from the SARS-CoV-2 seroprevalence study. Larger (not project-specific) biobanks are under consideration by both blood services. Methods for collecting more health and lifestyle data through questionnaires are being explored as are ways to link donor data to health registries for research. The value of biobanks will be amplified as more detailed information about donors is collected, increasing potential applications to public health surveillance and research.

Conclusion

The emergence of SARS-CoV-2 highlights the value of blood services to leverage operational capacity for rapid implementation of large-scale nationwide serosurveillance. Together Canadian Blood Services and Héma-Québec have near-national reach of a healthy adult population. Blood donations are collected daily and longitudinal sampling is possible. Demographic data, routine infectious disease testing information and screening questionnaire data such as current medications, recent vaccinations and travel history are collected from all donors. Avenues by which the blood services can contribute to public health surveillance post-pandemic are being actively explored. Potential areas include serosurveillance of vaccine-preventable infections, lookback and traceback investigations and monitoring for emerging vector-borne pathogens.

Authors' statement

All authors (SFO, SJD, AL, CO, MAD, CR) conceptualized and revised this paper. SFO drafted the paper.

Competing interests

None.

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COMMENTARY

The need for linked genomic surveillance of SARS-CoV-2

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Abstract

Genomic surveillance during the coronavirus disease 2019 (COVID-19) pandemic has been key to the timely identification of virus variants with important public health consequences, such as variants that can transmit among and cause severe disease in both vaccinated or recovered individuals. The rapid emergence of the Omicron variant highlighted the speed with which the extent of a threat must be assessed. Rapid sequencing and public health institutions' openness to sharing sequence data internationally give an unprecedented opportunity to do this; however, assessing the epidemiological and clinical properties of any new variant remains challenging. Here we highlight a "band of four" key data sources that can help to detect viral variants that threaten COVID-19 management: 1) genetic (virus sequence) data; 2) epidemiological and geographic data; 3) clinical and demographic data; and 4) immunization data. We emphasize the benefits that can be achieved by linking data from these sources and by combining data from these sources with virus sequence data. The considerable challenges of making genomic data available and linked with virus and patient attributes must be balanced against major consequences of not doing so, especially if new variants of concern emerge and spread without timely detection and action.

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Introduction

Since the start of the pandemic, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has evolved in multiple ways that increase its public health threat, with higher transmissibility (Alpha, Delta, Omicron variants) (1–4), partial immune escape (Beta, Omicron variants) (5,6) and greater severity (Alpha, Delta variants) (7–9). The continued emergence and spread of new variants of interest and variants of concern (VOC) have the potential to undermine our ability to manage the coronavirus disease 2019 (COVID-19) pandemic, with costly consequences to health, healthcare systems and economies. The SARS-CoV-2 virus faces heterogeneous selection: highly vaccinated communities and those with substantial immunity from previous infection are partially protected, while unvaccinated communities and those with waning immune protection are susceptible. With rising immunity levels, selection is expected to favour variants that better escape vaccine or infection-induced immunity (10). It is particularly crucial to know if a new virus variant emerges with mutations that increase 1) the ability to infect vaccinated or recovered individuals, 2) the transmissibility of the virus and/or 3) the severity of the disease. The rapid spread of the Omicron variant has led to the highest demand yet on hospitals in many areas, despite the disease being less severe on average (11), highlighting the urgency of developing the methods and data processes to answer these questions in time to take appropriate preventive action.

It is to be hoped that SARS-CoV-2 will not evolve higher transmissibility simultaneously with higher severity among vaccinated or recovered individuals. The cellular immune response is strong and complex (12–14), and breakthrough infections have had reduced severity compared to infections in unvaccinated individuals (15). Before Omicron emerged, vaccine-induced antibody responses remained strong across a variety of VOCs (16,17), but Omicron is a stark reminder that variants can emerge that substantially evade our immune responses (1–3,18), at least in terms of neutralizing antibodies (14,18–20), dramatically reducing vaccine-induced protection against infection (21). There is no guarantee that future variants will follow Omicron's path in terms of severity.

Virus sequencing initiatives and related genomic surveillance systems give a high-resolution and near-real-time view of how SARS-CoV-2 is evolving and spreading and of the mutations that are rising in frequency (22). Establishing surveillance systems that can detect evolving viral characteristics that impact clinical outcomes and effectiveness of control measures is a key aim of viral sequencing efforts (23). For a newly emerging variant with uncertain impact, rapidly assessing the degree of risk to control efforts is paramount and requires multiple sources of data.

Data and linkages that are required

While genomic data alone allow certain inferences (e.g. identifying which cases are related, and identifying which mutations occur in a new variant), substantially greater value can be obtained by combining a "band of four" key data sources: genetic data; epidemiological and geographic data; clinical and demographic data; and immunization (or recovery) data.

Genetic data refer to attributes of the virus. Here we focused on SARS-CoV-2 whole genome sequence data, but note that polymerase chain reaction testing can identify specific mutations or deletions without fully sequencing the virus genome and so can provide rapid VOC detection.

Epidemiological and geographic data refer to information about the transmission context, including the geographic location and the reason for testing or sequencing (e.g. whether the individual was part of a known outbreak, was a traveller, was randomly sampled, was a vaccine breakthrough infection, was someone previously infected or was tested for other reasons). Epidemiological data also include information about the source and location of exposure: workplace outbreak; household; travel; community exposure; animal exposure; and health care worker, as well as any other contact investigation information (e.g. indoors vs outdoors, ventilation, community setting).

Clinical and demographic data refer to attributes of individuals infected with SARS-CoV-2, including treatments provided, outcomes (e.g. symptoms, severity) and demographic aspects (e.g. age, comorbidities, exposure risks).

Immunization (or recovery) data refer to attributes of past COVID-19 infection or vaccination, including vaccine type(s), number of doses and dates of doses.

These data are typically gathered by different parts of a health system at different times and are used for a variety of purposes, creating challenges for data linkage. Medical facilities manage the clinical course of disease, contact tracing and other case data are gathered by epidemiological teams in public health, vaccination status may be in medical records or known only to the individual, while sequence information is often collected at specialized sequencing centres. Along the way, information may be lost or remain disconnected. Jurisdictions differ in the extent to which linkages among these data can be made; however, linking these four data sources is the most promising way to rapidly detect variants that have the potential to break through pandemic containment measures.

Opportunities with partial data

It is essential to understand vaccine effectiveness against a variety of outcomes (infection, symptoms, hospitalization, death), as well as intrinsic transmissibility and severity in vaccinated and unvaccinated individuals. These can change rapidly as new variants arise and spread. Links to genetic data can attribute transmissibility, severity and vaccine effectiveness to viral types, and thereby provide a better basis for projecting infections and healthcare burden in the context of vaccination. Viral evolution also causes a continual turn-over in how we classify a virus, as names are given only when a variant has spread and become sufficiently distinct (e.g. by Phylogenetic Assignment of Named Global Outbreak Lineages) (24). Consequently, case data with linked lineage information need to be updated as our classification system changes, and this is only possible if links to sequence data, as opposed to lineage names, are maintained.

With only viral sequences and sample dates, it is possible to identify unusual new variants, bursts of mutations, "mutator" lineages that evolve faster than predicted (25,26) or genetic changes that spread more rapidly than expected; however, rapid growth is difficult to interpret. Rapid growth could be due to viral characteristics, epidemiological fluctuations, travel-associated introductions or sampling artifacts (26). For example, the mutational profile of the Omicron variant was a cause for concern as it includes both new mutations and a number of mutations already seen in other VOC—including mutations known to enable the virus to evade neutralizing antibodies (27). Because of their genetic surveillance system, the Department of Health in South Africa sounded the alarm about Omicron (B.1.1.529; November 25, 2021) after detecting the new subvariant and witnessing its rapid spread in a matter of weeks (first collected on November 11, 2021). The researchers noted key outstanding questions about the effect of Omicron on transmissibility, effectiveness of vaccines and disease severity, which cannot be determined from data on the number of detected Omicron sequences alone (28).

The fields of phylogeography and phylodynamics have enabled the use of virus sequence data to infer the geographic movements of viruses (24,25), identify factors driving transmission across geographic regions (29), estimate the effective reproduction number over time (30,31) and link virus sequences to epidemiological models for a range of applications (32,33); however, there are limitations. Phylogeographic analyses are affected by geographic differences in both sampling rates and strategies. Phylodynamic estimates of reproduction numbers over time tend to be retrospective, apply to large virus populations at the national or international scale, have high degrees of uncertainty and are often not immediately actionable at smaller locations—where public health units need to act. Combining sequence data with the other three bands of data offers more opportunities to use virus sequences to understand transmission, severity and immunity. This combination does not necessarily require individual-level linked data; much could be done with data that are de-identified and even data reported for small groups rather than individuals. Even disaggregating outcomes by VOC status would have very high value, as noted recently for Omicron (34).

If the epidemiological context is known, it is possible to distinguish the emergence of a variant with a high growth rate from growth driven by chance "founder effects" (e.g. superspreader events, social gatherings among unvaccinated individuals, introductions vs transmission in care settings or increased sampling due to a particular outbreak) (35,36). Making this distinction increases the reliability of the inference and the value for both research and public health (36,37). For example, Volz *et al.* combined sequencing and polymerase chain reaction testing data with reason for sequencing (community samples) and geography in estimating transmissibility of the Alpha variant B.1.1.7 (1). Virus sequences can also be linked to travel history to monitor the spread of emerging variants and to inform public health measures aiming to limit importation (24,38,39).

In densely sampled outbreaks, linking virus sequences to epidemiology can offer information of immediate relevance to infection prevention, especially when analysis can be done in real time. Lucey *et al.* used whole genome sequence data to identify previously undetected transmission events in hospital-acquired infections, finding evidence that transmission occurred from both symptomatic and asymptomatic healthcare workers, and occurred disproportionately in patients who required high levels of nursing care, informing better prevention tools (40). In a real-time genomic epidemiology study in Australia, sequencing linked to epidemiological data indicated the probable source of infection and identified previously unknown connections between institutions (37,41). Linking virus sequences to additional host and epidemiological data, such as the location of exposure, would also make it possible to detect mutations that give the virus a context-specific advantage, such as transmitting more efficiently outdoors or among specific age groups.

Linking viral sequence data with host data on age, sex, race, occupation, dwelling type, comorbidities and other clinical/demographic data permits virus and host factors contributing to severe disease to be identified. For example, Bager *et al.* used linked data for virus sequences, hospitalization outcome and a large number of host covariates to demonstrate a higher adjusted risk ratio of hospitalization for the Alpha variant (42). Similarly, Fisman and Tuite estimated the increase in risk of hospitalization, intensive care unit admission and death from N501Y-containing variants and the Delta variant (43). Further resolution could be achieved with whole genome sequence in place of VOC screening data.

Linked immunization and sequence data are essential to determine whether newly emerging types and/or variants reduce vaccine effectiveness and to what extent. For example, Skowronski *et al.* linked VOC typing with vaccine status and testing information to show that a single dose of messenger ribonucleic acid (mRNA) vaccines was similarly effective against the Alpha and Gamma variants and non-VOC SARS-CoV-2 (44). Examining clusters or sets of closely related virus sequences together with immunization status informs us about potential transmission. If a cluster consists mainly of vaccinated individuals, this suggests considerable transmission among these individuals; however, if breakthrough infections are preferentially sequenced, an apparent cluster of breakthrough cases could be missing many unvaccinated individuals who comprised most of the transmission. Distinguishing between these requires linking sequences, vaccination status and reason for sequencing, which may include contact tracing or household information.

The entire band of four is needed to determine whether a virus variant can be transmitted by vaccinated individuals and cause severe disease among them: sequence data can tell us whether this is a new variant; epidemiological data and vaccination data can tell us whether it is being transmitted among vaccinated individuals and clinical data will indicate whether the variant is causing severe disease. Without these four linked pieces—shared sufficiently rapidly and over a large enough area to have strong statistical power—there will be gaps that substantially weaken our ability to monitor the virus' changing phenotype. Small-scale but aggregated and de-identified data may be sufficient for early warnings and help to avert concerns over privacy.

Data sharing and statistical power

Many jurisdictions may gather virus sequences and clinical, epidemiological and immunization data, but may not permit linkage among them due to structural or other barriers. Even where timely joint analysis of these data is possible, however, there is an additional challenge that an emerging variant or type is necessarily rare when it is first emerging. Sharing data across jurisdictions results in greatly improved statistical power by increasing the total amount of data available. Data delays are an additional problem. Even for countries sharing virus genomic data through the Global Initiative on Sharing All Influenza Data database, lags can span months (45). These extensive time

lags hamper international efforts to track variants and their mutations, determine which are rising in frequency and where, track variants' epidemiological and biological consequences and develop effective public health policy (45). Furthermore, even where sequences are shared in a timely manner to the Global Initiative on Sharing All Influenza Data database, they are typically not shared alongside epidemiological, clinical/demographic and immunization data. Indeed, the barriers to public health data sharing are extensive: van Panhuis *et al*. described technical, motivational, economic, political, legal and ethical barriers (46). Many of these are of daily relevance in the COVID-19 pandemic.

Timeliness matters

To make an immediate practical difference, these data linkages and analyses need to be conducted with as little delay as possible. The sooner a new VOC can be characterized, the more warning decision-makers have about the risk. Identifying the spread of a VOC requires strong real-time genomic surveillance with sampling that reflects community transmission, and it requires regular reporting on the makeup of the virus population.

There are significant challenges to developing timely surveillance for emerging VOC, and these challenges differ according to whether the concern is an increase in severity, immune escape, transmissibility or a combination. It takes many infections before we can estimate a difference in severity, yet changes in severity will shape the impact on the healthcare burden. But only a minority of individuals experience severe disease, and there are inherent delays between infection and eventual outcomes. By the time the risks of hospital and acute care needs can be estimated, many hundreds or thousands of infections will have occurred. To stratify severity estimates by viral factors requires even more hospital records and therefore more infections (potentially thousands). This can be ameliorated slightly by focusing on measures with minimal time lags (for example hospital admissions rather than occupancy) and with timely reporting.

Differences in transmissibility are likely to be apparent earlier than differences in severity, because transmission occurs for all infections (whereas severe outcomes occur for a small minority). Indeed, with both the Alpha and Delta variants, increases in transmissibility were detected well ahead of increases in severity (1,7). Differences in immune evasion may or may not be apparent soon after the relevant variants arise, depending on the genomic surveillance system (e.g. prioritization of breakthrough infections, extent of surveillance) and whether the new type causes severe disease among vaccinated individuals.

An effective surveillance system also requires linking timely detection with timely action. Public health and policy makers need to assess when to take action in the face of the uncertainty that is inherent in early assessments of variants that might increase transmission, severity or immune escape. Early localized actions that prevent a VOC from spreading widely, while costly in the short-term, reduce the risk of prolonged and global challenges to effective COVID-19 control.

Discussion

Timely and accurate surveillance requires a range of expertise spanning infectious disease epidemiology, statistics, virus evolution, genomics and public health. Benefits are gained not just from combining data but from conducting joint analyses, bringing together a sufficient range of expertise to increase the chance of early detection of an emerging threat. Many standard approaches used to estimate transmissibility, vaccine effectiveness and severity (e.g. attack rates, test negative study designs) are only possible after community transmission is well established. Designing systems to warn of possible elevated transmission, immune evasion and severity when there are still few cases requires integrating many sources of information and expertise and developing and using analytical methods designed to combine these data streams. Furthermore, progress in establishing linked surveillance for SARS-CoV-2 is likely to benefit surveillance for other respiratory pathogens, including newly emerging zoonotic viruses and high-burden pathogens such as influenza and respiratory syncytial virus. Improvements in sequencing technology also allow sequencing multiple viral pathogens sampled from patients or the environment, improving the ability to respond rapidly to any newly emerging virus (47).

There are precedents for strong genomic-based surveillance systems with linkage to clinical and epidemiological data. PulseNet Canada (48) is a virtual electronic network that delivers systemic surveillance for enteric disease and ensures that genomes of causal bacteria are rapidly sequenced. The presence of clusters of cases triggers coordinated outbreak investigations in which data are collected and linked to sequences to assess the full extent of the outbreak and identify the source. For SARS-CoV-2 surveillance, the Canadian COVID-19 Genomics Network (16) aims to establish large-scale virus and host sequencing at a national scale to inform decision-making and track the evolution and spread of the virus. Such national platforms can enable data linkage, either with public access or with privileged access given to approved researchers. Although to date such goals have been hampered in Canada, in part by limited or delayed access to virus sequences and limited linkage.

Throughout the SARS-CoV-2 pandemic, the United Kingdom has led the world in data linking, analyses and public communication in its efforts to understand SARS-CoV-2 evolution and impact on public health. The COVID-19 UK Genomics Consortium (49) performs and coordinates sequencing, with over 1.5 M publicly available viral genomes as of February 17, 2022 (50). Sequences are linked with clinical and epidemiological information and are stored securely. Public health agencies use genomic data linked to clinical, demographic and epidemiological data in the public health response and can provide de-identified COVID-19 patient information into the Cloud Infrastructure for Microbial

Bioinformatics (CLIMB-COVID-19) (51) database. There are systems in place for researchers to access the data.

A recent briefing (SARS-CoV-2 VOC and variants under investigation in England: technical briefing 36) from the UK Health Security Agency (21) provides an excellent example of the impact of research enabled by data linkage in the United Kingdom. This report summarizes research linking Phylogenetic Assignment of Named Global Outbreak lineage information to contact tracing data, permitting the discovery that the BA.2 sublineage of Omicron has shorter serial intervals than the BA.1 sublineage, which in turn impacts the interpretation of selection (higher rate of spread is in part due to faster transmission rather than more overall transmission). Linking to vaccination data, age profiles and severity permitted estimates of protection against severe disease and the likely health care burden of BA.2. Sequence and screen-based characterization of the rise of BA.2 allowed estimates of its rate of spread, which is needed to project the future burden of infection and disease. The report is a collaboration of teams that combine expertise in genomics, outbreak surveillance, contact tracing, epidemiology and data analytics, linking and analyzing emerging data with very rapid turn-around and thereby benefitting the global community.

Beyond national-level analyses, linking data at a local level can provide important insight into transmission routes and outbreak risks; for example, genomic epidemiology tools have been used to examine transmission at the scale of outbreaks (52–56). By linking sequences, clinical outcome, epidemiological data and vaccination status, such local analyses can alert public health to the emergence of a concerning cluster. If there was a growing cluster with transmission among vaccinated individuals and high severity, this could be detected early. Both national and local-scale analyses require linkage among disparate data systems through unique identifiers, collaboration across multiple disciplines, and a process by which researchers can access linked data to develop and validate methods.

Conclusion

The SARS-CoV-2 virus will continue to evolve. We cannot predict where new variants of concern will arise, nor rely on them being detected early in locations that have strong genomic surveillance. The more we build strong surveillance systems worldwide, with high-quality data and linkages, the earlier we will be able to detect new variants and act accordingly. Many wealthy countries have high rates of vaccination, which leads to selection of variants with the ability to transmit among vaccinated individuals. With extensive international travel, emerging variants will be able to rapidly migrate around the world, and any that evade immunity will not be as impacted by vaccination requirements. In the worst case, viral evolution could undermine the potential for vaccination to mitigate the pandemic, even in countries that have not yet reached high vaccination rates. Countries with the resources to conduct high volumes of sequencing and to develop strongly linked surveillance programs are also the ones that have most benefited from early and extensive vaccination programs. Developing and supporting strong genomic surveillance that enables monitoring the virus' phenotypes is important to help ensure that the vaccines remain effective for the rest of the world.

Authors' statement

CC — Conceived the project, led discussion with all authors, wrote the first draft
SO — Literature overview
NO — Literature overview
GJ — Literature overview
GvD — Literature overview

All authors performed writing-review and editing. All authors contributed text and approved the final manuscript.

Competing interests

None.

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Multijurisdictional outbreak of COVID-19 associated with a wake/funeral event in a northern Saskatchewan First Nations community

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Abstract

Background: Sixty-eight laboratory-confirmed cases of the coronavirus disease 2019 (COVID-19) (12 in Alberta [AB], 56 in Saskatchewan [SK]) were linked to a gathering at a hospital in Alberta on June 1–4, 2020, and a wake/funeral in a First Nations community in northern Saskatchewan on June 9–11, 2020.

Objective: The objectives were to provide a comprehensive description of the epidemiology of the outbreak and describe the chains of transmission to inform the hypothesis that there were multiple introductions of COVID-19 at the wake/funeral.

Methods: Case investigation and contact tracing was conducted by local public health in AB and SK. The Public Health Agency of Canada conducted a centralized case analysis. An epidemic curve and a Gantt chart for period of communicability were created to support or refute whether there had been multiple introductions of COVID-19 at the wake/funeral.

