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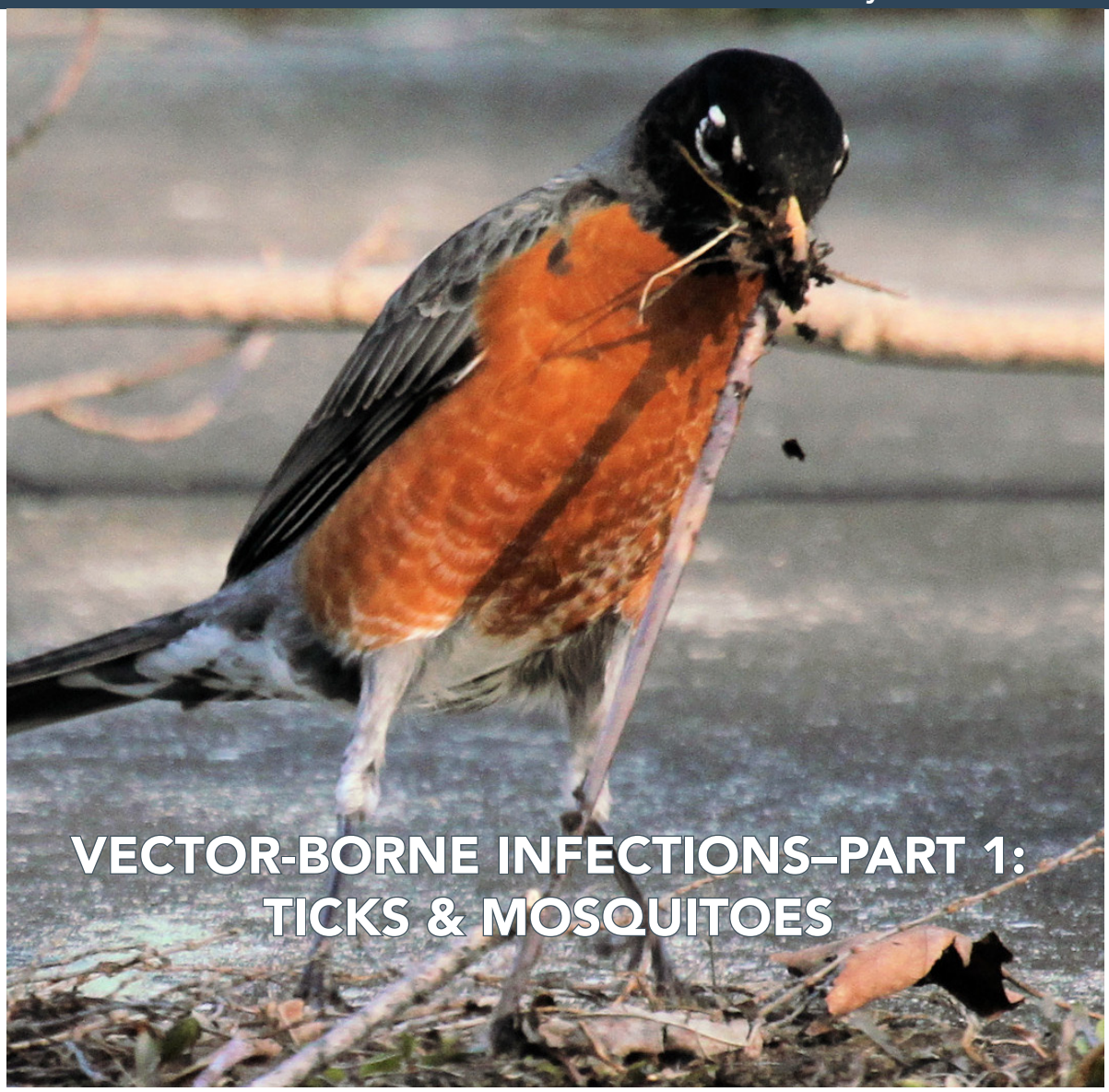

VECTOR-BORNE INFECTIONS–PART 1: TICKS & MOSQUITOES

GUEST EDITOR: ROBBIN LINDSAY

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CANADA COMMUNICABLE DISEASE REPORT

The *Canada Communicable Disease Report* (CCDR) is a bilingual, peer-reviewed, open-access, online scientific journal published by the Public Health Agency of Canada (PHAC). It provides timely, authoritative and practical information on infectious diseases to clinicians, public health professionals, and policy-makers to inform policy, program development and practice.