Results: Illness onset dates ranged from May 31 to July 1, 2020. Ages ranged from 2 to 80 years (median age=43 years). Five cases were hospitalized; there were no deaths. The available case exposure information supports the hypothesis that there had been multiple introductions of COVID-19 at the wake/funeral. Public health authorities in AB and SK declared the outbreak over on July 20, 2020; based on two incubation periods (i.e. 28 days) following the illness onset of the last primary case.

Conclusion: During multijurisdictional outbreaks, data sharing, coordination across health authorities and centralized analysis is essential to understanding the events that lead to the outbreak and possible hypotheses around chains of transmission.

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Keywords: COVID-19, SARS-CoV-2, outbreak, Indigenous community, mass gathering, funeral

Introduction

An outbreak of coronavirus disease 2019 (COVID-19) occurred in two Indigenous communities in northern Alberta (AB) and northern Saskatchewan (SK) in 2020. Sixteen individuals from AB and SK, including the index case (SK), visited a hospital in Edmonton, AB, on June 1–4. Nine of these individuals later travelled to an Indigenous community in northern Saskatchewan for a wake/funeral that was held on June 9–11. A large number of people attended the wake/funeral, including individuals from Indigenous communities in northern AB, where the deceased resided (whose death was unrelated to COVID-19). The index case and a household member hosted the wake indoors at their home on June 9–10. Public health measures, including physical distancing and masking, were not strictly observed at all times. The funeral ceremony took place in a church on June 11; 140 people attended these events.

The events on June 9-11 are refer to as "wake/funeral" because transmission and acquisition potentially occurred at either of these closely connected occasions and the investigation could not discern which of the 140 attendees came to which of the two events.

The objective of this report is to comprehensively describe the epidemiology of this COVID-19 outbreak using all cases and to describe the chains of transmission. It is important to highlight the value of collaborative interjurisdictional investigations in outbreaks; data sharing across jurisdictions can reveal associations that might not be uncovered during separate investigations.

Methods

Overview

Rapid point-of-care (POC) and polymerase chain reaction (PCR) testing are available to members of the northern Indigenous communities. Sufficient test kits are supplied to initiate testing for close contacts and exposed people, as the communities are remote. Samples are sent to the SK provincial laboratory for confirmation.

Saskatchewan public health was first alerted to an emerging outbreak when the index case was hospitalized on June 11, 2020. The individual was tested by rapid POC test on June 7, and the positive PCR test occurred on June 12. Saskatchewan public health launched its investigation and began contact tracing on June 11.

On June 11, Northern Inter-Tribal Health Authority (NITHA) public health in SK declared an outbreak of COVID-19 and launched an investigation. NITHA declared the outbreak over on July 20, 2020, based on two incubation periods (i.e. 28 days) following the illness onset of the last primary case.

Definitions

The definitions used during this outbreak investigation and in this report are as shown in **Table 1**.

The AB, SK and the Public Health Agency of Canada (PHAC) collaborated on the minimum set of data elements required to provide an epidemiological description of cases and describe the chains of transmission. Case-level line lists were shared with PHAC for centralized analysis. Data were received for 68 PCR-confirmed cases.

Investigations

Case investigation and contact tracing was conducted by public health nurses and trained case investigators from AB and SK using the standard COVID-19 case report form agreed upon by all provinces/territories in Canada. Most of the interviews were conducted in-person because reaching individuals by phone was difficult. Local Indigenous outreach workers helped with translation as needed. Community leaders, including the First Nations Chief and Council, worked closely with Indigenous Services Canada, Alberta Health, NITHA and Saskatchewan Health Authority throughout the investigation.

Alberta public health laboratory genetically sequenced the isolates and found the SARS-CoV-2 lineage to be identical for them all. Centralized genomic analysis comparing AB and SK isolates was not completed.

Epidemiologic and statistical analyses

Case demographics, including age, sex and severity of illness, were summarized. An epidemic curve was generated based on illness onset date (or earliest date based on the date sequence: onset date, specimen collection date and positive laboratory test result date).

Table 1: Definitions used in this COVID-19 outbreak investigation

Item	Definition
Primary outbreak case	• Confirmed or probable case (as per provincial/territorial surveillance case definitions) • **AND** epidemiologically linked to event: o For symptomatic individuals: exposure to the outbreak setting/site during their incubation period o For asymptomatic individuals: exposure to outbreak setting/site in the 14 days prior to their positive specimen collection date
Secondary outbreak case	• Confirmed or probable case (as per provincial/territorial surveillance case definitions) • **AND** epidemiologically linked to primary outbreak case • **AND** no exposure to the outbreak setting/site during their incubation period or 14 days prior to their positive specimen collection date
Outbreak setting/site[a]	• The hospital in AB • **OR** the wake and the funeral in SK
Close contact[b]	A person who had direct contact with a primary or secondary outbreak case during the case's period of communicability because they • Lived with or otherwise had close prolonged contact with a case (i.e. for more than 15 minutes and within 2 metres) • **OR** had direct contact with infectious body fluids of a case (e.g. was coughed or sneezed on or through contaminated surfaces)
Incubation period	Up to 14 days from exposure to onset of symptoms. The maximum incubation period of 14 days is used as a proxy for the likely exposure period
Period of communicability	For symptomatic individuals: 2 days prior to onset of symptoms and 10 days post onset of symptoms or symptom resolution, whichever is longer For asymptomatic individuals: 2 days prior to specimen collection date and 10 days post specimen collection date

Abbreviations: AB, Alberta; SK, Saskatchewan
[a] A primary outbreak case was present at least one of these sites (hospital, wake/funeral), and a secondary outbreak case was someone who was not present at any of these sites
[b] For the purpose of this investigation, all wake/funeral attendees were considered close contacts, as they were present for 15 minutes or longer. Individuals who were present for less than 15 minutes and wore masks were not considered close contacts

A Gantt chart with the cases' periods of communicability was overlaid with exposure information. As specific linkages between cases based on case identifier were not available, it was not possible to produce a social network analysis.

Because the exposure information did not include date of attendance at the wake and funeral, we assumed that cases were present on all three days (June 9–11). Travel dates were not available; the assumption that AB cases were in SK on June 8–11 is based on information from AB.

Interventions

The First Nations community in northern SK imposed travel restrictions that permitted essential travel only. Curfew was in effect from 11 p.m. to 7 a.m. daily, and groceries and essential supplies were delivered to minimize travel. Local public health issued a precautionary health advisory, as the attendance list for these events were not available. Anyone in attendance at an outbreak setting/site was advised to immediately self-isolate and self-monitor for symptoms of COVID-19 for 14 days and to call community health centre for evaluation and direction. Local radio broadcast key messages translated into the local language. Local radio and social media promoted public health strategies, such as the use of nonmedical face masks, physical distancing, personal hygiene measures and participating in responsible gatherings.

NITHA and the Saskatchewan Health Authority established rapid POC and PCR door-to-door and drive-through testing options. Isolation trailers were made available to ensure adherence to isolation requirements. Public health detention orders and warning letters were issued to individuals not complying with the self-isolation requirement.

Contact tracing and mass testing were also conducted in the First Nations community in northern AB. Accommodations for isolation/quarantine were made available for individuals returning to AB from SK following the wake/funeral.

Investigation findings

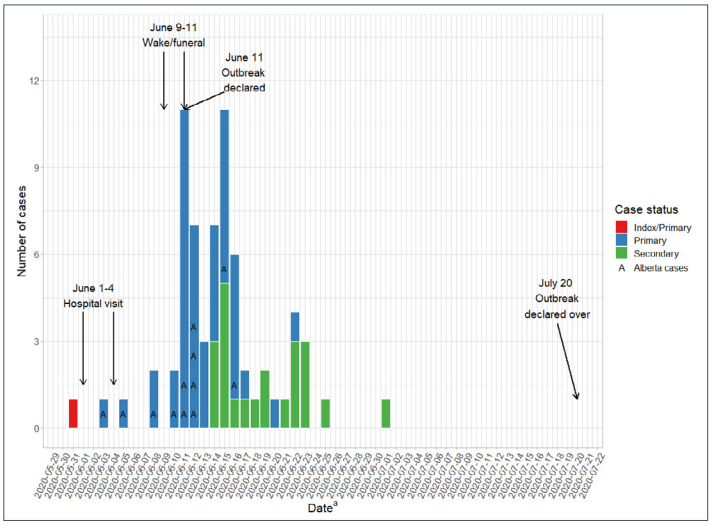
Descriptive epidemiology

There were three settings where transmission may have occurred. The first setting was the hospital visit in AB (June 1–4); of the 16 visitors, 9 (AB=7, SK=2) later tested positive for COVID-19. Of the 9 hospital visitors who tested positive, 8 attended the wake and funeral.

The second and third settings were the wake/funeral in the northern Saskatchewan First Nations community (June 9–11). Of the 140 attendees, 44 (AB=11, SK=33) later tested positive, an attack rate of 31%.

In total, 68 PCR-confirmed cases of COVID-19, including secondary cases (AB=12, SK=56), were identified as part of this outbreak (**Figure 1** and **Table 2**). A large proportion of cases (38%) remained asymptomatic throughout their period of communicability.

Figure 1: Epidemic curve of laboratory-confirmed SARS-CoV-2 cases by episode date[a] from two northern Indigenous communities linked to a wake/funeral in northern Saskatchewan, May 31 to July 20, 2020 (N=68)



[a] Based on date sequence (illness onset date, positive specimen collection date or date of first positive test result)

Table 2: Characteristics of SARS-CoV-2 cases included in the outbreak investigation from two northern Indigenous communities linked to a wake/funeral in northern Saskatchewan, May 31 to July 20, 2020 (N=68)

Characteristics	Description	Outcome
Breakdown by case status	Primary, n	45 (AB=12, SK=33)
	Secondary, n	23 (SK)
Episode dates	Earliest date (illness onset, positive specimen collection date or date of first positive test result)	May 31–July 1, 2020
Demographics	Median age, years (range)	43 (range: 2–80)
	Female gender, n (%)	34/68 (50%)
Asymptomatic cases[a]	Cases that never developed symptoms, n	26/68 (38%)
Case severity	Hospitalizations, n (% cases hospitalized)	5 (7%)
	ICU admissions, n (% hospitalizations admitted to ICU)	1 (20%)
	Deaths, n	0

Abbreviations: AB, Alberta; ICU, intensive care unit; SK, Saskatchewan
[a] Cases remained asymptomatic throughout their entire period of communicability

Ancillary analyses

The first transmission likely occurred in the hospital in AB. Nine cases (AB=7, SK=2) reported visiting the deceased (non-COVID-19-related death) in the hospital in AB between June 1 and June 4. During the visit, three of the cases were within their period of communicability and two were symptomatic (**Figure 2**). The two SK cases stayed together at a hotel in AB; one was the index case from SK. Seven of the AB cases reported close contact with the two individuals from SK.

On June 8, 12 AB cases travelled to SK for the wake/funeral in a convoy of six vehicles. Only one AB case (AB-4) did not attend any of the events in SK, because that person was ill, likely with COVID-19; however, that case was not tested until June 14.

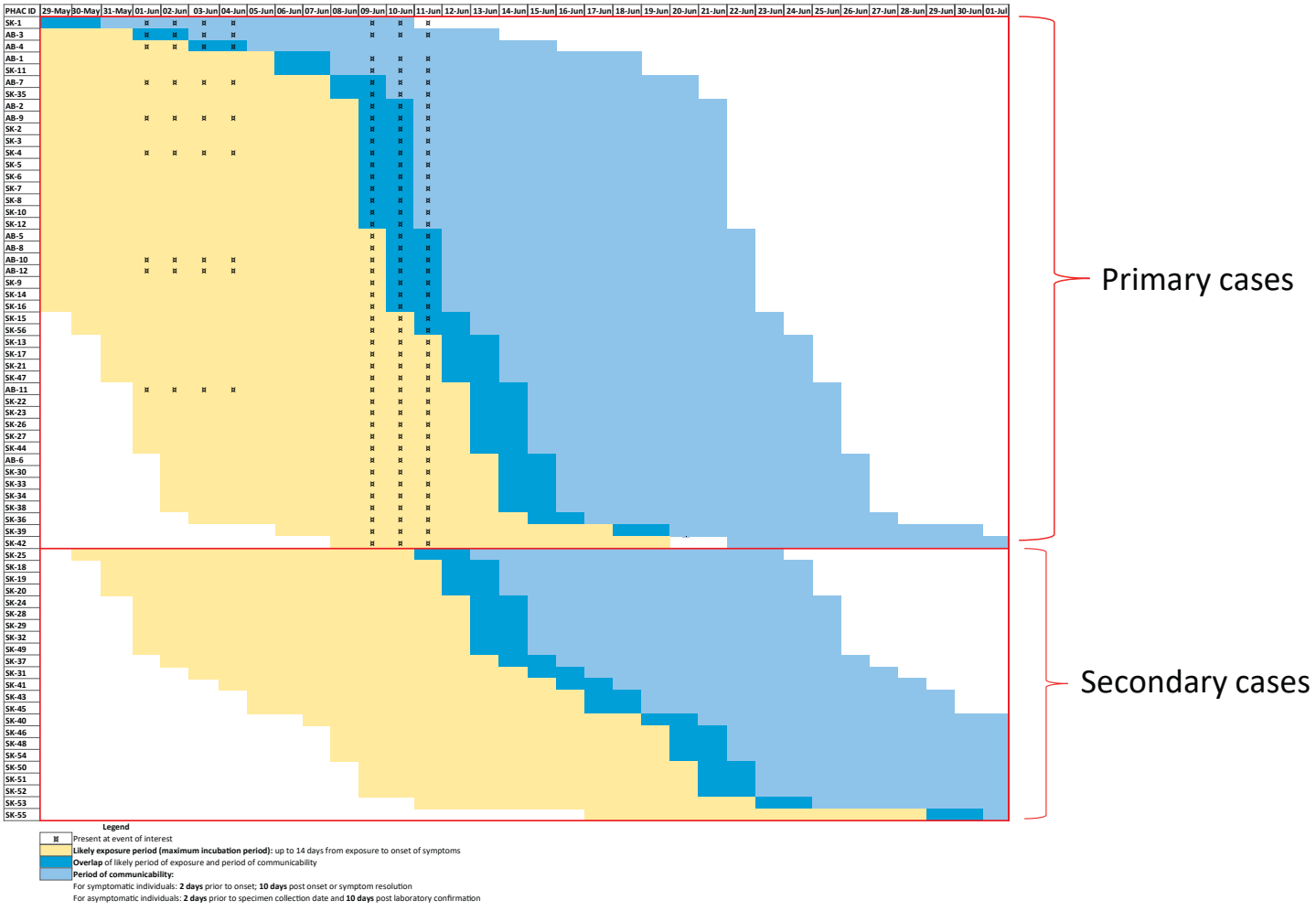
The second and third most likely transmission settings were the wake/funeral in SK. Forty-four cases attended the wake/funeral and 26 were in their period of communicability (Figure 2). These 26 individuals may have all potentially infected others with COVID-19. Based on onset date, 9 individuals (AB=5, SK=4) may have been symptomatic during the wake/funeral; 5 had visited the hospital (Figure 2).

There were 23 secondary cases who reported close contact with a known case linked to one of the outbreak settings, although they were not present themselves.

Complications

Five cases were hospitalized and one was admitted to the intensive care unit (ICU). No deaths were associated with this outbreak (**Table 2**).

Figure 2: Gantt chart of the period of communicability for all SARS-CoV-2 outbreak cases from two northern Indigenous communities linked to a wake/funeral in northern Saskatchewan, May 31 to July 20, 2020 (N=68)



Discussion

Key results

The centralized analysis suggested that the hospital visit in AB was critical to transmission, as three individuals were in their period of communicability during the visit and close contact occurred between the AB and SK visitors. Furthermore, if the hospital event was excluded, a subset of the secondary outbreak cases identified could not be explained based on the likely period of exposure (the maximum incubation period of 14 days is used as a proxy for the likely exposure period) and the period of communicability for COVID-19 (1).

The data supported the hypothesis of multiple introductions of COVID-19 at the wake/funeral. There were 26 individuals in their period of communicability and 9 may have been symptomatic based on onset date.

A large proportion of the cases remained asymptomatic throughout their period of communicability (38%). Also, a notable proportion of cases were asymptomatic when tested (n=16/68; 24%) but developed symptoms later, indicative of a rapid outbreak response.

Comparison

In Canada, there has been media coverage of COVID-19 outbreaks linked to funerals/memorial services and other mass gathering events (2–4).

South Africa reported that physical distancing (or "social distancing") guidelines are not always observed in many parts of the country, especially during funerals (5). In the Eastern Cape Province, 80% of all cases were linked to burial ceremonies (3). Cultural practices during burial ceremonies and lack of adherence to physical distancing protocols present an opportunity for transmission (5). Jaja *et al*. recommend that, in order to reduce spread of COVID-19, religious and cultural activities should be restricted and only immediate family members be allowed to bury their loved ones (5).

Early in the pandemic, the United States identified a multifamily cluster linked to gatherings, including a funeral (6). An individual with mild respiratory symptoms, later confirmed as a case, attended the funeral and a meal with family members of the deceased (6). The index case transmitted their infection to 10 other people, none of whom were household contacts (6). This funeral cluster occurred before physical distancing policies were implemented, and they support the recommendations to avoid gatherings and illustrate the importance of physical distancing (6).

Outbreak response

Outbreak response was timely; the outbreak was identified and the investigation launched on June 11, the day of the funeral. Public health employed multiple interventions, including imposing a curfew and travel restrictions to reduce the spread of COVID-19, both within the community and to surrounding communities, and supported the residents by bringing essential supplies into the community. The public health interventions were widely accessible—door-to-door or drive-through testing, messaging in the local languages and provision of isolation accommodations.

NITHA and Saskatchewan Health Authority have always benefited from a strong collaborative working relationship, and the organizations meet regularly to share information and discuss public health measures. Partnership with the Ministry of Health in Saskatchewan and PHAC, to coordinate with the Ministry of Health in Alberta, resulted in agreement on outbreak management, response and communication. Local, trusted or Indigenous nurses led the interviews and door-to-door initiatives to increase community uptake.

The investigation faced many challenges: the multijurisdictional nature of the outbreak, barriers to gathering data and contextual issues specific to the population.

Multiple public health organizations with different jurisdictions, including Indigenous population health needed to be involved to take into account that the cases lived in various geographic and administrative regions in two provinces. This required significant coordination. The pandemic response had put a strain on public health resources, making it difficult to find a convenient time for outbreak investigation partners to convene.

The lack of an attendance list for the wake/funeral made it difficult to notify individuals of their potential exposure. This has informed subsequent recommendations that event organizers maintain attendee lists for contact tracing.

There are many sensitivities related with sharing information between provinces and publicly about the affected Indigenous people. Trust issues remain between cases and investigators, including fear of stigma and/or discrimination, which made it difficult to obtain an accurate history. The transience of many community members added another layer of complexity. There were also cases who refused to isolate.

The investigation focused on forward contact tracing, and the role the hospital visits may have played in transmission was only identified during the centralized retrospective analysis. The subsequent outbreak investigation highlighted the value of backwards contact tracing (7).

Conclusion

The retrospective centralized analysis supported the hypothesis that there were multiple introductions of COVID-19 at the wake/funeral. As many as 26 attendees were in their period of communicability; 9 may have been symptomatic based on onset date at the time of the event. Public health measures including

masking and physical distancing were not strictly adhered to during the wake, although people who dropped in to pay their respects at the funeral did wear masks (none of whom were cases). The attack rate for the wake/funeral was 31% (44/140), which emphasizes the importance of protective measures at gatherings. The outbreak investigation also illustrated the importance of centralized analysis for multijurisdictional outbreaks. Information sharing is essential when gathering the details required to understand the events leading up to an outbreak and the hypotheses around chains of transmission.

Authors' statement

NM — Investigation, conceptualization, supervision, validation, writing–review & editing
SG — Investigation, conceptualization, data curation, validation, writing–review & editing
RZ — Investigation, conceptualization, data curation, validation, writing–review & editing
BQ — Investigation, conceptualization, validation, writing–review & editing
MK — Investigation, conceptualization, validation, writing–review & editing
EC — Investigation, conceptualization, data curation, validation, writing–review & editing
KF — Supervision, conceptualization, validation, writing–review & editing
EM — Conceptualization, formal analysis, visualization, writing–original draft, writing–review & editing

Competing interests

None.

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Summary findings from Tracks surveys implemented by First Nations in Saskatchewan and Alberta, Canada, 2018–2020

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Abstract

Background: The Public Health Agency of Canada's integrated bio-behavioural surveillance system—Tracks surveys—assesses the burden of HIV, hepatitis C and associated risks in key populations in Canada. From 2018–2020, Tracks surveys were successfully implemented by First Nations Health Services Organizations in Alberta and Saskatchewan.

Methods: First Nations-led survey teams invited community members who identified as First Nations, Inuit or Métis to participate in Tracks surveys and testing for HIV, hepatitis C and syphilis. Information was collected on social determinants of health, use of prevention services, substance use, sexual behaviours and care for HIV and hepatitis C. Descriptive statistics are presented.

Results: Of the 1,828 survey participants, 97.4% self-identified as First Nations and 91.4% lived in an on-reserve community. Over half (52.2%) were cisgender female, average age was 36.3 years, 82.5% lived in stable housing, 82% had access to primary healthcare and 73.8% reported having good to excellent mental health. Most participants (97%) had a family member who had experienced residential school. High proportions experienced stigma and discrimination (65.6%), financial strain (64.3%) and abuse in childhood (65.1%). Testing for HIV (62.8%) and hepatitis C (55.3%) was relatively high. Prevalence of HIV was 1.6% (of whom 64% knew their infection status). Hepatitis C ribonucleic acid prevalence was 5% (44.9% of whom knew their current infection status).

Conclusion: Historical and ongoing experiences of trauma, and higher prevalence of hepatitis C were identified, reaffirming evidence of the ongoing legacies of colonialism, Indian Residential Schools and systemic racism. High participation in sexually transmitted blood-borne infection testing and prevention reflect the importance of First Nations-led culturally sensitive, safe and responsive healthcare services and programs to effect improved outcomes for First Nations peoples.

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Keywords: First Nations, on-reserve communities, community-led, Indigenous Peoples, resilience, Tracks survey, STI, STBBI, Canada, HIV, hepatitis C, testing, care and treatment

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Introduction

Available evidence suggest First Nations, Inuit and Métis peoples continue to experience disproportionately higher rates of HIV and hepatitis C virus compared with non-Indigenous Canadians. In 2016, Indigenous peoples represented 4.9% of Canada's population but comprised an estimated 12.3% of all new HIV infections in Canada that year, increasing to 14% of all new HIV infections in 2018 (1). In 2016, rates of newly diagnosed HIV and newly diagnosed hepatitis C were three times higher in First Nations living on reserve than in the overall Canadian population (2,3).

First Nations communities in Saskatchewan (SK) and Alberta (AB) are particularly impacted by HIV and hepatitis C. In 2016, the rate of new HIV diagnoses in First Nations living on reserve in SK was three and seven times higher than for overall provincial and national rates, respectively (4). Rates of hepatitis C in SK First Nations communities were three and four times higher than for the overall provincial and national populations in 2016, respectively (4). In AB, between 2012 and 2016, HIV incidence was four and eight times higher among male and female First Nations, respectively, compared with their non-First Nations counterparts (5). Similarly, in 2016, hepatitis C incidence in AB was four times higher among First Nations than among non-First Nations (6). Despite the higher rates of HIV and hepatitis C in First Nations communities, there is a lack of information on factors associated with these increased rates.

The Public Health Agency of Canada (PHAC) coordinates an integrated bio-behavioural surveillance system—Tracks surveys—to assess the burden of HIV, hepatitis C and associated risk factors in key populations in Canada. Tracks surveys help identify underlying determinants contributing to higher rates of sexually transmitted and blood-borne infections (STBBI), including HIV and hepatitis C, in key populations. These data are used to inform public health responses aimed at reducing and preventing infections and improving treatment and support to those who need it most. Tracks information contributes to national estimates of HIV and hepatitis C prevalence and to assessments of Canada's progress towards global targets to eliminate HIV and hepatitis C as a public health threat by 2030 (7).

Compared with other ethnicities, Indigenous participants have been consistently over-represented in all four phases of Tracks survey of people who inject drugs, conducted periodically in sentinel sites across Canada since 2002 (8). Indigenous participants represented 42.2% of all participants of the Phase 4 Tracks survey among people who inject drugs, conducted in 2017–2019, up from 36.1% in Phase 3 conducted in 2005–2008. The first Tracks survey that focused on Indigenous Peoples was conducted in Regina, SK in 2011–2012 and was formerly known as A-Track. Self-reported injection drug use was not a criterion for eligibility to participate (9). The A-Track pilot survey provided valuable information on the challenges faced by urban Indigenous peoples and factors contributing to increased vulnerability for HIV and hepatitis C.

In the context of evidence of higher rates of HIV and hepatitis C in on-reserve communities and gaps in knowledge on factors contributing to higher rates in community contexts—from 2017 to 2020, First Nations Tribal Councils, communities, regional and federal public health authorities worked towards implementation of First Nations-led Tracks surveys in on-reserve community settings in AB and SK. This unique collaboration between First Nations Tribal Councils and communities, the Northern Inter-Tribal Health Authority, the First Nations and Inuit Health Branch of Indigenous Services Canada and PHAC was grounded in early and continuous First Nations involvement, participatory research and respect for First Nations data sovereignty.

The objective of this report is to present descriptive summary findings of combined Tracks surveys led and implemented in and by seven First Nations Health Services Organizations in AB and SK between September 2018 and March 2020. The generous agreement of all participating First Nations Health Services Organizations to contribute their site-specific data made this summary analysis and report possible. Findings include socio-demographic characteristics of survey participants, selected social determinants of health, access and use of healthcare, STBBI prevention and testing services including Indigenous health and healing services, injection and non-injection substance use (including drugs or alcohol) and experiences of substance-related poisoning, sexual risk behaviours, and HIV and hepatitis C care cascade, prevalence and awareness of infection status.

Methods

First Nations engagement and participation

Community engagement to determine interest and participation in Tracks surveys was conducted by the Northern Inter-Tribal Health Authority and Indigenous Services Canada's First Nations and Inuit Health Branch regions of AB and SK and included the following criteria: Chief and Council support, health director support; increasing rates of HIV/hepatitis C or higher than provincial average or identified risk; capacity to meet the requirements of the project including testing; and population size of community or group of collaborating communities of over 800.

In the fall/winter of 2018–2019 and of 2019–2020, seven First Nations-led survey teams were established to implement the Tracks survey and testing: four in SK (two First Nations communities in 2018 and two Tribal Council Health Services Organizations in 2019–2020) and three Tribal Council Health Services Organizations in AB in 2019–2020.

Data source and sampling methods

The protocol for the Tracks survey of determinants of HIV and hepatitis C among Indigenous peoples in Canada was approved by the Health Canada/PHAC Research Ethics Board. First Nations leadership reviewed and approved the proposed survey approach in each participating jurisdiction. Similar to other Tracks surveys of key populations in Canada, venue-based sampling methods were used, focusing recruitment efforts on where people are more likely to gather as determined by community survey teams. The survey was widely promoted including advertising at high traffic community locations such as stores, band offices, health centres, health fairs, harm reduction program venues and high schools, as well as on community and regional social media platforms. Survey participation mainly took place in community health centres but also at health fairs, high schools and using mobile outreach vehicles, and were often strategically timed to coincide with other health-related events such as mass influenza immunization clinics, "Liver Health Days" and HIV Awareness Day.

Anyone who self-identified as First Nations, Inuit or Métis and met the minimum age to provide informed consent (according to local research ethics requirements) was eligible to participate in the survey. Eligible and consenting participants completed a web-based questionnaire on an electronic tablet.

Questionnaire and biological sample

The Tracks survey collects information on socio-demographic characteristics, social determinants of health, use of health and prevention services (including testing), substance use (including drugs or alcohol) and injecting behaviours, sexual behaviours and care and treatment for HIV and hepatitis C. The questionnaire was comprised of validated questions from previous Tracks surveys, including from the 2011 A-Track pilot survey of Indigenous Peoples. The questionnaire was pre-tested in a small sample of First Nations community members in 2018 and was reviewed and approved by Health Canada/PHAC Research Ethics Board. Plain language definitions for more complex terms were embedded in the questionnaire. Trained survey staff were available to assist participants during survey completion upon request. The majority of participants (85%) self-administered the questionnaire on an electronic tablet while the remainder was assisted by an interviewer. Participants provided a blood sample in the form of a dried blood spot specimen (SK, 2019) or a full-blood sample (SK, 2018; AB, 2019) for HIV, hepatitis C and syphilis testing according to provincial testing protocols. Community public health nurses collected personal information necessary to return test results to participants. Anonymized test results were linked to survey data using a unique survey identification code.

Analysis, interpretation and contextualization of results

All seven First Nations Health Services Organizations contributed their site-specific survey data to this combined analysis. A Writing Group was established comprised of a representative from each participating First Nations organization, Northern Inter-Tribal Health Authority, First Nations and Inuit Health Branch and PHAC to review draft manuscripts and to ensure that survey findings were appropriately contextualized in a culturally relevant safe manner and that potential implications resonated with community realities and priorities. First Nations review and approval of the final manuscript was sought prior to publication.

Seven site-specific survey datasets were combined to generate an all-site dataset for the purposes of this analysis and report. Descriptive statistics were produced for selected indicators using SAS Enterprise Guide 7.1. Participants who responded "not stated", "refused" or "don't know" were excluded from the denominator of each indicator analysis, except for instances where "don't know" was an expected valid response to certain questions. As a proxy measure of the representativeness of the survey sample, age and sex characteristics of the sample were compared with those of the 2019 Registered Indian Population (10) for AB and SK using chi-square tests at a level of significance of 0.05.

Results

Socio-demographic characteristics

In total, 1,828 individuals who self-identified as being Indigenous participated in Tracks surveys implemented by First Nations Health Services Organizations in First Nations communities in AB and SK in 2019 and 2020. The majority of participants (97.4%) self-identified as First Nations and 91.4% lived in a First Nations on-reserve community (**Table 1**).

Table 1: Socio-demographic characteristics of Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828)

Socio-demographic characteristics		n	%	Total[a]
Indigenous identity	First Nations	1,780	97.4	1,827
	Inuit, Métis, or unspecified Indigenous identity	47	2.6	
Living in a First Nations (on-reserve) community		1,671	91.4	1,828
Age group	Younger than 25 years	458	25.4	1,807
	25–39 years	680	37.6	
	40–54 years	443	24.5	
	55 years or older	226	12.5	

Table 1: Socio-demographic characteristics of Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828) (*continued*)

Socio-demographic characteristics		n	%	Total[a]
Gender identity[b]	Cisgender female	952	52.2	1,825
	Cisgender male	822	45.0	
	Transmasculine[c]	30	1.6	
	Transfeminine[d]	21	1.2	
Sexual orientation	Heterosexual or straight	1,606	88.4	1,817
	Bisexual	110	6.1	
	Two-spirit	35	1.9	
	Gay or lesbian	20	1.1	
	Other[e]	46	2.5	

[a] Total represents total counts for the corresponding indicator excluding "don't know", "refused" and "not stated" values
[b] The Multidimensional Sex/Gender Measure was used to measure gender identity (11)
[c] Transmasculine includes those assigned female at birth who identified with either male or a non-binary gender
[d] Transfeminine includes those assigned male at birth who identified with either female or a non-binary gender
[e] Other included asexual, pansexual and other unclassifiable responses

Over one third of participants (37.6%) were 25 to 39 years of age. A quarter of participants were younger than 25 years (25.4%) and a similar proportion were 40 to 54 years (24.5%) while 12.5% were 55 years of age or older.

Just over half of participants (52.2%) identified their gender as cisgender female, 45% identified as cisgender male, 1.6% identified as transmasculine and 1.2% as transfeminine.

The assessment of representativeness comparing the age and sex characteristics of the survey sample to those of the on-reserve population in AB and SK did not show any statistically significant differences (age, p=0.999; sex, p=0.298).

The majority of participants (88.4%) reported their sexual orientation as heterosexual or straight. Small proportions identified as bisexual (6.1%), Two-spirit (1.9%), gay or lesbian (1.1%) or other sexual orientation (2.5%).

Social determinants of health

Equal proportions of participants either completed high school (20.4%) or completed more than high school (20.5%). More than half of participants completed some high school or less (59.1%) (**Table 2**).

A large majority of participants (82.5%) reported living in stable housing in the six months prior to completing the survey. Less than one third of participants (32.1%) reported having been incarcerated at some point in their lifetime and 6.2% reported being incarcerated in the year prior to the survey.

Table 2: Social determinants of health of Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828)

Social determinants of health		n	%	Total[a]
Education, highest level completed	Some high school or less	1,078	59.1	1,825
	High school	373	20.4	
	More than high school	374	20.5	
Housing status[b], past 6 months	Stable housing	1,506	82.5	1,826
	Unstable housing	320	17.5	
Incarceration	Ever incarcerated	585	32.1	1,824
	Incarcerated, past 12 months	113	6.2	1,823
Mental health, self-reported	Fair to excellent	1,742	95.4	1,826
	Good to excellent	1,347	73.8	
	Poor	84	4.6	
Experienced financial strain[c], past 12 months		1,175	64.3	1,827
Other social determinants of health	Experience of stigma and discrimination[d], ever	1,107	75.9	1,458
	Experience of stigma and discrimination[d], past 12 months	870	65.6	1,326
	Experience of childhood physical, sexual, and/or emotional abuse	1,068	65.1	1,641
	Experience of sexual partner physical, sexual, and/or emotional abuse	741	44.8	1,654
	Placed in an Indian Residential School	474	26.4	1,798
	Family member placed in an Indian Residential School	1,636	97	1,686

[a] Total represents total counts for the corresponding indicator excluding "don't know", "refused" and "not stated" values
[b] Stable housing included living in an apartment or house or a relative's apartment or house. Unstable housing included living in a hotel or motel room, rooming or boarding house, shelter or hostel, transition or halfway house, psychiatric institution or drug treatment facility, public place or correctional facility
[c] Defined as ever having difficulty making ends meet (e.g. having a hard time paying bills or buying enough food) in the year prior to the survey
[d] Defined as ever experienced any stigma or discrimination (e.g. avoidance, pity, blame, shame, rejection, verbal abuse, or bullying) based on racial or cultural background, hepatitis C status, HIV status, sexual orientation, use of drugs or alcohol or sex work
rejection, verbal abuse, or bullying) based on racial or cultural background, hepatitis C status, HIV status, sexual orientation, use of drugs or alcohol or sex work

A large majority of participants (95.4%) reported their mental health as fair to excellent and almost three quarters (73.8%) reported their mental health as good, very good or excellent. Fewer than 5% of participants reported poor mental health status.

Over one fifth of participants (23.4%) reported working full-time in the six months prior to completing the survey and 14.5% reported working part-time in the same period. Almost

two thirds of participants (64.3%) reported experiencing financial strain in the year prior to the survey. Over one third reported being unemployed (37.4%) or receiving social assistance (36.2%) in the six months prior to the survey.

Three quarters of participants (75.9%) experienced stigma and discrimination in their lifetime and two thirds (65.6%) experienced stigma and discrimination in the year prior to the survey. More than one quarter of participants (28.7%) reported experiencing discrimination because of their racial or cultural background in the year prior to the survey. Almost two thirds of participants (65.1%) experienced physical, sexual and/or emotional abuse in childhood and under half (44.8%) experienced these types of abuse with a sexual partner.

One quarter of participants (26.4%) had been placed in a residential school. Almost all participants (97%) had a family member who had been placed in a residential school and two thirds (67%) had a parent who was placed in a residential school.

Access and use of health care, sexually transmitted and blood-borne infection prevention and testing services

The majority of participants (81.9%) had access to primary health care; almost two thirds (63.6%) had a regular healthcare provider or had access to a community health centre or nursing station (64.5%) (**Table 3**). Over one third of participants (36.4%) used Indigenous health or healing services in the year prior to the survey, while one quarter of participants (26.4%) used mental health counselling services in the same period. Just under one in five participants (18.3%) reported avoiding healthcare services due to stigma and discrimination in the year prior to the survey.

Table 3: Access and use of health care, STBBI prevention and testing services among Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828)

Access and use of health care and STBBI prevention services	n	%	Total[a]
Access to primary health care	1,492	81.9	1,822
Access to a primary healthcare provider	1,158	63.6	1,822
Use of community health centre or nursing station	961	64.5	1,491
Use of services that included Indigenous health or healing practices, past 12 months[b]	663	36.4	1,822
Use of mental health counselling services, past 12 months	481	26.4	1,823
Avoidance of healthcare services because of stigma and discrimination, past 12 months[c]	291	18.3	1,590
Use of prevention services, past 12 months			
Received STBBI prevention counselling	671	37.3	1,800
Use of a condom distribution program	639	35.2	1,816
Use of treatment services for drug or alcohol use[d]	175	9.6	1,815
Use of a needle and syringe distribution program	142	7.8	1,816
Use of methadone, suboxone or other opioid substitution therapy	111	6.1	1,814
Awareness of PrEP and nPEP			
Awareness of oral HIV PrEP	202	11.1	1,821
Awareness of nPEP for HIV	511	28.1	1,822
Use of STBBI Testing Services			
Tested for HIV			
Ever	1,036	62.8	1,649
Past 12 months	564	34.3	1,646
Tested for hepatitis C			
Ever	846	55.3	1,529
Past 12 months	467	30.6	1,526
Tested for chlamydia			
Ever	909	51.8	1,756
Past 12 months	488	27.8	
Tested for gonorrhea			
Ever	817	47.1	1,735
Past 12 months	446	25.7	
Tested for syphilis			
Ever	721	41.9	1,719
Past 12 months	428	24.9	
Tested for any STI			
Ever	1,078	65.0	1,658
Past 12 months	619	40.5	1,529

Abbreviations: HIV, human immunodeficiency virus; nPEP, non-occupational post-exposure prophylaxis; PrEP, pre-exposure prophylaxis; STBBI, sexually transmitted and blood-borne infection; STI, sexually transmitted infection

[a] Total represents total counts for the corresponding indicator excluding "don't know", "refused" and "not stated" values

[b] Indigenous health or healing practices included a Traditional Healer, a Community Elder, the Hope for Wellness Help line or other Indigenous-specific services

[c] Defined as worry about stigma by staff or neighbours, worry about or experienced violence, police harassment or arrest

[d] Included services such as live-in treatment, group counselling or a Traditional Healer

Over one third of participants (37.3%) received STBBI prevention counselling in the year prior to the survey and a similar proportion (35.2%) used a condom distribution program in the same period. Smaller proportions reported using treatment services for drug or alcohol use (9.6%), needle and syringe distribution programs (7.8%), or methadone, suboxone or other opioid substitution therapy (6.1%) in the year prior to the survey.

Just over one in ten participants (11.1%) were aware of oral HIV pre-exposure prophylaxis while over one quarter (28.1%) were aware of non-occupational post-exposure prophylaxis for HIV.

Just under two thirds of participants (62.8%) had ever been tested for HIV (i.e. tested at some time in their lifetime) while over one third (34.3%) were tested for HIV in the year prior to the survey. Over half of participants had ever been tested for hepatitis C in their lifetime (55.3%) and under one third were tested in the year prior to the survey (30.6%).

Almost two thirds of participants (65%) reported ever being tested for any sexually transmitted infection and 40.5% reported being tested for a sexually transmitted infection in the year prior to the survey. Approximately one quarter of participants were tested for chlamydia (27.8%), gonorrhea (25.7%) or syphilis (24.9%) in the year prior to the survey.

Injecting behaviours

One sixth (16.7%) of participants reported injecting a substance or drug for non-medicinal purposes at some point in their lifetime (**Table 4**). The average age of first injecting drugs was 25.3 years; the largest proportions reported first injecting at ages 16 to 24 years (44.3%) and 25 to 39 years (38.1%).

Table 4: Injecting behaviours among Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828)

Injecting behaviours	n	%	Total[a]
Injected substances or drugs for non-medical purposes			
Ever	304	16.7	1,826
Past 6 months	148	8.1	1,824
Daily in the past month[b]	42	28.4	148
Age at first injection[c]			
Younger than 16 years	28	9.6	291
16–24 years	129	44.3	
25–39 years	111	38.1	
40 years or older	23	7.9	
Injecting behaviours, past 6 months[b]			
Injected drugs in a public space	57	38.5	148
Used sterile needle and syringe at last injection	125	84.5	148
Borrowed used needles and/or syringes	34	23.1	147
Borrowed used needles and/or syringes from people known well[d,e]	30	90.9	33
Borrowed used other injecting equipment (i.e. water, filters, cookers, tourniquets, swabs, acidifiers)	70	48.3	145
Borrowed used other injecting equipment from people known well[e]	62	91.2	68
Related non-injection borrowing behaviours, past 6 months			
Borrowed used non-injection drug paraphernalia (i.e. straws, dollar bills and pipes)	502	33.7	1,489

[a] Total represents total counts for the corresponding indicator excluding "don't know", "refused" and "not stated" values
[b] Among those who injected in the past six months
[c] Among those who had ever injected
[d] People known well was defined as family, friends or sex partners
[e] Among those who borrowed used needles and/or syringes

Under one tenth (8.1%) of all survey participants reported injecting in the six months prior to the survey. Of these, a large majority (84.5%) used a sterile needle and syringe when they last injected. Of those who injected in the month prior to the survey, 85.7% used a sterile needle and syringe at last injection.