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The cover photo is of an American Robin pulling a worm. American Robins are important reservoires for West Nile virus. This image was taken by Dr. Ian Barker, Formerly of the Ontario Veterinary College.

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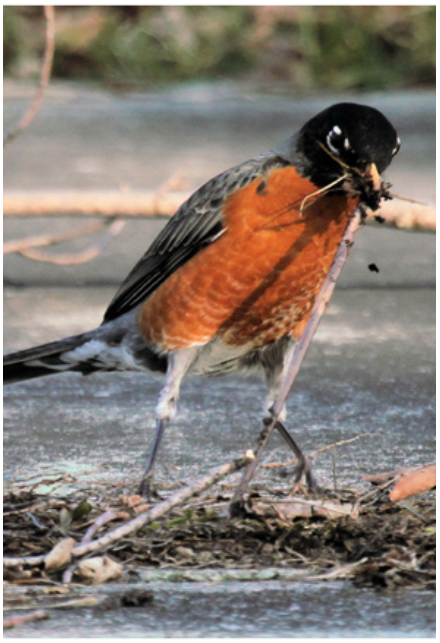
VECTOR-BORNE INFECTIONS: TICKS & MOSQUITOES



Guest Editor:
Robbin Lindsay has been a research scientist within the Public Health Agency of Canada at the National Microbiology Laboratory in Winnipeg since 1998. He is the Chief of the Field Studies section of the newly form One Health section of the Research Science and Surveillance division. The focus of his work has been on reference diagnostics, laboratory and field-based surveillance and research on various zoonotic disease agents including tick-borne infections like Lyme disease; mosquito-borne infections such as West Nile virus and Zika virus, and rodent-borne zoonosis like hantavirus pulmonary syndrome and tularemia. Robbin trained to become a medical entomologist during his Masters at the University of Manitoba and his subsequent PhD from the University of Guelph.

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OVERVIEW

An overview of the National West Nile Virus Surveillance System in Canada: A One Health approach

Dobrila Todoric[1]*, Linda Vrbova[1], Maria Elizabeth Mitri[1], Salima Gasmi[1], Angelica Stewart[1], Sandra Connors[1], Hui Zheng[1], Annie-Claude Bourgeois[1], Michael Drebot[2], Julie Paré[3], Marnie Zimmer[4], Peter Buck[1]

Abstract

National West Nile virus (WNV) surveillance was established in partnership with the federal, provincial and territorial governments starting in 2000, with the aim to monitor the emergence and subsequent spread of WNV disease in Canada. As the disease emerged, national WNV surveillance continued to focus on early detection of WNV disease outbreaks in different parts of the country. In Canada, the WNV transmission season occurs from May to November. During the season, the system adopts a One Health approach to collect, integrate, analyze and disseminate national surveillance data on human, mosquito, bird and other animal cases. Weekly and annual reports are available to the public, provincial/territorial health authorities, and other federal partners to provide an ongoing national overview of WNV infections in Canada. While national surveillance allows a jurisdiction-by-jurisdiction comparison of data, it also helps to guide appropriate disease prevention strategies such as education and awareness campaigns at the national level. This paper aims to describe both the establishment and the current structure of national WNV surveillance in Canada.

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Introduction

West Nile virus (WNV) was first isolated in 1937 from the blood of a febrile patient in the West Nile district of Uganda (1). Since its first discovery, it has spread through Africa, the Middle East, Asia, southern Europe, Oceania and, more recently, the Western Hemisphere (2). In North America, the virus was first detected in New York City in late August of 1999 (3) during an outbreak of meningoencephalitis. This outbreak was the first recognized introduction of WNV into North America.

West Nile virus belongs to a family of viruses called Flaviviridae. The virus is typically maintained in a mosquito-bird enzootic transmission cycle and is transmitted to humans and other mammals by the bite of an infected female mosquito. West Nile virus is primarily transmitted by the *Culex* species of mosquitoes in Canada, with principal vectors being *Culex pipiens* and *Culex tarsalis* (1). The *Culex* mosquitoes that are implicated in this cycle feed exclusively on avian blood and are referred to as amplification vectors, while the *Aedes* and *Ochleratus* mosquitoes and other *Culex* species that transmit WNV to humans, horses and non-avian vertebrates have more general feeding habits and are referred as bridge vectors (4). Humans and other mammals are considered dead-end hosts as they are unable to transmit the disease due to insufficient viremia. Although WNV is primarily a mosquito-borne disease, transmission of WNV to humans via blood transfusion and tissue and organ transplantation has also been reported on rare occasions (5).

In human WNV infections, 70% to 80% of people remain asymptomatic (1). Symptomatic individuals may experience a range of signs and symptoms including fever; however, fewer than 1% will develop severe neurological manifestations, including meningitis and encephalitis (1). The overall case fatality rate in patients that develop neurological manifestations is 4% to

14%, with a higher rate in older populations (1). Currently, there is no WNV vaccine for humans, and prevention of transmission depends on the use of personal protective measures and sustained vector control.

The objective of this article is to describe the establishment and structure of national WNV surveillance in Canada (6). This is a system that has adopted a One Health approach in connecting partners as well as integrating surveillance data, given the interconnectedness of human health with that of animals and the environment. The description covers the four main system components: human surveillance; mosquito surveillance; dead bird surveillance; and animal surveillance.

National West Nile Virus Surveillance in Canada

Establishment of the surveillance system

Following the incursion of WNV in and around New York City, and given its close geographic proximity to Canada, the Laboratory Centre for Disease Control, Health Canada and the Council of Chief Medical Officers of Health created a National Steering Committee (NSC) in late winter 2000. The principal mandate of the NSC was to develop pan-Canadian surveillance guidelines that could assist with detection and response to the virus in Canada. The committee was composed of representatives from other government and non-government departments: the Canadian Food Inspection Agency, Canadian Wildlife Health Cooperative (CWHC) and provincial/territorial human and animal health partners. The NSC agreed to develop a surveillance system to track and monitor WNV across Canada that closely followed a template employed by the United States (7) that set out the guidelines on criteria for disease surveillance, prevention, education and vector control (8). In September 2004, the Public Health Agency of Canada (PHAC) was established in response to growing concerns regarding Canada's public health system (9); in December 2006, the NSC was confirmed as a legal entity by the *Public Health Agency of Canada Act*. As such, the WNV surveillance system, previously under Health Canada, moved to PHAC.

Dead bird surveillance in Canada started in 2000 and was conducted from the Atlantic provinces to Saskatchewan; no evidence of WNV activity was detected that year. West Nile virus was first reported in Canada in the municipality of Windsor, Ontario, in August 2001 (10); the virus was detected in the wild bird population. Dead corvids, including species such as ravens, jays and crows, are known to be reliable indicators of WNV activity in a given geographical area (10). Subsequently, 12 health units across southern Ontario reported 128 WNV-infected wild birds during the 2001 transmission season. The movement of WNV from the United States to Canada has been linked to the migration of birds (10). Likewise, it has been suggested that the westward movement of WNV across Canada is largely associated with the flight routes of migratory birds (11). Dispersion of the virus in Canada in 2001 was correlated with some of the notable flyways of migratory birds which include the Atlantic, Mississippi, Central and Pacific flyways (11).

During 2000 and 2001, parts of Atlantic Canada, Ontario and Québec surveyed adult and larval mosquito populations to determine the presence/absence of mosquito populations in selected rural and peri-urban locations (12). On August 31, 2001, Ontario isolated WNV from *Culex pipiens/restuans* mosquito pools (12). Mosquito pool surveillance started in 2002, with an aim to obtain baseline information on the number of mosquito species present and their relative abundance in a given area.

The first human cases of WNV in Canada were detected in Québec and Ontario in August 2002. Also, during that same year, the first cases of WNV infections in equine populations were reported in Saskatchewan, Manitoba, Ontario and Québec.

Evolution of the surveillance system

In June 2003, WNV became a nationally-notifiable human disease. Since 2003, WNV human infection has been a reportable disease in the provinces and territories. As a result, when a probable or confirmed case is diagnosed by a laboratory, it must be reported to the local public health authority in the respective jurisdiction; however, reporting at the national level is maintained only on a voluntary basis.