Over one third (38.5%) of participants who injected in the six months prior to the survey reported injecting drugs in a public space and over one quarter (28.4%) reported injecting daily in the month prior to the survey.

Over one fifth (23.1%) of participants who injected in the past six months reported borrowing used needles and/or syringes and of these, a large majority (91%) borrowed from people they knew well. Almost half (48.3%) reported borrowing used other injecting equipment such as water, filters and cookers; mostly from people they knew well (91.2%). Of note, of the survey participants who reported using a non-injection substance in the previous six months, one third (33.7%) reported borrowing previously used non-injection drug paraphernalia such as straws and pipes in the six months prior to the survey.

Substance use and experiences with overdoses (poisonings)

Alcohol and cannabis were the most commonly used non-injection substances by survey participants in the six months prior to the survey; almost two thirds (64.6%) reported alcohol use and over half (55.6%) used cannabis (**Table 5**). Lower proportions reported using cocaine (16.7%), codeine (15.1%), methamphetamine (14.3%) or crack (12.9%).

Table 5: Substance use and experiences with overdoses (poisonings) among Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828)

Drug use and experiences with overdoses (poisonings)	n	%	Total[a]
Most common non-injection substances used, past 6 months[b]			
Alcohol	1,174	64.6	1,817
Cannabis	1,010	55.6	
Cocaine	304	16.7	
Codeine	275	15.1	1,816
Methamphetamine	260	14.3	1,817
Crack	234	12.9	1816
Most common injection drugs used, past 6 months[b,c]			
Methamphetamine	96	64.9	148
Morphine	57	38.5	
Fentanyl	55	37.4	147
Heroin	43	29.1	148
Cocaine	42	28.4	
Hydromorphone	41	27.7	
Awareness, access and use of an overdose kit			
Heard of overdose kits	839	46.0	1,826
Ever used an overdose kit	144	17.2	838

Table 5: Substance use and experiences with overdoses (poisonings) among Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828) (*continued*)

Drug use and experiences with overdoses (poisonings)	n	%	Total[a]
Awareness, access and use of an overdose kit (*continued*)			
Overdose kits are available in participants' community[d]			
Yes	586	69.9	838
No	56	6.7	
Don't know	196	23.4	
Overdose experiences			
Overdosed in the past 6 months	122	8.2	1,495
Most common drugs or substances used at last overdose[e]			
Alcohol	46	38.3	120
Fentanyl	44	36.7	
Methamphetamine	29	24.2	
Cannabis	22	18.3	
Cocaine	19	15.8	
Heroin	16	13.3	

[a] Total represents total counts for the corresponding indicator excluding "don't know", "refused" and "not stated" values
[b] Participants recorded all drugs (that they had injected, consumed or used at last overdose) for non-medicinal purposes in the six months prior to survey. The most commonly reported drugs among all participants are presented. Responses are non-mutually exclusive
[c] Among participants who injected in the past six months
[d] Among participants who had heard of overdose kits
[e] Among participants who overdosed in the past six months and who provided a response. Overdose was defined as 'a negative reaction to using too much drugs. Symptoms may include slow breathing, slow heart rate, slow pulse, muscle spasms, seizures, or decreased consciousness

Of the 8.1% of participants who reported injecting non-medicinal drugs in the six months prior to the survey, methamphetamine was the most commonly injected drug (64.9%), over one-third injected morphine (38.5%) or fentanyl (37.4%), and over one quarter injected heroin (29.1%), cocaine (28.4%) or hydromorphone (27.7%).

Just under half (46%) of all participants had heard of overdose kits. Of these, the majority (69.9%) knew that overdose kits were available in their community while almost one quarter (23.4%) did not know. Under one fifth (17.2%) had used an overdose kit on someone else.

Under one tenth (8.2%) of participants said they had overdosed in the six months prior to the survey. The most commonly reported substances used at last overdose were alcohol (38.3%), fentanyl (36.7%), and methamphetamine (24.2%).

Sexual risk behaviours

Of participants who reported ever having had sex, approximately one quarter (26.1%) had two or more sex partners in the six months prior to the survey (**Table 6**). The majority (89.3%) of participants who had a regular sex partner reported inconsistent condom use during vaginal and/or anal sex. Among participants who had a casual sex partner, almost 80% reported inconsistent condom use during vaginal and/or anal sex. About four out of ten participants (43.5%) reported substance use before or during sex in the six months prior to the survey.

Table 6: Sexual risk behaviours among Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,828)

Sexual risk behaviours, past 6 months	n	%	Total[a]
Two or more sex partners	410	26.1	1,573
Inconsistent condom use during vaginal and/or anal sex with a regular sex partner[b]	1,049	89.3	1,175
Inconsistent condom use during vaginal and/or anal sex with a casual sex partner[b]	432	79.9	541
Substance use before or during sex	606	43.5	1,394
Engaged in transactional sex	53	3.8	1,394
Condomless sex at last transactional sex[c]	19	35.9	53

[a] Total represents total counts for the corresponding indicator excluding "don't know", "refused" and "not stated" values indicators and excludes participants who never had sex
[b] Inconsistent condom use defined as not always using a condom (i.e. never, sometimes or frequently)
[c] Among those who engaged in transactional sex

A small proportion (3.8%) of participants had engaged in transactional sex at least once in the six months prior to the survey and of these, over one third (35.9%) reported not using a condom at last transactional sex.

HIV and hepatitis C prevalence and awareness

The majority (95%) of participants provided a blood sample for testing for HIV and hepatitis C testing (n=1,736) and HIV prevalence was 1.6% (or under two in 100 participants). Of those who tested positive for HIV, almost two thirds (64%) were aware of their HIV-positive status (**Table 7**).

Table 7: HIV and hepatitis C prevalence, awareness of infection status, and care cascade among Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,736)

Prevalence of HIV and hepatitis C	n	%	Total[a]
HIV prevalence	27	1.6	1,736
Awareness of HIV-positive status[b]	16	64.0	25
HIV care cascade (among participants aware of their HIV-positive status)			
Linked to care for HIV-related services[c]	13	81.3	16
Currently taking ART treatment	13	81.3	
Adherence to ART, no missed doses in last month	<10	-	13
Self-reported undetectable HIV viral load	7	53.9	
Avoidance of HIV services or treatment because of stigma and discrimination, past 12 months	<5	-	
Hepatitis C prevalence and awareness of infection status			
HCV antibody prevalence	193	11.2	1,728
HCV RNA prevalence	87	5.0	1,725
Awareness of hepatitis C RNA positive status[d]	35	44.9	78

Table 7: HIV and hepatitis C prevalence, awareness of infection status, and care cascade among Tracks survey participants in First Nations communities in Alberta and Saskatchewan, 2018–2020 (n=1,736) (*continued*)

Prevalence of HIV and hepatitis C	n	%	Total[a]
Hepatitis C care cascade (among participants aware of their hepatitis C RNA-positive status)			
Linked to care for hepatitis C[e]	21	60.0	35
Ever taken hepatitis C treatment	<10	-	
Currently taking hepatitis C treatment	<10	-	
HIV and hepatitis C co-infection			
HIV-positive and hepatitis C RNA-positive	8	0.5	1,724

Abbreviations: ART, antiretroviral therapy; HCV, hepatitis C virus; HIV, human immunodeficiency virus; RNA, ribonucleic acid; -, data suppressed to protect privacy
[a] Total represents total counts for the corresponding behavioural indicator excluding "don't know", "refused" and "not stated" survey values. For biological test results, total is among participants who provided a biological sample of sufficient quantity for testing
[b] Among participants who tested positive for HIV antibodies and who reported their HIV diagnosis
[c] Defined as under the care of a doctor or healthcare provider for HIV-related services at the time of the survey
[d] Among participants who tested HCV RNA positive and who reported their current hepatitis C status. The denominator excludes participants with missing data
[e] Defined as under the care of a healthcare provider for hepatitis C-related services at the time of the survey

Lifetime exposure to hepatitis C infection measured by the prevalence of hepatitis C antibodies was 11.2%. One in 20 (5%) of participants were hepatitis C ribonucleic acid (RNA)-positive, an indication of having active hepatitis C infection at the time of the survey. Of these, under half (44.9%) were aware of their hepatitis C RNA-positive status.

HIV and hepatitis C cascade of care

Of the 16 survey participants who were aware of their HIV-positive status, 13 (81.3%) were linked to a healthcare provider for HIV-related services and were on antiretroviral treatment at the time of the survey (Table 7). Of those currently taking treatment for HIV, fewer than 10 participants reported adherence to treatment in the month prior to the survey. Seven of 13 individuals self-reported undetectable viral load. Fewer than five participants reported avoiding HIV services or HIV treatment in the year prior to the survey.

Of the 35 participants who were aware of their hepatitis C RNA-positive status, 21 (60%) were linked to a healthcare provider; fewer than 10 of 35 had taken treatment for hepatitis C at some point or were taking hepatitis C treatment at the time of the survey. The most common reasons for not taking hepatitis C treatment were that the participant was feeling good (33.7%), they were using substances (14.9%) or they only recently linked with medical care (11.9%).

The proportion of participants who were both HIV-positive and hepatitis C RNA positive was five in 1,000 individuals (0.5%). The prevalence of syphilis antibodies (an indicator of lifetime exposure to syphilis) was 2.5%.

Discussion

Seven First Nations Health Services Organizations and their respective survey teams successfully implemented Tracks surveys in participating First Nations communities in AB and SK. These First Nations-led Tracks surveys represent the first assessments of their kind in on-reserve community settings. Early First Nations involvement, leadership support, participatory research, and respect for First Nations data sovereignty were fundamental to meaningful community engagement and successful survey implementation in communities. A commitment to return biological test results to survey participants, while assuring anonymity of all personal data for public health surveillance purposes, was also key. Public health professionals from First Nations Health Services Organizations-led community survey teams to conduct survey promotion, participant recruitment and data collection. Their expertise and participation in the writing group to guide data analysis and interpretation was critical to assuring the culturally relevant and appropriate contextualization of survey findings for this report. First Nations active involvement throughout the project lifecycle, from conceptualization to knowledge translation, supported commitments to advance reconciliation and First Nations self-determination of health services and programs to reduce the impacts of STBBI in their communities.

It is recognized that health, structural and social inequities directly and indirectly influence vulnerability to and resilience against HIV, hepatitis C and other STBBI (12). These factors are further compounded by the legacy and ongoing impacts of colonialism, residential school and systemic racism experienced by First Nations, Inuit and Métis people. Consistent with previous Tracks surveys involving Indigenous participants in urban centres (8), personal or close family member residential school experience, past and ongoing experiences of stigma and discrimination and physical, sexual and/or emotional abuse (in childhood or with a sexual partner), as well as financial strain, were commonly reported by participants. Despite these significant challenges and traumas, several survey indicators reflected the strength and resilience of communities with a relatively high proportion reporting good to excellent mental health, stable housing, access to primary health care and to Indigenous-specific health or healing services.

The STBBI prevention and testing indicators were encouraging with high rates of lifetime testing for HIV and hepatitis C, testing for any sexually transmitted infection and use of STBBI prevention counselling or condom distribution programs. Awareness of oral HIV pre-exposure prophylaxis and non-occupational post-exposure prophylaxis were 11.1% and 28.1%, respectively; equivalent or higher than found in a sub-analysis of Indigenous participants of the Tracks survey among people who inject drugs across Canada in 2017–2019 at 11.5% and 10.8%, respectively (8). High participation in STBBI

prevention and testing programs reflects the effectiveness of First Nations-led and delivered programs and services in their communities. It should also be noted that pre-exposure prophylaxis and non-occupational post-exposure prophylaxis are covered for registered First Nations and Inuit under the Non-Insured Health Benefits program of Indigenous Services Canada as are medications for treatment for HIV and hepatitis C (13).

Alcohol and cannabis were the most commonly reported non-injection substances. Stimulant use, including cocaine, methamphetamine and crack, was reported to a lesser extent. Fewer than 10% of all participants reported injecting substances in the six months prior to the survey among whom predominant use of methamphetamine and opioids, including morphine and fentanyl, was noted. While most used sterile needles and syringes, borrowing used needles, syringes and other used injecting equipment, mostly from people they knew well, was also reported. Similarly, borrowing previously used paraphernalia such as straws or pipes for non-injection substance use was also reported. These findings suggest increased public health education and awareness are warranted to alert communities to the increased risks associated with sharing used drug consumption equipment and/or paraphernalia even with trusted contacts.

One in ten participants experienced drug and/or alcohol poisoning (overdose) in the six months prior to the survey, with alcohol and fentanyl being the most commonly reported substances used at last overdose. It is encouraging that almost half of the participants had heard of overdose kits such as naloxone and a large proportion of these knew that kits were available in their community. However, almost one quarter of participants did not know if kits were available locally, suggesting that promotion of availability of kits in communities could be bolstered.

Caution must be taken when comparing the prevalence from studies using different methods, and among different populations and settings and in different time periods. However, to provide some context, HIV prevalence among survey participants was relatively low at 1.6% compared with 5.2% HIV prevalence in the A-Track pilot survey of urban Indigenous peoples in Regina, SK in 2011–2012 (9) and higher than national modelled estimates of HIV prevalence among Indigenous Peoples of just under 0.4% in 2016 (14) and under 0.2% in the general Canadian population in 2018 (1). While HIV testing rates were high in communities, six of the 25 (or one in four) participants who tested positive for HIV did not know their status. Over 81% of those who did know their HIV-positive status were previously linked to care and treatment and of these, over half reported undetectable viral loads. These findings suggest more work is needed to optimize testing, linkage to HIV care and treatment to better meet community needs and to come closer to reaching the 90-90-90 global HIV testing and treatment targets (7).

Similar caution must be taken if attempting to compare hepatitis C prevalence in different populations, settings and time periods. Just over one in ten (11.2%) survey participants tested positive for the hepatitis C antibody (an indicator of lifetime exposure). This is lower than the 41.6% of participants who tested positive for the hepatitis C antibody in the 2011–2012 A-Track survey of Indigenous peoples in an urban (*versus* on-reserve) setting (9). It is also higher than estimates of hepatitis C antibody-positive rate of just under 1% in the general Canadian population in 2017 (15). The current Tracks surveys in First Nations communities found 5% of participants tested positive for hepatitis C RNA (an indicator of active hepatitis C infection) and of these, more than half were unaware of their active hepatitis C status. These findings support redoubling of efforts to advance community-driven strategies to normalize culturally safe and accessible screening and testing, facilitate more timely linkage to care and treatment and move closer to the goal of eliminating hepatitis C in First Nations communities.

Strengths and limitations

Tracks surveys use an integrated bio-behavioural surveillance approach endorsed by the World Health Organization/Joint United Nations programme on HIV/AIDS to increase knowledge on factors contributing to HIV among populations most at risk towards improving public health responses. Tracks surveys in First Nations communities in AB and SK were First Nations-led and supported by Tribal Council leadership. The combined population of participating communities and Tribal Councils represents over one quarter (28%) of all First Nations living on reserve in AB and SK. Over 95% of survey participants agreed to provide a blood sample for HIV, hepatitis C and syphilis testing. The surveys were widely promoted at local community and healthcare venues in all participating jurisdictions, inviting community members to participate. While this non-probabilistic method of participant recruitment means survey findings may not be fully representative of all First Nations communities in AB and SK, First Nations-led survey promotion, participant recruitment and data collection likely helped mitigate this limitation. The similarity of age and sex characteristics of the survey population to those of the on-reserve population in both provinces is also reassuring. The majority (85%) of surveys were self-administered thereby reducing potential observer and/or social desirability biases associated with interviewer-administered surveys; however, as with all self-reported data, it is possible that some risk behaviours were over or under-reported. Regional variations in some indicators are not reflected in this summary of combined results. Despite the limitations, and considering notable strengths, these surveys provide unique insights into factors that may affect vulnerability to STBBI in First Nations communities and help inform targeted strategies to address them.

Conclusion

First Nations-led Tracks surveys are the first of their kind in on-reserve community settings and represent an innovative model of a successful community, public health and surveillance collaboration at local, regional and national levels. Early

engagement, leadership support, respect for First Nations data sovereignty, First Nations-led survey implementation and active participation in all phases of the project were key to success and help contribute to the path towards reconciliation. This project generated new insights on HIV and hepatitis C prevalence in First Nations communities in AB and SK. Survey findings will help inform community STBBI testing, prevention and treatment services and harm reduction programs on where best to focus their efforts. High prevalence of hepatitis C in particular signals that renewed and sustained efforts are needed to address the drivers of infection and to increase access to testing and treatment. This, together with ongoing experiences of stigma, discrimination and racism, including when accessing health services, reaffirms evidence of ongoing impacts of colonization, Indian Residential Schools and systemic racism on First Nations peoples. Despite these challenges, the high uptake of STBBI testing and prevention programs reflect the importance of culturally sensitive, safe and responsive healthcare services and programs that are First Nations-led to effect meaningful progress towards improved STBBI-related and other health outcomes for First Nations peoples. Subject to the support and priorities of the collaborating First Nations Health Services Organizations, further analyses may be undertaken to assess associations between behavioural and social determinants and infection rates. Future surveys in community settings will depend on the priorities and needs of First Nations as well as the capacity needed for successful survey implementation.

Authors' statement

KLH — Conceptualization, formal analysis, methodology, project administration, writing (original draft and review and editing)
LJ — Conceptualization, formal analysis, data curation, methodology, project administration, writing (review and editing)
LM — Conceptualization, project administration, writing (review and editing)
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BG — Conceptualization, project administration, writing (review and editing)
BM — Conceptualization, project administration, writing (review and editing)
AN — Conceptualization, project administration, writing (review and editing)
MA — Conceptualization, project administration, writing (review and editing)
DN — Conceptualization, project administration, writing (review and editing)
DTY — Writing (review and editing)
SG — Writing (review and editing)
NN — Conceptualization, project administration, writing (review and editing)
IK — Conceptualization, writing (review and editing)
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Competing interests

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SURVEY

Antibiotic prescribing for respiratory tract infection across a national primary care network in 2019

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Abstract

Background: Respiratory tract infection (RTI) is the leading reason for avoidable antimicrobial use in primary care, yet provider-level feedback on its use is only available in some provinces. The aim of this study was to validate case definitions for RTI across the Canadian Primary Care Sentinel Surveillance Network (CPCSSN) and determine baseline provider-level variability in antimicrobial prescribing in 2019.

Methods: The RTI case definitions were developed using demographic, diagnostic coding and keywords in electronic medical record. Manual chart abstraction was performed to identify cases of acute otitis media. Remaining RTI definitions were validated using a random sample of 5,164 patients with encounters in 2019. The proportion of patients with an RTI treated with antibiotics was determined by provider, per patient, per episode and per patient encounter.

Results: Negative predictive value, positive predictive value and prevalence were as follows: 1.00 (0.99–1.00), 0.99 (0.96–0.99) and 4.14% (4.10–4.19) for common cold; 1.00 (0.99–1.00), 0.94 (0.88–0.98) and 1.09% (1.07–1.12) for acute otitis media; 0.98 (0.96–1.00), 0.93 (0.87–0.97) and 1.2% (1.18–1.22) for acute pharyngitis; 0.99 (0.99–1.00), 0.88 (0.81–0.93) and 1.99% (1.96–2.02) for sinusitis; 0.99 (0.97–0.99), 0.95 (0.89–0.98) and 4.01% (3.97–4.05) for acute bronchitis/asthma. By provider, median (interquartile range [IQR]) proportion treated with antibiotics (per patient) was 6.72 (14.92) for common cold, 64.29 (40.00) for acute otitis media, 20.00 (38.89) for pharyngitis, 54.17 (38.09) for sinusitis, 8.33 (20.00) for acute bronchitis/asthma and 21.10 (20.56) for overall RTI.

Conclusion: The CPCSSN can provide national surveillance of antimicrobial prescribing practices for RTI across primary care. Baseline variability underscores the need for provider feedback and quality improvement.