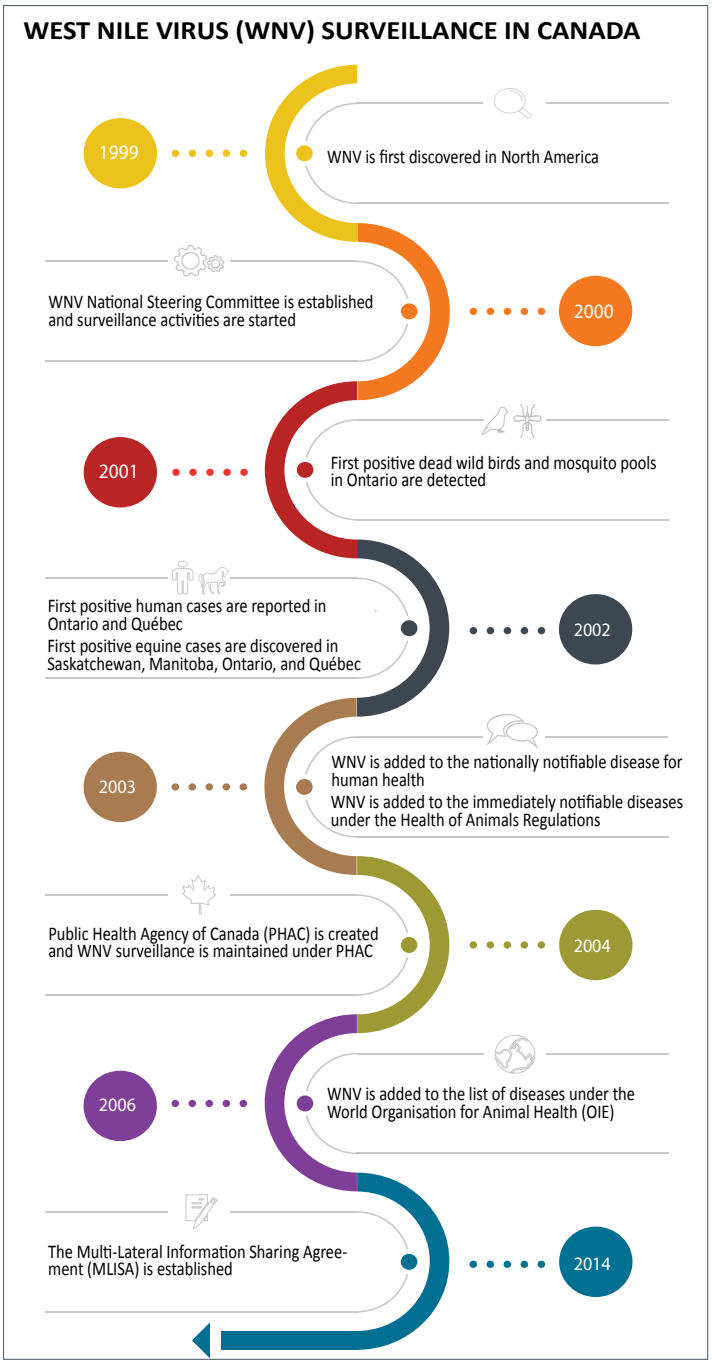
The WNV surveillance system quickly evolved into a multi-species surveillance system focusing on human, dead bird, mosquito and animal data (**Figure 1**). Initially, dead bird surveillance proved to be an efficient early predictor of where human cases could occur. Dead bird surveillance was particularly useful in the detection of new areas with WNV activity as the virus was introduced into and spread across Canada; however, this type of surveillance became less useful as the virus became established. As such, many jurisdictions eventually turned their efforts to mosquito pool testing, which provides a more specific indication of spatial and temporal risk for human infection.

A multi-species surveillance system for WNV was important since the interaction of bird populations and mosquitoes is integral to the dynamics of WNV transmission and infection. Furthermore, different vectors have specific transmission efficiencies that might trigger localized outbreaks of WNV (13). Over the years, the surveillance system has undergone reviews and updates, including on elements such as the national case definition (14) and reporting practices. Considering the complexity of the WNV transmission cycle, a One Health approach (15) was implemented to enhance understanding of species involved and develop an effective and sensitive surveillance system. Over time, the system and its purpose evolved to the following objectives that guide the national WNV surveillance system:

- To track WNV disease and describe national trends and burden of disease in humans

- To monitor changes in WNV carrying mosquito populations and other non-human vertebrate hosts each week in advance of epidemic activity affecting humans
- To provide timely information (e.g. weekly surveillance reports) on WNV across all provinces/territories that informs the development of public health messaging to prevent human infections
- Work carried out at the local-level (i.e. public health units), regional-level and national-level complies with global regulations such as meeting the 2005 International Health Regulations obligations (16).

Figure 1: National West Nile Virus Surveillance System timeline in Canada



The WNV surveillance system comprises four components: 1) human surveillance; 2) mosquito surveillance; 3) dead bird surveillance; and 4) animal surveillance.

Human surveillance

Human surveillance of WNV is a passive case-based system. Human cases are reported voluntarily (i.e. no legal obligation) to PHAC by provincial or territorial public health authorities. Canadian Blood Services/Héma-Québec participate in the surveillance system via provincial health authorities, by testing for WNV in donations collected from Canadian blood donors (17–19). At the national-level, human case data are reported to PHAC during the WNV season, from June to November; however, at the provincial and regional levels, data are collected on a year-round basis.

Key variables collected include age, sex, disease onset date, case classification (probable and confirmed) and clinical status (asymptomatic, non-neurological and neurological). Health authorities at the provincial-level perform laboratory testing related to the WNV infections.

Mosquito surveillance

The aim of mosquito surveillance is to help detect proximal risk of WNV in a specific region, so proactive measures can be taken. West Nile virus risk varies across Canada; as a result, the mosquito pool surveillance is conducted in some jurisdictions and not others. During 2001, WNV activity in mosquitoes was detected in Saskatchewan, Manitoba, Ontario, Québec and Nova Scotia, and intensified surveillance was put in place for mosquito pool testing (12). Over the years, the amount of mosquito surveillance has fluctuated and currently, four provincial partners—Saskatchewan, Manitoba, Ontario and Québec—conduct active mosquito surveillance. Mosquito pool testing for WNV occurs from June to November and data are shared by provincial partners on a weekly basis.

Mosquitoes are trapped by using a variety of techniques. The trapping is carried out weekly at fixed and mobile (changed based on current season) sites that represent the most likely WNV mosquito vector habitat in that specific community (20). Some of the traps used are to sample host-seeking mosquitoes. The most commonly used traps are based on the Centers for Disease Control and Prevention (CDC) miniature light trap that use carbon dioxide (CO_2) as an additional attractant (20). The main advantage of the CDC miniature light trap is that it attracts a wide range of mosquito species. Another common trap is the gravid trap that specifically targets gravid females—mosquitoes carrying mature eggs. The advantage of gravid traps is that they attract female mosquitoes who already took a blood meal, increasing the prospect of detecting WNV in the specific region where the sampling is occurring (20). In addition to the CDC miniature light traps and gravid traps, there are several other traps that can be used such as the CDC resting trap, which uses aspirators, and host-baited traps (20).

Dead bird surveillance

Dead bird surveillance consists of testing dead wild birds for WNV in jurisdictions across Canada. The information obtained from this passive surveillance serves as an early indicator of viral activity in the natural reservoir host of this virus, and thus the potential to spread to mosquitoes, humans and other animals (21).

In 2000, the CWHC (21), formerly known as Canadian Cooperative Wildlife Health Centre, started dead bird surveillance and *post mortem* testing on birds across Canada. Since 2009, approximately 300 birds are tested each year for WNV (21); however, the annual amount of wild bird testing is influenced by the severity of the WNV season. The CWHC tests dead birds for WNV from late April until the first hard frost.

Animal surveillance

Under the *Health of Animals Regulations*, WNV has been an immediately notifiable disease in animals since 2003. All veterinary laboratories in Canada are required to report suspect or confirmed WNV cases in all animal species to the Canadian Food Inspection Agency. In horses, the case definition is based on clinical signs and laboratory diagnostic results (22). West Nile virus surveillance assists with export certification, meeting international reporting obligations to the World Animal Health Organisation and informing public health on possible risk areas. Furthermore, among domestic animals, horses are susceptible to encephalitis related to WNV infection and can therefore serve as indicators of viral activity in rural communities (7) and provide national insight on the epidemiology of WNV in Canada (23). The Canadian Food Inspection Agency shares surveillance data with PHAC's Canadian WNV surveillance system on a weekly basis during the WNV season (22). It includes mostly equine cases of WNV, but occasionally other mammals (alpacas, sheep and goats), domestic birds and poultry, and some zoo animals. Because testing is owner-requested and funded, wildlife cases are mostly unavailable. Equine WNV surveillance data, which is the most consistently reported, is leveraged to help address gaps in environmental surveillance for geographical regions where mosquito and bird surveillance are not currently in place (7,23) and can provide complementary coverage in areas where no human cases have been diagnosed. Since horses can be vaccinated against WNV and the frequency of vaccination is variable, the surveillance numbers are likely an underreporting of actual infections.