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Keywords: antimicrobial stewardship, primary care, audit and feedback, respiratory tract infection, validation

Introduction

Antimicrobial resistance has significant socioeconomic impacts in Canada, which are only expected to be magnified over the next decade (1). Antimicrobial stewardship efforts to curb this trend has focused on hospitals, yet nearly 90% of antimicrobials are dispensed in the community sector, with a large proportion of these prescriptions arising from primary care (2).

Respiratory tract infection (RTI) is the leading cause of avoidable antimicrobial use in primary care (2,3). A national campaign led by Choosing Wisely Canada has developed prescriber-led practice changes and clinical tools to help facilitate avoidance of antibiotics in the management of RTI (4,5). One key challenge is that many primary care providers have never received feedback on their antimicrobial prescribing for RTI and may not recognize the need to make practice changes.

Accurate measurement of antimicrobial prescribing practices by primary care providers has been challenging in Canada due to

the lack of a national antimicrobial surveillance system. While some provinces are already providing feedback to prescribers (6), the only large-scale data available regarding antibiotic use for RTI across Canada is an estimate based on population-based health services research, which is not available across all provinces (2).

The Canadian Primary Care Sentinel Surveillance Network (CPCSSN) is a national network of primary care clinics representing over two million patients and 1,500 primary care clinicians across eight provinces and one territory (7). Each participating sentinel contributes electronic medical record (EMR) data to their respective network and the pan-Canadian data repository for the purposes of public health surveillance, quality improvement and research. Case definitions that incorporate keywords from EMRs have already been validated, which allows CPCSSN to generate surveillance on a wide range of diseases (8–10). We hypothesized that CPCSSN would be ideally suited to accurately measure RTI in primary care as well as provider-level antimicrobial prescribing practices. If successful, this approach could in turn be used to generate provider feedback across CPCSSN based on peer comparison, which is known to improve antimicrobial prescribing practices in primary care (6,11). We undertook the following study to validate case definitions for RTI across a sample of CPCSSN sites and determine baseline provider-level variability in antimicrobial prescribing in the year preceding the coronavirus disease 2019 (COVID-19) pandemic.

Methods

Data source

Point-of-care de-identified data are extracted from the EMRs semiannually and transformed to a standard CPCSSN schema to form a regional and pan-Canadian data repository. The CPCSSN extracts clinical primary care data from 11 different EMR systems. Each EMR system has a different architecture and, even within one EMR system, may also have province-specific differences in the structure of the database where medical information is stored. As such, the transformation from EMR to the CPCSSN data repository includes advanced data cleaning and coding techniques. The architecture and approach have been previously described, including data flow, quality, mapping, cleaning and de-identification (12). This project uses pan-Canadian data extracted from January 1 to December 31, 2019. Data included socio-demographics, providers, encounters, health conditions, risk factors, biometrics, laboratory results, procedures, medications and referral information (12). Research Ethics Board approval was obtained at the site where manual chart abstraction was performed (approval #20-0037), in addition to University of British Columbia research ethics board where the case definition was examined using manual chart reviews to a subset of the CPCSSN data (approval #H20-02722) and Queen's University (approval #6034400) in order to apply the case definition to the entire pan-Canadian repository.

Development of case definitions

Several steps were performed to develop and validate the RTI case definition. First, a team of clinicians and researchers from CPCSSN and Choosing Wisely Canada, including two family physicians and one infectious diseases physician, met virtually to create the five case definitions (**Table 1**) that make up the majority of RTIs. Like previous work (1), these case definitions were primarily based on International Classifications of Diseases (ICD-9) codes found in EMRs. In addition to the ICD-9 codes, a set of related keywords, which could be found in a patient's record, was also included. These keywords were utilized to improve the specificity of the case definitions. The case definitions were modified and iterated upon until consensus was reached amongst the team members. Table 1 provides the final case definitions of the five RTI syndromes.

Table 1: Case definitions and minimum sample size for validation of five common respiratory tract infection syndromes in primary care

Syndrome	ICD-9 codes for inclusion	Chart audit keywords	Exclusion (i.e. ICD-9 subcodes, keywords, etc.)	Population at risk
Acute otitis media (6 months of age or older)	381: Eustachian tube disorders/otitis media, serous 382: Otitis media, suppurative	Otitis media, AOM, otitis, acute otitis media	Chronic suppurative otitis media 381.6: Obstruction of eustachian tube 381.7: Patulous Eustachian tube 381.8: Other disorders of eustachian tube 381.9: Unspecified eustachian tube disorder	17 years or younger
Uncomplicated pharyngitis	034: Streptococcal sore throat/scarlet fever 463: Acute tonsillitis 464: Acute laryngitis, tracheitis, croup, epiglottis 462: Acute pharyngitis	Pharyngitis, streptococcal throat, URI, URTI, viral URI, viral infection, viral URTI, laryngitis, bacterial pharyngitis, croup, tracheitis, epiglottis, acute laryngitis, acute tracheitis, acute laryngotracheitis	Abscess (peritonsilar, nasopharygneal, etc.), mononucleosis	All ages

Table 1: Case definitions and minimum sample size for validation of five common respiratory tract infection syndromes in primary care (*continued*)

Syndrome	ICD-9 codes for inclusion	Chart audit keywords	Exclusion (i.e. ICD-9 subcodes, keywords, etc.)	Population at risk
Uncomplicated sinusitis	461: Acute sinusitis	Uncomplicated sinusitis, bacterial sinusitis, viral sinusitis, sinusitis, maxillary, sinusitis, frontal, sinusitis, ethmoidal, sinusitis, sphenoid, sinusitis, other, sinusitis, unspecified	473: Chronic sinusitis	All ages
Common cold	460: Upper respiratory infection/nasopharyngitis, acute/pharyngitis/upper respiratory infection/acute nasopharyngitis (common cold)	Upper respiratory tract infection, URTI, cold, common cold, viral pharyngitis, nasopharyngitis, acute nasopharyngitis	N/A	All ages
Acute bronchitis/asthma (i.e. chronic lung condition exacerbations)	466: Acute bronchitis 491: Chronic bronchitis 492: Emphysema 493: Asthma, allergic bronchitis 496: Other COPD	Bronchitis, emphysema, must include COPD, chronic bronchitis, acute bronchitis, acute bronchiolitis, bronchitis, bronchiolitis	Must NOT include COPD (using the CPCSSN definition for COPD) 1. ICD-9 codes 490–492, 496 2. Problem list: bronchitis, emphysema, COPD/cold 3. Medication list: beta agonists, anticholinergics, inhalant corticosteroids 4. Risk factors: smoker	All ages

Abbreviations: AOM, acute otitis media; COPD, chronic obstructive pulmonary disease; CPCSSN, Canadian Primary Care Sentinel Surveillance Network; ICD-9, International Classifications of Diseases; N/A, not applicable; URI, upper respiratory infection; URTI, upper respiratory tract infection

Abstraction of electronic medical records for cases of acute otitis media

A manual chart review of one RTI syndrome was completed at one CPCSSN site. Previous case validations have used manual charts review as a common standard of measurement (8,9,13); however, manually reviewing potentially thousands of charts is both resource intensive and time consuming (14). We chose to complete a manual chart review of otitis media because it was a specific definition with a well-defined population and required a small sample size. A standardized data collection form was created using a secure web-based Qualtrics survey (Qualtrics, Provo, Utah, United States) to ensure that a systematic approach was used to review the designated patients. The manual chart review was completed by one research team member who verified presence or absence of RTI for each patient by manually reviewing their EMR. A programmatic method, based on billing, encounter diagnosis information and age, of selecting patients for manual review was performed by a family physician at the selected clinic. A total of 418 patients representing 771 cases of otitis media were reviewed as part of this manual chart review. The chart review also included any further evidence of RTI by reviewing unstructured data (e.g. free text notes). The abstracted data were then reviewed by both the abstractor, the internist and the family physician to determine classification of RTI status.

Validation of other respiratory tract infection case definitions

To validate the remaining RTI definitions, a random sample of 5,164 patients from the pan-Canadian CPCSSN dataset was selected. The case definition was then applied and estimates of the prevalence of the five conditions were obtained. To ensure that these cases were correctly identified, a minimum of 100 random cases of each condition were selected, as well as a minimum of 100 cases with none of the five conditions, for additional database review by a blinded abstractor, as per the methodology described by Williamson *et al.* (9). Finally, we applied the resulting definitions to the pan-Canadian CPCSSN 2019 dataset.

Antibiotic prescribing associated with respiratory tract infection syndromes

Following validation of RTI syndromes, we examined the proportion of patients with an RTI that received an antibiotic prescription. The sample was restricted to all patients who had a visit in 2019 and had a recorded birth year and gender. No limit was applied to the number of RTI diagnoses included per patient over the study period. An RTI case was considered "treated" if the patient received a prescription, on the same day or within one day of the RTI diagnosis, for any medication typically used to treat RTI including penicillin VK, amoxicillin, amoxicillin-clavulinic acid, cefuroxime, cefaclor, cefadroxil, clarithromycin, azithromycin, moxifloxacin and levofloxacin.

Statistical analysis

To properly power the case definition validation, sample size calculations were performed. Sample size calculations were set to a precision of 0.10. Sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) were calculated using 2x2 tables comparing each of the constructed case definitions (case/no case) with the chart review diagnosis (case/no case). We constructed 95% confidence intervals (CI) for each parameter using the Clopper-Pearson approach for proportions. Since we were examining data across the pan-Canadian CPCSSN, we considered all measures greater than 80% to be acceptable. Summary data were tabulated for all RTI, as well as by each of the five clinical syndromes. The proportions were reported by patient, encounter and by episode. The proportion of patients with an RTI was tabulated by counting any patient with at least one RTI in 2019, out of all patients with at least one billing record in 2019. The proportion of patients treated was determined by counting a patient as "treated" if they had an associated antibiotic prescription on the same day or within one day of meeting the case criteria for an RTI, out of all the patients with at least one RTI in that year. The proportion of encounters with an RTI was tabulated by counting all encounters (unique date) that met the criteria for an RTI case in 2019, out of all encounters (defined as at least one billing on a unique day) in 2019. The proportion of RTI encounters treated was determined by counting an RTI case as "treated" if the case was associated with an antibiotic prescription, out of all the RTI cases in that year. If a patient's RTI case indicator (unique billing or encounter date) was more than 31 days from a previous RTI case indicator it was classified as a unique episode. The proportion of RTI episodes treated per individual provider was tabulated by counting all episodes of an RTI as "treated" if the episode was associated with an antibiotic prescription, out of all RTI episodes in that year. All data were analyzed in SAS version 9.4 (SAS Institute Inc., Cary, North Carolina, United States).

Results

For otitis media, among 418 patients manually reviewed to assess performance characteristics of the algorithm, 399 (95%) were confirmed to have acute otitis media while 19 (5%) did not. The algorithm correctly identified 392 (98%) cases and 15 (79%) patients without the infection. **Table 2** summarizes the performance characteristics of the algorithm for acute otitis media.

Table 2: Performance characteristics of case definition algorithm compared with manual chart review for acute otitis media

Performance characteristic	Detection of acute otitis media	95% CI
Sensitivity	0.98	0.96, 0.99
Specificity	0.79	54.43, 93.95
PPV	0.99	0.98, 1.00
NPV	0.68	0.50, 0.82

Abbreviations: CI, confidence interval; NPV, negative predictive value; PPV, positive predictive value

Table 3 presents the performance characteristics of all five RTI syndromes based on random sampling of pan-Canadian CPCSSN database. In this random sample of 5,164 patients, 2,981 (57.7%) were female and the median age was 44.7 years. When the case definitions were applied to the entire national CPCSSN database, we found that, of the 873,180 patients that visited their primary care provider in 2019, 11.33% (95% CI, [11.27, 11.40]) were diagnosed with an RTI. Evaluating each syndrome individually, we found the following prevalence (per patient): otitis media, 1.09% (95% CI, [1.07, 1.12]); pharyngitis, 1.20% (95% CI, [1.18, 1.22]); sinusitis 1.99% (95% CI, [1.96, 2.02]), common cold, 4.14% (95% CI, [4.10, 4.19] and acute bronchitis/asthma, 4.01% (95% CI, [3.97, 4.05]).

Table 3: Performance characteristics of five upper respiratory tract infection case definitions applied to random sample of pan-Canadian database

RTI syndrome	Number of cases sampled	Sensitivity		Specificity		Negative predictive value		Positive predictive value	
		n	95% CI	n	95% CI	n	95% CI	n	95% CI
Common cold	172	1.00	0.98, 1.00	0.99	0.99, 0.99	1.00	0.99, 1.00	0.99	0.96, 0.99
Acute otitis media	122	1.00	0.97, 1.00	0.99	0.98, 0.99	1.00	0.99, 1.00	0.94	0.88, 0.98
Acute pharyngitis	122	0.88	0.81, 0.93	0.99	0.97, 0.99	0.98	0.96, 0.99	0.93	0.87, 0.97
Acute sinusitis	121	0.99	0.95, 1.00	0.98	0.96, 0.99	0.99	0.99, 1.00	0.88	0.81, 0.93
Acute bronchitis/asthma	121	0.93	0.88, 0.97	0.99	0.98, 1.00	0.99	0.97, 0.99	0.95	0.89, 0.98

Abbreviations: CI, confidence interval; RTI, respiratory tract infection

Evaluating the data per encounter, we found that, of the 3,747,610 encounters (identified by a unique date) in 2019, 3.52% (95% CI, [3.50, 3.54]) were diagnosed with an RTI. Evaluating each syndrome individually, we found the following prevalence (per encounter): otitis media, 0.35% (95% CI, [0.34, 0.35]); pharyngitis, 0.32% (95% CI, [0.32, 0.33]); sinusitis 0.56% (95% CI, [0.55, 0.57]), common cold, 1.16% (95% CI, 1.15, 1.17], acute exacerbation of chronic obstructive pulmonary disease, 1.32% (95% CI, [1.31, 1.33]). **Figure 1** depicts the proportion prescribed an antibiotic per patient, per encounter, and per episode, across the five upper respiratory tract infection syndromes.

Figure 2 shows the proportion of antibiotics prescribed per patient at the prescriber level across CPCSSN. There was significant variability identified for each syndrome with a median and interquartile range (IQR) of 64.29 (40.00) for acute otitis media, 20.00 (38.89) for uncomplicated pharyngitis, 6.72 (14.92) for common cold, 54.17 (38.09) for uncomplicated sinusitis, 8.33 (20.00) for acute bronchitis/asthma and 21.10 (20.56) for overall RTI.

Figure 1: Variability in antibiotics prescribing in primary care for different upper respiratory tract infection syndromes per patient, per episode and per patient encounter

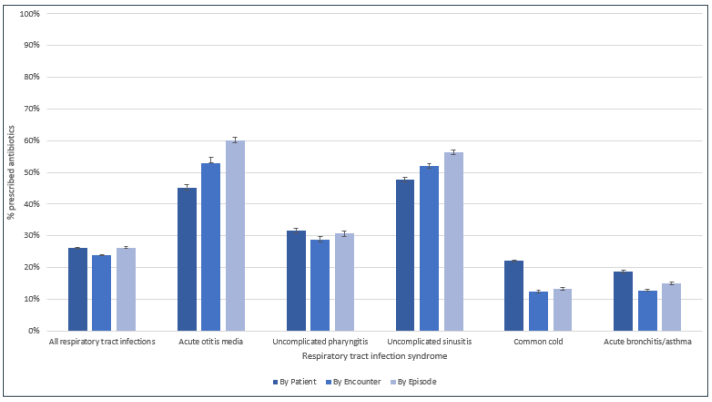
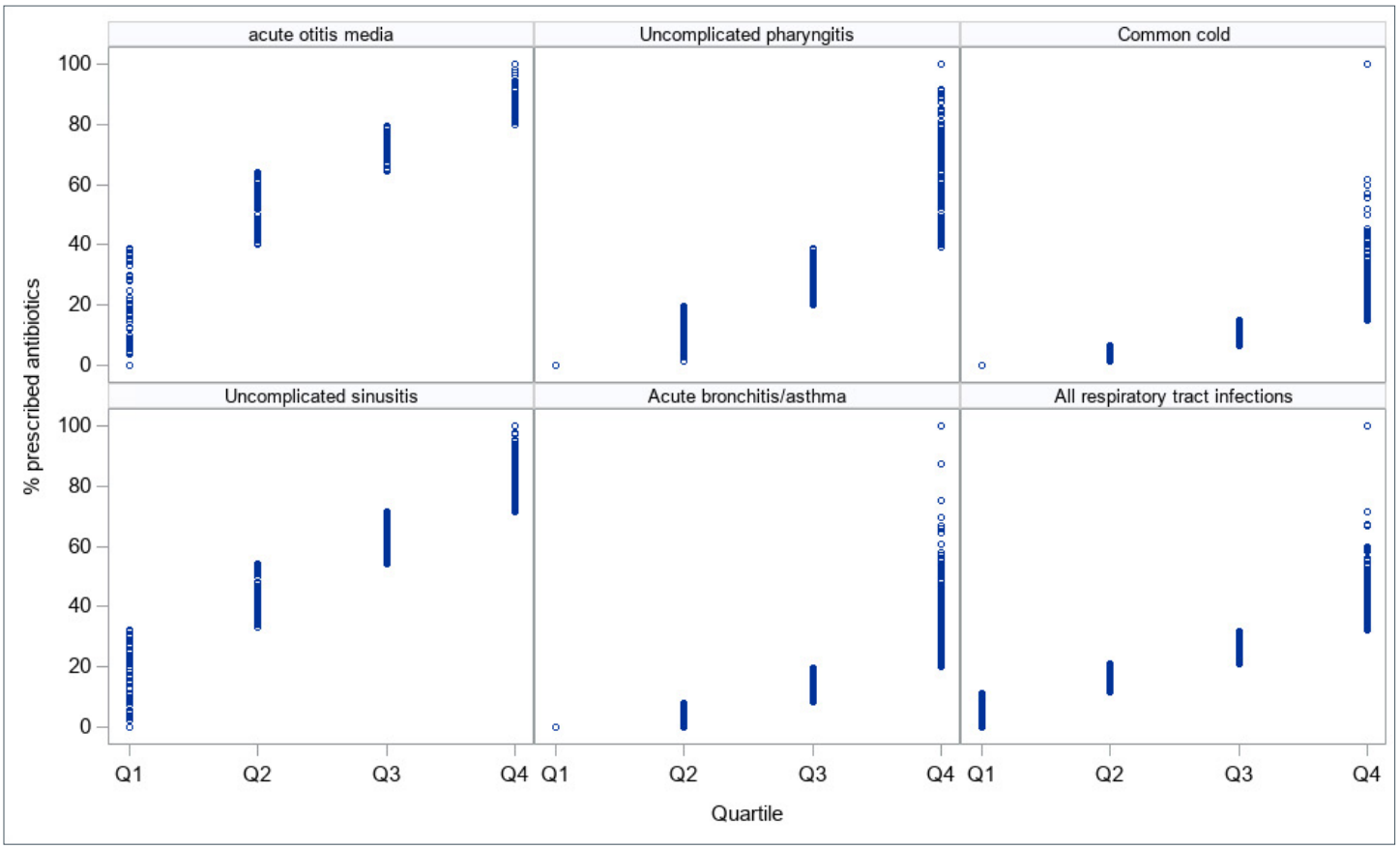


Figure 2: Antibiotic prescribing associated with different validated respiratory tract infection syndromes episodes by primary care provider, divided by quartile[a]



[a] Divided by quartile from lowest (Q1) to highest (Q4) proportion prescribed antibiotics

Discussion

This study found that CPCSSN can provide highly accurate surveillance for five common RTI syndromes across primary care. The variability in antibiotic prescribing practices identified underscores the need for feedback to providers and quality improvement as part of Canada's strategy to curb antimicrobial resistance.

Until now, surveillance of RTI and antibiotic prescribing practices in primary care has relied on provincial administrative databases that rely on physician billing claims (3,6). Previous validation studies of physician RTI billing claims found a PPV that ranged between 0.84 and 0.96 (15,16). In this study, we found that CPCSSN, which utilizes a combination of demographic factors, diagnostic codes and search terms in electronic medical records, similarly showed high PPV for surveillance of multiple different RTI case definitions.

Measuring antibiotic utilization in relation to RTI case definitions was assessed in different ways in our study. Antibiotic use per patient over the course of a year likely overestimated antibiotic prescribing, while antibiotic use per visit with RTI likely underestimated prescribing rates for patients with repeat visits. While the difference between these two approaches remained small, we found that antibiotic use per RTI episode, defined by incidence of a maximum of one RTI specific case definition per 30 days, fell between both measurements and may therefore provide the most accurate estimate of antibiotic prescribing practices.