Evolution of laboratory diagnostics for West Nile virus surveillance

Laboratory diagnostics are out of the scope of this paper; however, it is important to mention that currently there are several laboratory diagnostic procedures available for documenting WNV cases. Laboratory diagnostics can be divided into the following three categories: virus isolation/culture; serological assays for detecting viral specific antibodies; and WNV antigen detection/nucleic acid sequence-based amplification (7). The advancement from immunohistochemistry-immunofluorescence assay to nucleic acid sequence-based amplification is a notable evolution in the laboratory methodology for the detection of WNV in various field collected specimens (e.g. bird tissues) from the early years of WNV surveillance. Polymerase chain reaction-based testing continues to be the procedure of choice for detection of WNV-positive mosquito pools. These advancements allowed for the technical transfer of molecular procedures to testing sites outside of the National Microbiology Laboratory in Winnipeg, Manitoba. Further refinements and availability of commercial IgM enzyme-linked immunoassay (ELISA) tests for screening human sera for WNV antibodies was a major contributor to higher throughput screening of samples from suspect cases of virus infection.

Collaboration to knowledge translation

To coordinate surveillance at the national-level, collaboration is needed between various federal/provincial/territorial partners and non-governmental organizations. During the WNV surveillance season, data on human cases, animal cases and positive mosquito pools are submitted directly to PHAC by participating provincial/territorial governments on a weekly basis. Data reported to PHAC between 2002 and present day are stored in a database before being analyzed and disseminated through various channels (**Figure 2**).

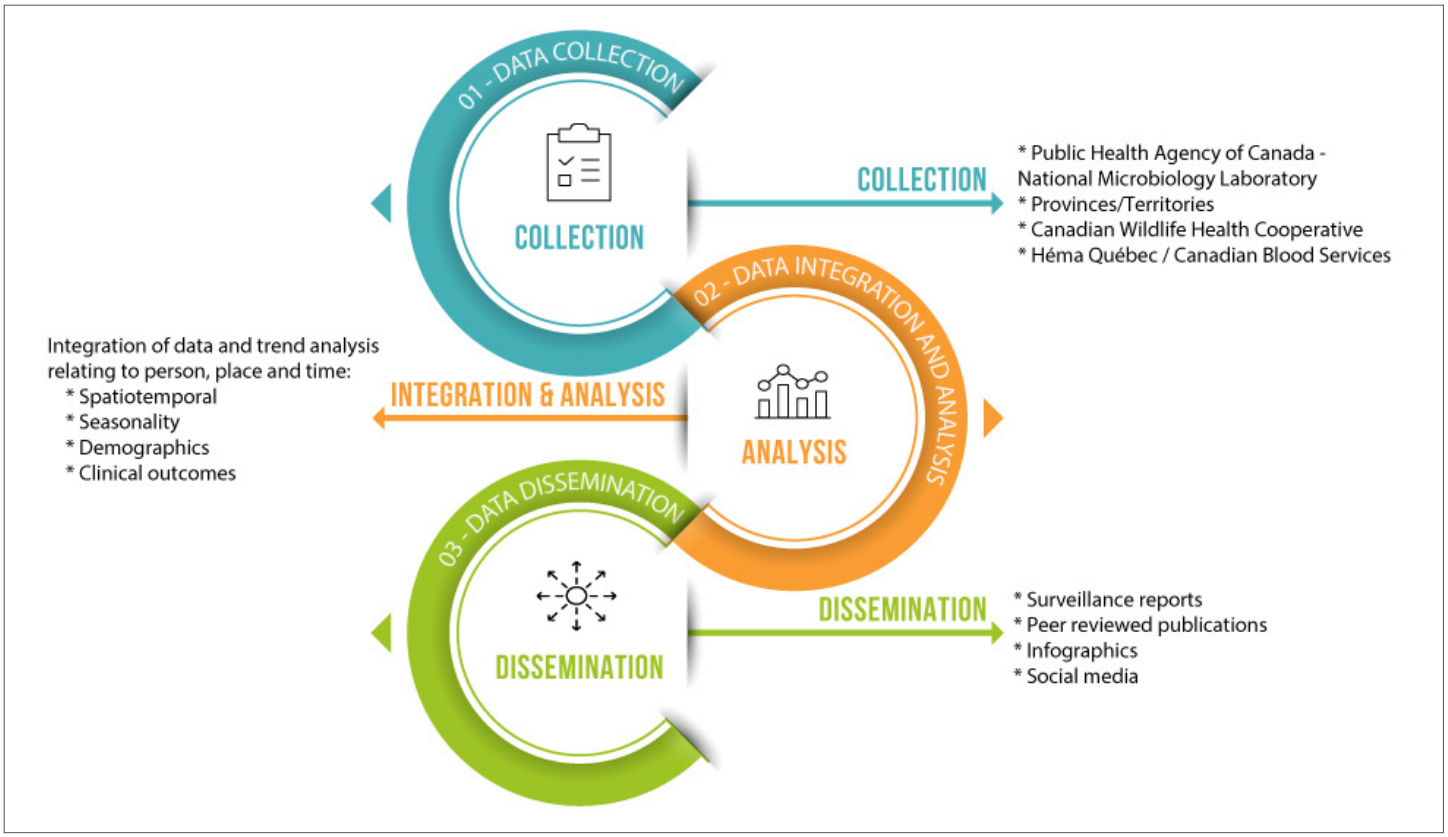
Multi-Lateral Information Sharing Agreement