Antibiotics for RTI are recognized to be the most common indication for unnecessary prescribing in primary care. Using our validated case definitions, we identified significant variability in antibiotic prescribing patterns with opportunity for improvement especially among those in the upper quartiles of antibiotic prescribing. Although our data do not directly measure appropriateness, this inter-provider variability in prescribing has been identified previously and was not explained by clinical patient differences (2,3,17). In this study, prescribers in the fourth quartile (those who prescribe the most) were found to prescribe antibiotics for nearly 100% of episodes of otitis media and sinusitis, and over half of pharyngitis and common colds. While there are no established benchmarks, the prescribers in the top quartile had rates of prescribing rates of close to zero for the common cold and pharyngitis as would be expected, and less than 30% for sinusitis and otitis media.

To address high-volume prescribing in primary care, multiple prior randomized controlled trials have demonstrated that peer comparison and feedback can significantly curb antimicrobial use (6,11,18). A recent trial in Ontario found that mailing a single letter to primary care providers notifying them that they are among the highest quartile of antibiotic prescribers compared with their peers resulted in a 4.2% relative difference in overall ambulatory antibiotic prescribing and $1.7 million in drug cost savings (6). Our validation of RTI case definitions across CPCSSN and identification of the high-volume prescribers will allow for similar targeted feedback interventions across this national primary care network.

Limitations

Our study has several important limitations. First, CPCSSN currently represents less than 10% of all primary care providers and therefore our findings may not represent antibiotic prescribing practices across Canada; however, greater representation may be possible in the future by scaling up the number of practices participating in this national primary care network. Second, the performance characteristics of our RTI case definitions vary by syndrome but the overall high PPV makes these data conducive to use for audit-and-feedback (19). Finally, this study was conducted based on chart abstraction of cases prior to the COVID-19 pandemic which has greatly affected the incidence and management of RTI (20). Further follow-up will be required in the post-COVID-19 era to reassess the incidence of different RTI syndromes and antibiotic prescribing practices.

Conclusion

National surveillance of antimicrobial prescribing practices in the community will be a vital strategy for curbing antimicrobial resistance. Our validation study confirmed that CPCSSN can provide this surveillance for RTI, which is the most common reason for antibiotic prescriptions in primary care. Future studies should focus on feedback to high-volume prescribers at a national scale, in combination with clinical tools that support practice improvement.

Authors' statement

All authors contributed to the preparation of this manuscript.

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Competing interests

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Impact of the first vaccine dose on COVID-19 and its complications in long-term care facilities and private residences for seniors in Québec, Canada

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Abstract

Background: Residents of long-term care facilities (LTCFs) and private residences for seniors (PRSs) were given priority for vaccination against coronavirus disease 2019 (COVID-19). Given the shortage of vaccine in the winter of 2021, the *Comité sur l'immunisation du Québec* recommended postponing the administration of second doses to ensure more rapid and widespread administration of first doses. The objective of this study was to measure the impact of first-dose vaccination on 1) the incidence of cases and complications in LTCFs and PRSs and 2) the frequency of outbreaks in LTCFs.

Methods: In this ecological study, COVID-19 incidence and complications in residents of LTCFs and PRSs in Québec were compared with the general (community) population at a point in time when there was still only limited eligibility for vaccination.

Results: After vaccination in LTCFs, the incidence rate of COVID-19 decreased by 92% compared with 49% in the community, and deaths decreased by 95%. By six weeks post-vaccination, almost no facility reported five or more cases per 100 beds per week. The incidence rate decreased by 91% in PRSs compared with 2% in the community. Hospitalizations and deaths in PRSs decreased by 94% and 90%, respectively.

Conclusion: As a result of 1) vaccination of residents with one dose, 2) natural immunity already acquired in LTCFs and PRSs, 3) vaccination of healthcare workers and 4) other non-pharmaceutical prevention measures implemented, the circulation of the coronavirus in these settings was largely interrupted.

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Introduction

Between March 1, 2020, and February 15, 2021, coronavirus disease 2019 (COVID-19) affected more than 2,500 long-term care facilities (LTCFs) or private residences for seniors (PRSs) in Canada, causing more than 55,000 infections in residents (over approximately 830,000 total cases in Canada), of which nearly 15,000 died (over approximately 21,000 total deaths in Canada, all ages) (1,2). In Québec, elderly or frail people frequently move into PRSs or LTCFs (3). This population has been particularly affected by COVID-19, representing only 2% of the Québec population but accounting for 12% of all cases (n=19,838/163,744), 32% of hospitalizations (n=4,248/13,280) and 56% of deaths related to COVID-19 (n=4,292/7,631) as of December 12, 2020 (data from the *Ministère de la Santé et des Services sociaux; Infocentre de santé publique*).

Limited quantities of the first COVID-19 vaccines were delivered to Canada in early December 2020. On January 12, 2021, the National Advisory Committee on Immunization recommend

delaying the administration of the second dose of vaccine until 42 days after the first dose, rather than the 21–28 days advocated by manufacturers (4). On March 3, 2021, the National Advisory Committee on Immunization increased their recommended timeframe for administration of second dose to four months, bringing all provinces and territories into compliance (5). In Québec, the COVID-19 vaccination campaign began on December 14, 2020 and an unlimited interval extension between vaccinations was adopted as of December 31, 2020 (6). The first priority group for vaccination was LTCF residents, followed by healthcare workers and people living in PRSs (7). Additional non-pharmaceutical measures were implemented, including another lockdown for the general population and tightening of measures in isolated and confined living environments (8–10).

The objective of the study is to measure the impact of first-dose vaccination on the incidence and complications of COVID-19 in LTCFs and PRSs and on the frequency of outbreaks in LTCFs.

Methods

Study design and population

This ecological study involved all residents of LTCFs (42,002 beds registered in the M02 Directory of Institutions of the *Ministère de la Santé et des Services sociaux*) and PRSs (129,626 residents), who were compared with the rest of the Québec population ("general" or "community" population, excluding healthcare workers) based on the registry of persons insured by the *Régie de l'assurance maladie du Québec* (comprising 7,991,678 inhabitants) (11,12). Healthcare workers (n=354,038) excluded from the community population included physicians and employees from the health and social services network, on the payroll of public and private institutions; community pharmacists and research personnel were not excluded. Thirty-six LTCFs (with a total of 2,510 registered beds) which mission was not focussed on seniors were excluded from the analyses as they were not given priority in the vaccination campaign. The observation period was from August 23, 2020 to April 10, 2021.

Variables

Data on COVID-19 cases (symptomatic and non-symptomatic cases, hospitalizations and deaths, date of episode, living environment, name of the LTCF of residence and healthcare worker status) were extracted from the provincial electronic file of confirmed COVID-19 cases (*Trajectoire de santé publique* platform, accessed at the *Infocentre de santé publique*) on April 25, 2021 for the LTCF analyses and on June 15, 2021 for the PRS analysis. The *Trajectoire de santé publique* platform is the only database documenting all laboratory-confirmed and epidemiologically-linked cases of COVID-19 in Québec and is therefore the gold standard. It is supported by surveys conducted by regional public health departments, which report, among other things, basic demographic data on cases, their living environment (home/LTCF/PRS/other, name of facility and address) and whether they are healthcare workers. The platform has not undergone validity studies; however, cases occurring in LTCFs and PRSs are investigated on a priority basis and are therefore very well documented, whereas non-severe cases in the rest of the population are underestimated since their reporting depends on individuals' propensity to consult or be screened (13). In contrast, hospitalized or deceased COVID-19 cases are much better captured. The list of facilities with a LTCF mission was developed from the *Ministère de la Santé et des Services sociaux* directory of institutions, which contains the number of licenced beds for each LTCF (11). Information on the progress of vaccination coverage in each of the three groups was extracted from the *Registre de vaccination du Québec*—a population-based registry consulted at the *Infocentre de santé publique*, which is the only source for such data (12). Doses must be entered into the registry within hours of administration. The LTCF and PRS residents were identified by their address as declared to the *Régie de l'assurance-maladie du Québec* and by the justification for their vaccination.

First-dose vaccination of LTCF residents began in December 2020, but occurred primarily in January 2021, with coverage increasing from 17% to 80% between January 5 and 20, 2021. Similarly, the majority of PRS residents were vaccinated between February 10 and 28, 2021, when coverage increased from 18% to 80%. The administration of second doses in LTCFs and PRSs began on April 22, 2021. As of April 10, 2021, 91% of LTCF residents and 92% of PRS residents were vaccinated with at least one dose. Vaccination with a first dose for the community population began sequentially in March 2021, but as of April 10, 2021, only a minority of this group (19%) had been reached.

Analyses

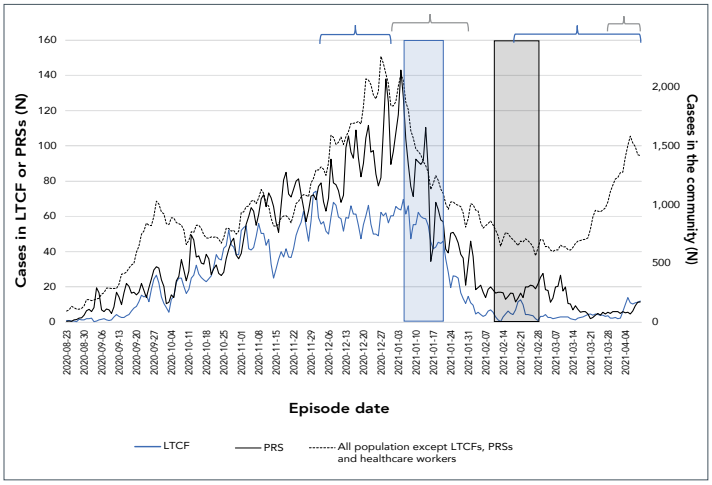
The number of cases occurring in each group (LTCF, PRS, and general population) was calculated and presented according to the episode date (the date of onset of symptoms when available, otherwise the sampling date or the reporting date if neither of these two dates was available). Differences in daily pre/post-vaccination incidence rates were calculated by comparing the period December 1 to 31, 2020 *vs* February 17 to April 10, 2021 for LTCFs and January 1 to 31, 2021 *vs* March 28 to April 10, 2021 for PRSs. The buffer period between the pre/post-vaccination periods included both the vaccination and the subsequent 28 days required for the vaccines to reach their full effect. The same analysis was done for hospitalizations and deaths; however, because LTCF residents had access to health care in their living environments, we did not analyze the hospitalization trends in this population. Finally, the number of cases per 100 beds was calculated by LTCF and by CDC week before or after the start of vaccination in the LTCF to identify the number of "affected" (defined as at least one case per week) and "more severely affected" (defined as at least five cases per 100 beds) LTCFs per week. This calculation was used as an approximation of outbreaks. This calculation was not possible for PRSs since the information was not available.

Results

Long-term care facilities

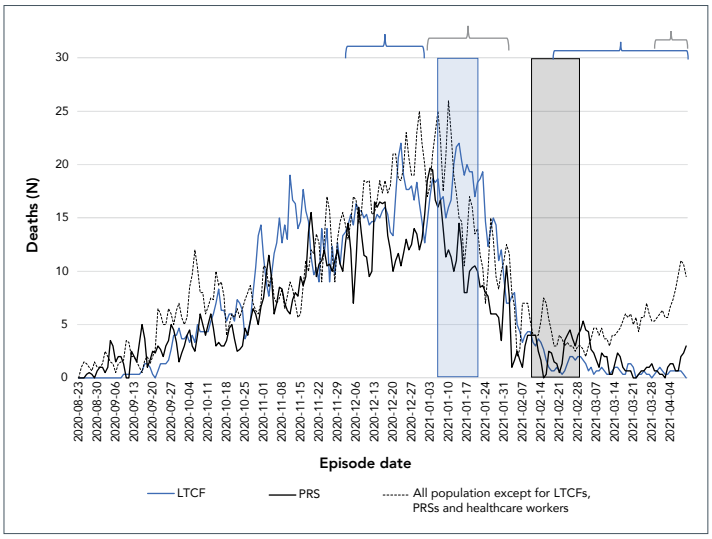
Between August 23, 2020 and April 10, 2021, 6,027 cases of COVID-19 were reported among residents in the 418 LTCFs that were tracked; 1,723 (29%) of these cases died. There was a gradual increase in the incidence of cases during the fall of 2020, both in LTCFs and in the community (**Figure 1**). In the community, incidence began to decline in very early January 2021, reaching a low point between mid-February and mid-March 2021 and rising again during the third wave. The pattern was significantly different in the LTCFs, where a much steeper decline began on January 10, 2021, reaching a very low plateau during the entire month of March before increasing only slightly again during the first two weeks of April 2021. The same trend was observed for deaths (**Figure 2**). During the post-vaccination period (February 17–April 10, 2021), the incidence rate had decreased by 91.8% in the LTCF and 48.9% in the community (general population; excluding LTCFs, PRSs and healthcare workers) compared with December 2020 (**Table 1**).

Figure 1: Cases in long-term care facilities, private residence for seniors and among the general population[a], August 23, 2020–April 10, 2021



Abbreviations: LTCF, long-term care facilities; PRS, private residence for seniors
[a] Excluding LTCFs, PRSs and healthcare workers

Figure 2: Deaths in long-term care facilities, private residences for seniors and among the general population[a], August 23, 2020–April 10, 2021



Abbreviations: LTCF, long-term care facilities; PRS, private residence for seniors
[a] Excluding LTCFs, PRSs and healthcare workers

For the same periods, the mortality rate decreased by 94.9% in LTCFs and 73.0% in the community. The number of LTCFs affected (defined as at least one case) or reporting at least five cases per 100 beds decreased beginning in the second and third weeks after the vaccination blitzes (**Figure 3**); these numbers stabilized beginning in the sixth week after vaccination, when approximately 10 LTCFs were affected each week, with none or only one LTCFs more severely affected.

Private residences for seniors

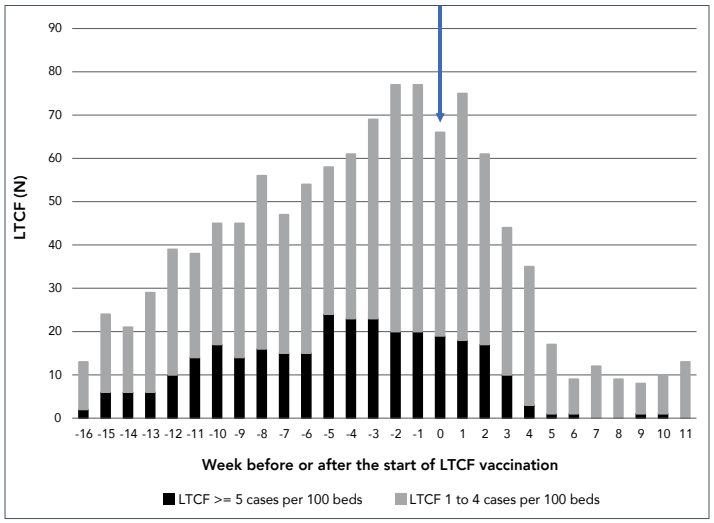
Over the entire observation period, 9,396 cases of COVID-19 were reported in PRSs; of these cases, 2,412 (26%) were hospitalized and 1,359 (14%) died. The decrease in PRS cases occurred in two stages (Figure 1). The largest decrease occurred from early January to mid-February, when few vaccines had been administered. A resurgence of cases occurred from late February to early March, then declined again to levels not seen

Table 1: Changes in case incidence and mortality rates in long-term care facilities and in the general population[a] before and after intensive vaccination of residents[b]

Outcome	LTCFs (rate per 100,000 person-days)			General population (rate per 100,000 person-days)		
	Pre-vaccination	Post-vaccination	Difference (%)	Pre-vaccination	Post-vaccination	Difference (%)
Cases	138.6	11.4	-91.8	21.4	10.9	-48.9
Deaths	37.6	1.9	-94.9	0.2	0.1	-73.0

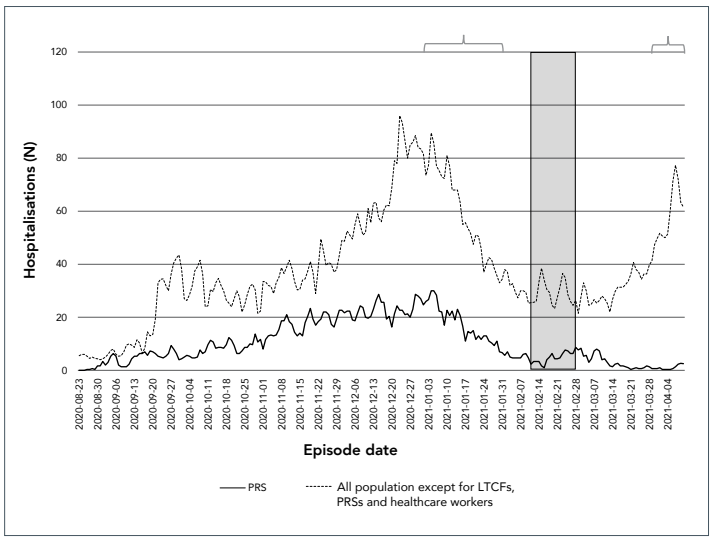
Abbreviation: LTCF, long-term care facilities
[a] Excluding long-term care facilities, PRSs and healthcare workers
[b] Pre-vaccination period: December 1 to 31, 2020; post-vaccination period: February 17 to April 10, 2021

Figure 3: Number of long-term care facilities affected, based on the number of cases per 100 users, per week before or after the start of the vaccination



Abbreviation: LTCF, long-term care facilities

Figure 4: Hospitalizations in private residences for seniors and in the general population excluding long-term care facilities, private residences for seniors and health care workers, August 23, 2020–April 10, 2021



Abbreviations: LTCF, long-term care facilities; PRS, private residence for seniors

since the very beginning of September 2020. The cases in the comparison group followed approximately the same pattern up to that point. The impact of vaccination in PRSs became more apparent toward the end of March, as cases increased substantially in the comparison population, while cases in PRSs reached a low plateau, without a substantial increase at the end of the period. Hospitalizations and deaths followed the same temporal trends as cases (Figure 2 and **Figure 4**). The incidence rate in PRSs decreased by 91% between January 2021 and the post-vaccination period (March 28–April 10, 2021), whereas the decrease was only 2% in the general population (**Table 2**). Post-vaccination hospitalization and mortality rates for PRS residents had decreased by 94% and 90% compared to January, while these decreases were 7% and 53%, respectively, in the community.

Table 2: Changes in case and hospitalization incidence rates and mortality rates in private residences for seniors and in the general population[a] before and after intensive resident vaccination[b]

Outcome	PRS (rate per 100,000 person-days)			General population (rate per 100,000 person-days)		
	Pre-vaccination	Post-vaccination	Difference (%)	Pre-vaccination	Post-vaccination	Difference (%)
Cases	56.0	5.0	-91.0	16.9	16.7	-1.6
Hospitalizations	13.6	0.8	-93.8	0.8	0.7	-6.5
Deaths	8.6	0.8	-90.2	0.2	0.1	-52.6

Abbreviation: PRS, private residence for seniors
[a] Excluding long-term care facilities, PRSs and healthcare workers
[b] Pre-vaccination period: January 1 to 31, 2021; post-vaccination period: March 28 to April 10, 2021

Discussion

This study measured the impact of the first-dose of the vaccination campaign in Québec LTCFs and PRSs, that is, a combination of vaccine efficacy, vaccine coverage and an additional reduction in virus transmission via herd immunity. Rapid vaccination of residents was followed by a significant decrease in cases (91% in LTCFs and 92% in PRSs), hospitalizations (94% in PRSs), deaths (95% in LTCFs and 90% in PRSs) and outbreaks related to COVID-19 in these settings. The decrease was maintained until the administration of the second and even the third dose in October 2021 (data from the *Trajectoire de santé publique* platform). Improvement in the community case counts, hospitalizations and deaths also occurred in January and February 2021, but to a lesser extent, and were followed by increases during the third wave of COVID-19 in April 2021.

In LTCFs, vaccination blitzes were followed by a 91% reduction in the infection incidence rate among residents compared with a 49% reduction among the community population. This important decrease in cases and disease severity in LTCFs is most likely attributable to vaccination. In addition, while cases increased again in the community during the third wave in Québec, cases in LTCFs remained low. The number of deaths followed the same trend. In Ontario, where second doses were administered promptly in LTCFs, a similar decrease in incidence rates was observed eight weeks after the start of vaccination (14). We also note that after vaccination, almost no LTCF was severely affected (five or more cases/100 beds) despite the occurrence of sporadic cases, which suggests the existence of herd immunity generated by the vaccination in a substantial proportion of the residents and the workers in these settings. A study in Catalonia, Spain, showed a maximum decrease of 90% (95% CI: 76–93) between expected and observed cases six weeks after 70% of residents received a second dose (15). Our data suggest that a comparable outcome was achieved with a single dose of the vaccine.

In PRSs, the large decrease in the number of cases, which started before resident vaccination began, is likely related to the reduction in transmission in the general population resulting from general non-pharmaceutical public health measures implemented in late December 2020, the vaccination of healthcare workers and the tightening of prevention measures instituted in PRSs after the December holiday season. The impact of vaccination of residents seems clear during the third wave, which was caused primarily by the Alpha variant (B.1.1.7). This wave greatly affected unvaccinated persons in the community, leading to another lockdown in some areas; but PRSs were almost completely spared.

Strengths and limitations

A major strength of this study is that it is a population-based study—there was no random error, as the differences reported were those observed in the target population as a whole—and the trends are very clear. Nevertheless, in addition to the other measures and phenomena concomitant with resident vaccination mentioned in the introduction, this ecological study has some limitations. The provincial registry of COVID-19 cases is intended to record all cases reported to public health authorities, but cases that did not result in an epidemiological investigation were not included. An underestimation of cases in LTCFs and PRSs is possible, especially before vaccination when the high incidence of cases led to an overload of work for the teams responsible for the surveys and a prioritization of the information to be captured. The living environment (home/LTCF/PRS/other, name of facility and address), however, continued to be important information. The impact of a first dose may have been underestimated since the post-vaccination period began four weeks after 80% coverage had been achieved, whereas vaccine coverage is now over 95%. Since LTCFs and PRSs were severely affected by COVID-19 prior to vaccination, for many residents, the first dose of vaccine was in addition to natural immunity. The unknown role of these factors may reduce the reproducibility of this study. It should be noted that an ecological design was entirely appropriate for measuring the impact of a vaccination campaign in the target population in order to capture data reflective of herd immunity as well. Finally, while it would have been interesting to measure the impact of age and health status of the residents and type of facility, this information was not available. Furthermore, it was not necessary, since it would be unlikely that the composition of the study population had changed significantly between the pre- and post-vaccination periods.

Conclusion

Although the vaccination of healthcare workers and the enhanced preventive public health measures instigated in early 2021 likely reduced the transmission of COVID-19, administration of the first dose of vaccine to the residents in the LTCFs and PRSs appears to have contributed to the marked decrease in COVID-19 incidence, hospitalizations and mortality in these settings—even before the second dose was administered.

Authors' statement

EF — Conceptualization, data analysis and interpretation, writing or revising the article
PDW — Conceptualization, data analysis and interpretation, writing or revising the article
DT — Conceptualization, data analysis and interpretation, writing or revising the article
MO — Data analysis and interpretation, writing or revising the article
GD — Conceptualization, data analysis and interpretation, writing or revising the article
CS — Conceptualization, writing or revising the article
RG — Data analysis and interpretation, writing or revising the article
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The contents and views expressed in this article are those of the authors and do not necessarily reflect those of the Government of Canada.

Competing interests

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Regional differences in access to direct-acting antiviral treatments for hepatitis C across Ontario: A cross-sectional study

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Abstract

Background: Direct-acting antivirals (DAAs) are curative treatments for hepatitis C virus (HCV) infection, a condition affecting over 100,000 Ontarians. Although DAAs are covered under the public drug programs in Ontario, receiving prescriptions depends on access to healthcare. The aim of this study is to understand the relationship between DAA treatment rates and distance to prescriber in Ontario, Canada.

Methods: We conducted a cross-sectional study and identified patients who filled a DAA prescription through the Ontario Drug Benefit (ODB) in 2019. We calculated crude (per 100,000 ODB recipients) and adjusted (by a regional HCV infection rate) DAA treatment rates by public health unit (PHU). We reported median distances to provider for all visit types, in-person visits, virtual visits, and proportions of visits that were virtual.

Results: In 2019, the crude DAA treatment rate for Ontario is 83.0 patients per 100,000 ODB recipients. The HCV-adjusted DAA treatment rate ranges from 28.2 (Northwestern Ontario) to 188.5 (Eastern Ontario) per 100,000. In our primary analysis, patients in rural PHUs, including Northwestern and Porcupine, were among the highest median distances to prescriber for all visit types (1,195 km and 556 km, respectively). These PHUs also had the highest proportions of virtual visits (greater than 60%). Urban PHUs, such as Toronto and Ottawa, had smaller median distances for all visit types, with smaller proportions of virtual visits (10.8% and 12.4%, respectively).

Conclusion: We observed heterogeneity in treatment rates, distance to DAA prescribers and use of virtual care in the management of HCV. Increasing use of telemedicine in regions with limited utilization of DAAs may improve access.

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Introduction

Over 100,000 Ontarians are living with hepatitis C virus (HCV) infection (1). While the first six months of infection is acute, chronic HCV infection is a potentially life-threatening condition. In 2014, curative treatments, direct-acting antivirals (DAAs), have become available to Ontarians living with HCV infection under the publicly-funded Ontario Drug Benefit (ODB) programs (2–7). Over 90% of DAAs dispensed in Ontario are covered by the ODB. Prior to March 2017, the ODB required that individuals have liver fibrosis in order to obtain coverage for DAAs. Furthermore, from March 2017 to June 2021, ODB coverage required that a specialist prescribed the medication and that patients had two laboratory-confirmed HCV ribonucleic acid (RNA) tests taken at least six months apart to confirm chronic infection (8,9). As a result, access to publicly-funded DAAs required an advanced liver disease stage over an extended period of time (10,11).

In general, prior to broad access to virtual care and telemedicine, healthcare access was inversely correlated with distance to healthcare services, with low access contributing to shorter life expectancies (12,13). For example, those living in northern Ontario had shorter life expectancies and poorer health outcomes compared with people living in southern Ontario (14). In addition, the number of specialist physicians in rural and north Ontario was low and has decreased over time (15). One barrier to accessing healthcare is the large distances between patients and their providers (14,16); thus, virtual care can play an important role in increasing access to physicians and services (17). This is especially important for Ontarians living in northern and remote small population centres where access to in-person healthcare is limited (18).

Those living with HCV infection face many structural barriers to DAAs (11). Large distances to specialized healthcare may lead to delays in diagnosis and treatment. The DAAs cure over 95% of HCV infections and understanding which regions in Ontario have lower treatment rates can assist in the development of targeted initiatives to increase these treatment rates (19,20). Targeted initiatives, including harm reduction, may benefit those living with HCV infection who are part of marginalized communities, including people who use or inject drugs, those who are homeless/underhoused and those in Indigenous communities (21,22). As such, we described the DAA treatment rates across Ontario, distance to prescriber and use of virtual care.

Methods

Study design

We conducted a cross-sectional study among patients who were dispensed at least one course of DAAs ("treatment") through the ODB from January 1, 2019, to December 31, 2019.

Data sources

We utilized January 1, 2019–March 31, 2019, healthcare administrative data through ICES, an organization that houses routinely collected healthcare administrative data. We used the ODB database to identify patients who received a publicly-funded course of DAAs, and the number of ODB-eligible Ontarians. Ontario Drug Benefit-eligible Ontarians included those 65 years of age or older, with financial needs (due to high drug costs and/or low income; individuals who spent at least 4% of their after-tax household income on medications), living in long-term care, who received home care or disability benefits and individuals 24 years of age or younger (23). Beginning April 1, 2019, ODB coverage for those 24 years of age or younger was restricted to patients without private insurance. Notably, over 90% of DAAs dispensed in Ontario were reimbursed by the ODB (6). We determined prescriber location through the ICES Physician Database. These databases are securely linked using unique, encoded identifiers and are analyzed at ICES.

Analysis

We calculated three rates to describe HCV infections and DAA dispensing in Ontario by PHU (see **Annex**, **Figure A1**). First, we calculated the HCV infection rate per 100,000 population, using the average annual incidence of newly diagnosed HCV patients (including acute infections and previously undiagnosed chronic infections) from 2014 to 2018 on Public Health Ontario's tool (24). We utilized incidence as a measure of HCV in each PHU due to the relationship between incidence and prevalence. This measure was used as a proxy to indicate the level of HCV in each PHU because we do not anticipate the duration of disease greatly shifting from 2014–2018, with the first DAAs becoming accessible in Canada in 2014 (25,26). Previous research has found a strong correlation between incidence rates and prevalence (25,27,28). Second, we calculated the crude DAA treatment rate, adjusted by the number of ODB-eligible individuals in each PHU. Third, we calculated the HCV-adjusted DAA treatment rate by dividing the crude rate by an HCV prevalence adjustment factor.

We calculated the distance between each patient's home address and their DAA prescriber (at first prescription) using patient residence and prescriber's primary practice postal code, as a measure of treatment access. In our primary analysis, we reported median distance to prescriber of first prescription and the proportion of patients with distances greater than 50 km for all visit types. In our secondary analysis, we reported each distance in kilometers, stratified by visit type, and calculated the proportion of virtual visits by PHU. To define the type of physician visit (in-person or virtual) we identified the physician visit that occurred closest to the DAA ODB claim date (within the past year), where the physician matched the prescriber of the filled DAA prescription. Virtual visits were defined as those with an Ontario Hospitalization Insurance Plan billing code associated with telemedicine (codes: B099, B100 and B200). We excluded individuals who did not have a physician visit in the past year from distance analyses (n=847; 17.7%) since we were unable to determine their visit type, yet included them in the DAA treatment rate calculations.

Initial analyses at ICES were completed using SAS software, Version 9.3 (29). We created maps showing treatment rates and median distances to a prescriber overall and stratified by visit type (30). These maps are published online in the Ontario Drug Policy Research Network (ODPRN) website.

Results

Crude and hepatitis C virus-population adjusted treatment rates

The crude provincial DAA treatment rate was 83.0 per 100,000 ODB-eligible Ontarians (**Table 1**). Eastern Ontario PHU had the highest HCV-adjusted treatment rate, with a rate of 188.5 per 100,000; before adjustment, this rate was 129.3 per 100,000. In

contrast, Northwestern had the lowest HCV-adjusted treatment rate at 28.2 per 100,000. The treatment rate was 144.6 per 100,000 prior to adjustment but lowered after accounting for the high HCV prevalence in this PHU (169.4 per 100,000; **Figure 1**, Table 1).

Table 1: Number and rate of direct-acting antiviral users and distance to prescriber in 2019, by public health unit from highest to lowest hepatitis C virus-adjusted direct-acting antiviral treatment rate

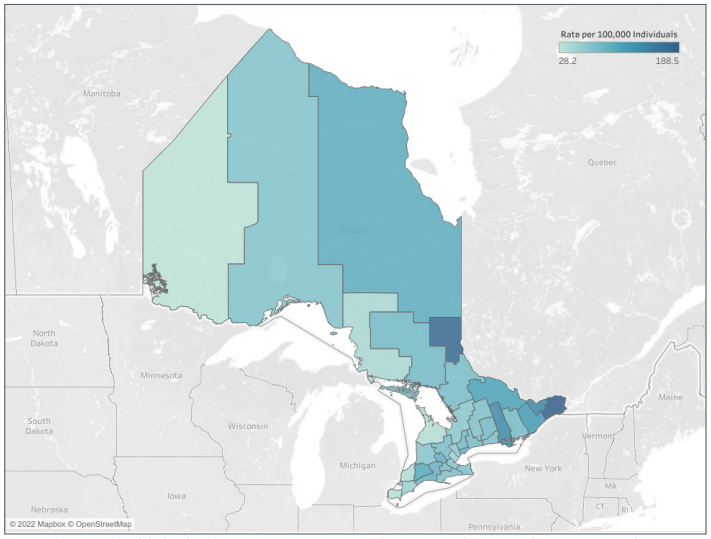
Public health unit	HCV rate[a]	Number treated and DAA treatment rate[b]		HCV-adjusted DAA treatment rate[c]	Distance to prescriber (all visit types)				Distance to prescriber (in-person visits)				Distance to prescriber (virtual visits)				Proportion of virtual visits	
		Treatment			Median		>50 km		Median		>50 km		Median		>50 km			
		N	Rate		km	IQR	N	%[d]	km	IQR	N	%[d]	km	IQR	N	%[d]	N	%[e]
Ontario	33.1	3,937	83.0	N/A	20	5–87	1,359	34.5%	13	4–49	801	24.6%	133	69–339	558	81.9%	681	17.3%
Eastern Ontario	22.7	104	129.3	188.5	86	76–278	87	83.7%	80	48–87	48	73.8%	93	86–401	39	100%	39	37.5%
Timiskaming	29.6	21	157.9	176.6	501	209–502	21	100%	489	209–501	≥5	≥5	501	209–502	16	100%	16	76.2%
City of Ottawa	25.5	348	110.0	142.4	13	5–120	125	35.9%	10	4–118	89	29.2%	355	342–444	36	83.7%	43	12.4%
Perth District	14.7	17	61.3	137.8	46	40–54	≥5[f]	≥5[f]	46	40–54	≥5	≥5	0	0	0	0	0	0.0%
Hastings and Prince Edward Counties	37.8	109	156.5	137	59	16–167	57	52.3%	27	13–86	33	38.8%	171	161–192	24	100%	24	22.0%
Leeds, Grenville and Lanark District	39.5	100	142.6	119.4	75	47–300	69	69%	56	30–83	38	56.7%	302	280–392	31	93.9%	33	33.0%
Renfrew County and District	27.3	36	91.4	110.5	135	97–276	36	100%	137	121–161	21	100%	122	73–299	15	100%	15	41.7%
Middlesex-London	49.4	266	153.6	102.9	7	4–166	78	29.3%	7	4–164	70	27.1%	166	121–338	8	100%	8	3.0%
Porcupine	44.7	39	132.0	97.7	556	224–576	33	84.6%	10	2–224	≥5	≥5	557	554–598	29	100%	29	74.4%
City of Toronto	25.1	629	72.2	95.2	7	3–12	34	5.4%	7	4–12	33	5.9%	5	2–9	≥5	≥5	68	10.8%
Waterloo	23.7	121	68.0	94.7	18	3–82	38	31.4%	6	3–32	19	19.8%	93	81–95	19	76%	25	20.7%
Southwestern (Oxford, Elgin and St. Thomas)	38.4	80	106.4	91.7	44	31–48	19	23.8%	43	30–46	13	17.6%	140	139–140	6	100%	6	7.5%
York Region	15.6	139	39.1	82.7	20	11–37	21	15.1%	18	10–30	10	8%	64	60–120	11	78.6%	14	10.1%
Peterborough County-City	55.8	82	137.4	81.4	63	3–111	51	62.2%	21	2–99	26	45.6%	124	110–202	25	100%	25	30.5%
Sudbury and District	69.3	131	170.4	81.3	11	5–31	27	20.6%	10	4–20	11	9.6%	339	225–350	16	100%	16	12.2%
Kingston, Frontenac and Lennox and Addington	67.2	126	162.1	79.8	34	4–75	43	34.1%	30	4–74	38	31.4%	≥5	≥5	≥5	≥5	≥5	≥5
Brant County	46.8	63	111.3	78.7	4	2–41	15	23.8%	4	2–30	8	15.4%	87	2–92	7	63.6%	11	17.5%
North Bay Parry Sound District	60.5	74	143	78.1	60	6–254	40	54.1%	22	3-96	18	35.3%	274	195–296	22	95.7%	23	31.1%
Durham Regional	24.2	122	57.0	77.8	19	5-49	25	20.5%	15	5–39	18	17.1%	49	42–140	7	41.2%	17	13.9%
Wellington-Dufferin-Guelph	24.5	55	56.6	76.4	24	14–64	18	32.7%	23	8–38	11	22.9%	71	64–72	7	100%	7	12.7%
Haldimand-Norfolk	37.8	35	82.8	72.5	49	40–81	16	45.7%	49	38–67	14	45.2%	≥5	≥5	≥5	≥5	≥5	≥5
Haliburton, Kawartha, Pine Ridge	47.7	81	104.6	72.4	86	46–119	59	72.8%	73	46–99	44	67.7%	126	105–181	15	93.8%	16	19.8%
Niagara Regional Area	51.4	206	111.8	72.0	30	20–56	65	31.6%	28	13–32	26	15.6%	70	57–85	39	100%	39	18.9%
Thunder Bay District	118.8	135	250.6	69.8	10	4–911	54	40%	6	3–11	12	13%	924	907–926	42	97.7%	43	31.9%

Table 1: Number and rate of direct-acting antiviral users and distance to prescriber in 2019, by public health unit from highest to lowest hepatitis C virus-adjusted direct-acting antiviral treatment rate (*continued*)

Public health unit	HCV rate[a]	Number treated and DAA treatment rate[b]		HCV-adjusted DAA treatment rate[c]	Distance to prescriber (all visit types)				Distance to prescriber (in-person visits)				Distance to prescriber (virtual visits)				Proportion of virtual visits	
		Treatment			Median		>50 km		Median		>50 km		Median		>50 km			
		N	Rate		km	IQR	N	%[d]	km	IQR	N	%[d]	km	IQR	N	%[d]	N	%[e]
Huron County	32.5	16	66.1	67.3	87	67–92	14	87.5%	87	67–92	13	86.7%	≥5	≥5	≥5	≥5	≥5	≥5
City of Hamilton	40.1	160	78.6	64.8	6	3–21	25	15.6%	5	3–12	14	9.7%	≥5	≥5	≥5	≥5	≥5	≥5
Peel Region	22.3	192	42.9	63.6	18	7–33	40	20.8%	17	7–33	37	20.6%	29	21–52	≥5	≥5	12	6.3%
Simcoe Muskoka District	38.1	149	73.4	63.6	85	51–126	112	75.2%	52	22–88	43	53.8%	105	85–145	69	100%	69	46.3%
Halton Region	19.2	53	29.8	51.5	18	8–41	≥5	≥5	18	7–30	≥5	≥5	42	41–43	0	0.0%	≥5	≥5
Chatham-Kent	58.8	39	90.0	50.6	91	16–107	24	61.5%	89	16–103	23	60.5%	≥5	≥5	≥5	≥5	≥5	≥5
The District of Algoma	70.1	43	87.9	41.5	5	2–128	14	32.6%	5	2–126	12	29.3%	≥5	≥5	≥5	≥5	≥5	≥5
Lambton	84.8	49	95.1	37.1	4	2–88	14	28.6%	2	1–43	8	18.6%	254	172–254	≥5	≥5	6	12.2%
Grey Bruce	24	17	25.4	35	128	116–160	16	94.1%	128	115–143	13	92.9%	≥5	≥5	≥5	≥5	≥5	≥5
Windsor-Essex County	40.1	66	40.8	33.7	114	6–332	34	51.5%	18	4–160	15	32.6%	332	323–333	19	95%	20	30.3%
Northwestern	169.4	34	144.6	28.2	1,195	305–1,291	28	82.4%	178	7–308	7	53.8%	1,212	1,182–1,310	21	100%	21	61.8%

Abbreviations: DAA, direct-acting antiviral; HCV, hepatitis C virus; IQR, interquartile range; N/A, not applicable
[a] Average annual HCV infection rate in Ontario, from 2014–2018 (includes acute and chronic, newly detected infections); rates are per 100,000 population
[b] Rates are per 100,000 population eligible for the Ontario Drug Benefit
[c] Adjusted by a factor calculated by dividing the HCV rate for each public health unit by the provincial HCV rate; rates are per 100,000
[d] Number of unique patients that were prescribed DAAs and travelled more than 50 km
[e] Proportion of clients who received their DAA through virtual care
[f] Values of five or fewer have been censored to prevent patient identification

Figure 1: Map of Ontario by public health unit, showing hepatitis C virus-adjusted treatment rates of direct-acting antiviral users[a]

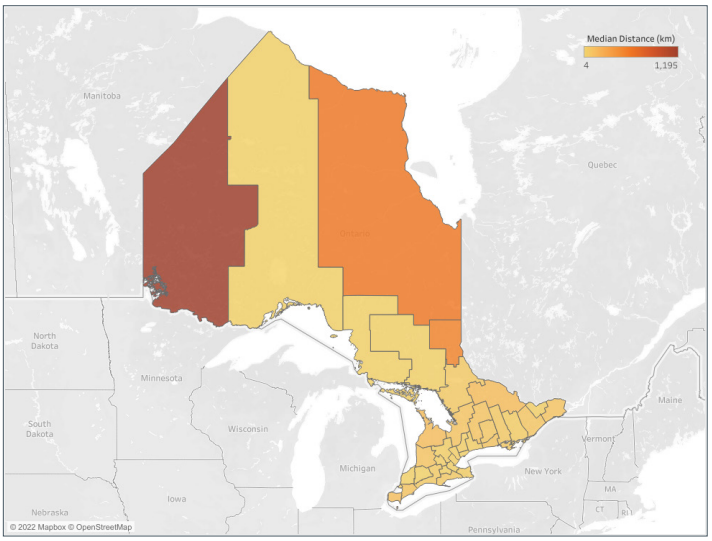


[a] Complete tool published online at Ontario Drug Policy Research Network (ODPRN) website

Distance to prescriber

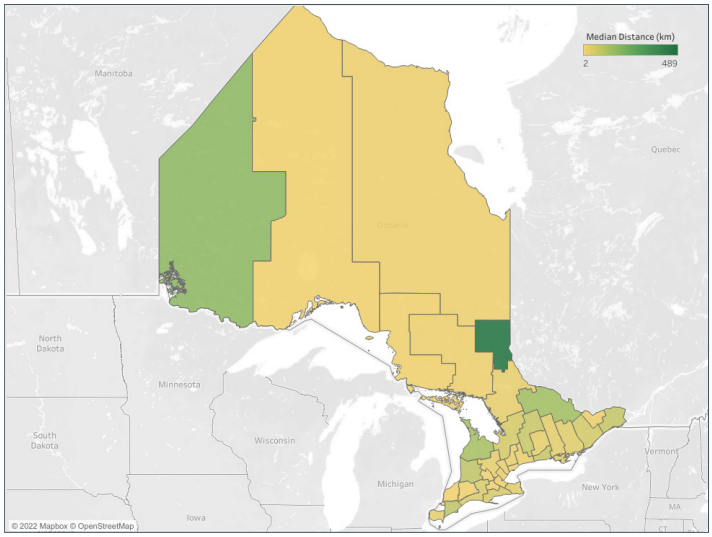
The median distance to prescriber in Ontario (all visits) was 20 km (interquartile range [IQR] 5–87 km) (Table 1). In our analysis of all visit types, patients in rural PHUs had the longest distances, with Northwestern (median of 1,195 km [IQR 305–1,291 km]), followed by Porcupine (median 556 km (IQR 224–576 km]) and Timiskaming (median 501 km [IQR 209–502 km]) (**Figure 2**). These three PHUs also had the highest proportions of patients receiving virtual care (61.8%, 74.4%, and 76.2%, respectively) yet had fewer than 100 patients in total (Table 1). Nonetheless, Timiskaming and Porcupine had high HCV-adjusted treatment rates (176.6 and 97.7 per 100,000, respectively), while Northwestern had the lowest rate. In contrast, those receiving DAAs in urban centres like Toronto and Ottawa generally had short median distances to their prescriber (Toronto: 7 km; Ottawa: 10 km) and smaller proportions of virtual visits (Toronto, 10.8%; Ottawa, 12.4%) (Table 1).

Figure 2: Map of Ontario by public health unit, showing median distance to prescriber (all visit types)[a]



[a] Complete tool published online at Ontario Drug Policy Research Network (ODPRN) website

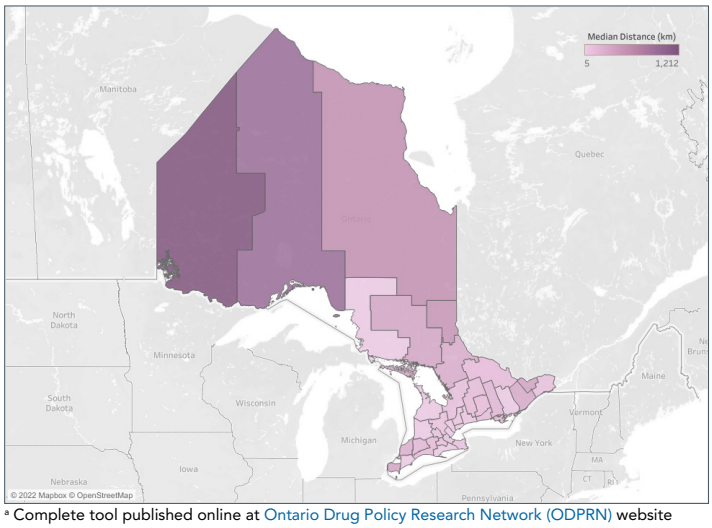
Figure 3: Map of Ontario by public health unit, showing median distance to prescriber (in-person visits)[a]



[a] Complete tool published online at Ontario Drug Policy Research Network (ODPRN) website

In our secondary analysis, distances between patients and their prescriber for in-person visits (median 13 km, IQR 4–49 km) were shorter than for virtual (median 133 km, IQR 69–339 km). Northern and rural PHUs (e.g. Northwestern, Thunder Bay) had the largest distances to prescribers for virtual visits. Within PHUs, there were large differences in the median distances to prescriber based on visit type: in the Northwestern PHU, in-person median distance was 178 km whereas virtual distance was 1,212 km. We also observed large IQR values within geographically large PHUs. Furthermore, there was considerable variation between PHUs in distance travelled for in-person visits, ranging from 178 km (IQR 7–308 km, 61.8% virtual) for Northwestern PHU to 6 km (median 6 km, IQR 3–11 km, 31.9% virtual) for Thunder Bay (Table 1, **Figure 3** and **Figure 4**). Interestingly, Hamilton and Peel had small distances to in-person visits yet had relatively low treatment rates. This was in contrast to Ottawa, which also had a small distance to in-person visits yet a relatively high treatment rate.

Figure 4: Map of Ontario by public health unit, median distance to prescriber (virtual visits)[a]



[a] Complete tool published online at Ontario Drug Policy Research Network (ODPRN) website

Discussion

Our study illustrates almost a seven-fold difference in HCV-adjusted DAA treatment rates across Ontario. Patients in rural PHUs generally lived further from their prescribers and had high proportions of virtual visits yet had few patients treated overall. The HCV-adjusted treatment rates were the lowest among PHUs in some rural regions, suggesting that expanded access to virtual care in rural PHUs may improve treatment rates.

Regions with large in-person distances to prescriber had greater utilization of virtual care than PHUs with shorter distances. Most visits in Timiskaming and Porcupine were virtual, with these regions having relatively high HCV-adjusted DAA treatment rates. Increasing virtual care may assist in improving treatment rates in Northwestern PHU. In this rural PHU, almost 40% of visits were in-person with a median distance of 178 km; however, Northwestern's lower HCV-adjusted DAA treatment rate may be due, in part, to a high HCV infection rate. In contrast, in urban PHUs, like Toronto and Ottawa, patients travelled shorter distances to prescribers and had fewer virtual visits while still maintaining high treatment rates. These high treatment rates were likely due to greater availability of providers and services per capita in urban PHUs.

Differences in treatment rates may be attributed to the fact that in 2019, ODB coverage criteria required a specialist physician to prescribe the medication and two laboratory tests at least six months apart (8). Both specialist physicians and laboratory testing may be particularly difficult to access in rural communities. In general, rural and northern communities have been found to have lower access and greater in-person distances to healthcare providers (18). Our results are consistent with other studies examining the relationship between rurality and DAA dispensing (31). Generally, there is variation in DAA dispensing in rural settings based on region, rather than on urban/rural status alone, as rural communities have distinct characteristics. Solutions to increase use of services can include working with PHUs and provincial specialty networks to develop specific plans that would benefit each PHU (e.g. harm reduction).

Northwestern PHU has the highest HCV infection rate, which doubled from 2009 to 2013. This was driven by increased testing among First Nations communities; a priority population identified by the *Blueprint to Inform Hepatitis C Elimination Efforts in Canada* (1,32). Despite this high incidence, Northwestern PHU had the lowest adjusted treatment rate across Ontario. We acknowledge that many in Northwestern PHU access healthcare in Manitoba or do not rely on the ODB for drug coverage as they can access DAAs through the Non-Insured Health Benefits (NIHB), First Nations and Inuit Health Branch. Yet for those eligible, the ODB is the first payer for medications (6,33). Telehealth can increase access to DAAs and assist in overcoming distance.

As local interventions have an impact on access to diagnosis and therapy, these may play a role in closing this treatment gap in Ontario. A diagnosis is the first step to receiving treatment, but many of those living with HCV infection can be asymptomatic for years (1). Access to testing for HCV must especially be increased in regions with high HCV rates. Additionally, family physicians and nurse practitioners are more accessible in the community than specialist physicians (34). Allowing non-specialists to prescribe DAAs, as was implemented in Ontario in March 2020, may enable more patients in underserved communities to obtain prescriptions (1,18,35). Finally, increased utilization of telemedicine may assist in reaching patients who face traditional barriers to treatment, such as distance to healthcare provider. Regions with high utilization of virtual care may have reduced the need for travel long distances to an appointment, indicating the impact virtual care can have. While virtual care can be beneficial, access and comfort using devices and internet required to facilitate virtual care can be challenging in rural regions (36). Thus, movement towards increasing virtual care should consider reducing the barriers to accessing these services by increasing infrastructure that can support internet and phone access.

Limitations

Our results have several limitations that warrant discussion. We calculated HCV rates in Ontario using an average annual incidence from 2014 to 2018. Thus, we do not know the true chronic HCV prevalence, which would provide an estimate of individuals who were untreated. Although we expect that the average incidence closely approximates prevalence of HCV (27,28,37), future studies are needed to determine the true prevalence of HCV by PHU. This calculation serves as an estimator of HCV infection rates, allowing us to control for the rates across PHUs. Second, we calculated distances based on each prescriber's primary office location. As a result, we were not able to account for prescribers who had multiple practices or who travelled to patients. We estimate that these would be a small proportion of visits. Lastly, we utilized the ODB database to identify DAA prescriptions; thus, prescriptions accessed through the NIHB or were paid for by private insurance or out-of-pocket were not included. Nonetheless, approximately 90% of all DAA prescriptions in Ontario are reimbursed by the ODB and would have been captured in our data (6). Lastly, we report rates of prescribing per PHU, and no tests of association between distance and treatment rates were done.

Conclusion

Ontario is a Canadian province with a wide range of disparities in distance to prescriber and treatment rates. This research provides observations relevant for other regions that also struggle with these inequalities. Interventions to increase DAA dispensing include diversifying the pool of prescribers, working with communities to address their needs and increasing virtual care and the infrastructure to facilitate its use. Future research could examine Ontario's HCV prevalence and explore how access to DAAs has shifted post-coronavirus disease 2019, especially with the increased use of virtual care.

Authors' statement

All authors were involved in the design, interpretation of results, writing, or revision of the manuscript (NK, MT, AS, DM, VPP, ACM, TG, MM). DM is the guarantor of the data and analysis.

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

No authors have any competing interests to declare.

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Annex

Equations used to calculate hepatitis C virus (HCV) and direct-acting antivirals (DAA) treatment rates

1) *Public health units* (*PHU*) *HCV infection rate* (*per* 100,000)

$$= \frac{HCV\ rate\ (2014) + HCV\ rate\ (2015) + HCV\ rate\ (2016) + HCV\ rate\ (2017) + HCV\ rate\ (2018)}{5} \times 100{,}000$$

2) *Crude DAA Treatment rate* (*per* 100,000) $= \frac{total\ treated\ per\ PHU}{total\ eligable\ for\ Ontario\ Drug\ Benefit\ (ODB)\ per\ PHU} \times 100{,}000$

3) *HCV – Adjusted DAA treatment rate* (*per* 100,000) $= \frac{crude\ DAA\ treatment\ rate}{adjustment\ factor} \times 100{,}000$

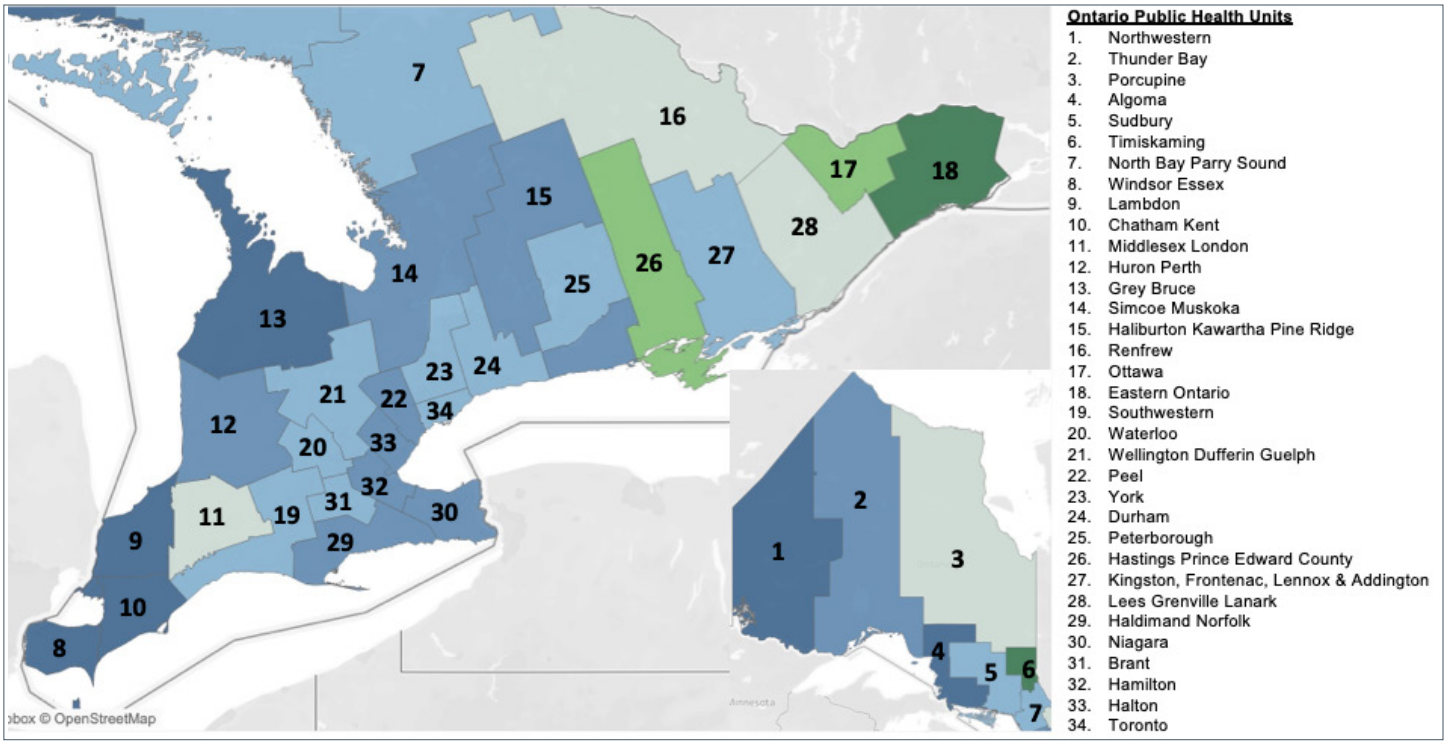
a. Provincial HCV rate (*per* 100,000) $= \frac{total\ HCV\ cases\ in\ Ontario}{total\ eligable\ for\ ODB\ in\ Ontario} \times 100{,}000$

b. Adjustment factor $= \frac{PHU\ HCV\ rate}{provincial\ HCV\ rate}$

Relationship between incidence and prevalence

Prevalence = incidence × duration of disease

Figure A1: Map of public health units in Ontario



Source: Association of Public Health Agencies (alPHa). Public Health Units. Accessed March 9 2022. https://www.alphaweb.org/page/PHU

Are there clinically significant interactions between COVID-19 vaccination and post-COVID-19 condition (long COVID)?

Source: Emerging Science Group of the Public Health Agency of Canada. Evidence Brief on the associations and safety of COVID-19 vaccination and post-COVID-19 condition: January 13, 2022. Full report available from: ocsoevidence-bcscdonneesprobantes@phac-aspc.gc.ca

Background: "Long COVID" has been studied both as post-acute sequelae (PAS), defined as symptoms 4 to 12 weeks post diagnosis, and as post-COVID-19 condition (PCC), defined by the World Health Organization as persistent or recurring symptoms lasting for at least 8 weeks and occurring 12 or more weeks after an acute COVID-19 infection (1). It is important to know if there are any beneficial or harmful effects of COVID-19 vaccination on PAS or PCC, or if PAS or PCC increases the risk of adverse events following vaccination. This report addresses three questions: Does COVID-19 vaccination before or after COVID-19 infection decrease the risk of developing PAS or PCC? Among those who already have PAS or PCC, does COVID-19 vaccination affect their symptoms? Is it safe to receive a COVID-19 vaccine after PAS or PCC?

Methods: Twenty databases and key websites were searched for relevant reviews, peer-reviewed publications and preprints up to January 13, 2022. Search terms included the following: immuniz*, immunis*, vaccin*, long covid, long-covid, post covid, post-covid, chronic covid, chronic-covid, long-term sequelae, long hauler and long-hauler. The search netted 97 citations, which were screened for relevance. Data were extracted from relevant studies into three evidence tables to address each of the questions.

Results: Fourteen relevant studies were identified: four prospective cohort studies; four retrospective cohort studies; and six cross-sectional studies. One was peer-reviewed, twelve were preprints and one was a letter to the editor. Twelve studies reported on vaccines authorized for use in Canada and are reported on here; the two others were on a vaccine authorized for use in India (2,3).

COVID-19 vaccination prior to developing PAS or PCC

All studies in this area were on PCC. Four situations were assessed: four studies assessed one or two doses of COVID-19 vaccine before COVID-19 infection and the risk of developing PCC; and two studies assessed having one or two doses of a COVID-19 vaccine after COVID-19 infection, but before developing PCC.

COVID-19 vaccination before COVID-19 infection

No studies found an increased risk of developing PCC subsequent to infection. All studies were retrospective or cross-sectional studies; thus, the evidence of a protective effect from vaccination was not strong.

- Two studies assessed one dose of a vaccine prior to COVID-19 infection. One study identified a decreased risk of PCC (odds ratio [OR] 0.22) (4) and one study found no difference (5).
- Two studies assessed two doses of a vaccine prior to COVID-19 infection. One study identified a decreased risk of PCC (hazard ratio [HR] 0.87) (6), two studies reported a lower proportion of some PCC symptoms among vaccinated people (5,7) and one study found no difference (5).

COVID-19 vaccination after infection and before post-COVID-19 condition

This was reported in two studies; both found a decreased risk of developing PCC.

- A prospective cohort described a temporary reduction in the risk of PCC (13%) post first dose and a 9% reduction post second dose followed by further decreases of 0.8% per week regardless of the vaccine received (8). Timing of the vaccine post-infection did not appear to affect results.
- A retrospective cohort that assessed at least one dose of a vaccine received 0–20 weeks post-COVID-19 diagnosis found a reduced risk of PCC, and this was most protective when received closer to diagnosis (OR 0.38 at 0–4 weeks *vs* OR 0.75 at 8–12 weeks) (4).

One study did not differentiate between vaccination before or after COVID-19 and reported no association with vaccination and development of PCC overall, however those vaccinated had a lower risk of certain symptoms (9).

COVID-19 vaccination after developing PAS or PCC

Five studies examined the effect of COVID-19 vaccination after developing PAS or PCC. Three studies showed a small beneficial effect and two studies showed no difference.

- A large prospective cohort study found that the PCC remission rate in vaccinated individuals was 16.6% *vs* 7.5% in unvaccinated individuals (10).

- A smaller prospective cohort study found that the PCC remission rate in vaccinated individuals was higher than the unvaccinated (23.2% *vs* 15.4%), the proportion with worsening symptoms was lower (5.6% *vs* 14.3%) and in the majority of vaccinated and unvaccinated people PCC symptoms were the same (71.1% *vs* 70.3%) (11).
- A third prospective cohort study found that there were fewer general practitioner consultations among individuals with PAS after vaccination compared with before vaccination (12).
- A retrospective cohort on PCC (13) and a cross-sectional study on PAS (14) found that there was no change in symptoms with vaccination status.

Safety of COVID-19 vaccination in those with PAS or PCC

Two studies reported on vaccine adverse events after one dose of a COVID-19 vaccine in individuals with PCC.

- A cross-sectional study of one dose of an mRNA vaccine found that there was no significant difference in the number or duration of vaccine adverse events in those with PCC (n=30) *vs* those without (n=944) (15).
- A large prospective cohort study of individuals with PCC concluded vaccination was safe with fewer than 1% reporting a serious adverse event (0.88%) (10).

Conclusion: Preliminary research findings suggest COVID-19 vaccination may decrease the risk of developing PCC and, in those who already have PCC or PAS, receiving a COVID-19 vaccination was not associated with an increase in adverse events and was associated with remission of PAS or PCC symptoms in some people. There is low confidence in these findings as the evidence was limited by the number of studies, lack of peer review and risk of bias in the retrospective studies. Peer-reviewed longer-term prospective studies are needed.

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