In 2014, the federal/provincial/territorial Multi-Lateral Information Sharing Agreement (MLISA) (24) was completed to address some of the information sharing challenges between provincial/territorial public health data contributors and surveillance programs at the national level. The Agency worked closely with the Pan-Canadian Public Health Network's National Surveillance Information Task Group to develop this agreement. While continuing to respect the existing legislation within jurisdictions, MLISA outlines when, what, and how infectious disease and emerging public health event information will be shared between and among jurisdictions (24). The WNV surveillance system complies with the regulations in the main clauses of the MLISA. These clauses include regulations ensuring that a review period is provided to key partners and stakeholders, as well as custodians of the data, to comment on various surveillance products and publications before being released into the public domain.

Knowledge translation and public awareness campaigns

Data from WNV surveillance inform policy decisions and awareness campaigns that contribute to the reduction of WNV disease in Canada. Some of these efforts include public health messaging through various social media platforms, and digital signage on Service Canada/Passport Centre screens. In addition, weekly surveillance reports and annual surveillance reports are posted on the Government of Canada website (25) for public access along with periodic publications in the *Canada*

Figure 2: Flow of information for the National West Nile Virus Surveillance System



Communicable Disease Report or other scientific peer-reviewed journals.

In First Nations communities, First Nations and Inuit Health Branch regional staff advise Chiefs, councils and federal departments on emerging needs for WNV public health control measures. First Nations residents obtain information about specific WNV activity in their community through their assigned Environmental Public Health Officers, Community Health Centre and/or Nursing Stations. This includes information on surveillance activities and case counts.

Along with local and provincial/territorial information that is released to the public, information on WNV prevention (including handling of dead wild birds) and WNV risk, symptoms and treatment is publicly available on www.canada.ca. The Agency also provides information to health professionals on WNV clinical assessment, diagnosis and prognosis.

Future opportunities

When establishing the WNV surveillance system in Canada, a One Health approach evolved to respond to the inherent complexities of this emerging disease and its transmission dynamics. The integrated surveillance approach provides a template for surveillance systems on other mosquito-borne diseases such as Bunyaviruses, including the California serogroup (Jamestown Canyon and Snowshoe hare virus) and Cache valley viruses (26) in Canada. Furthermore, the COVID-19 pandemic has underscored the importance of having effective surveillance systems in place to deal with emerging diseases.

Conclusion

The Canadian WNV surveillance system is based on a collaboration of federal/provincial/territorial partners involved in public and animal health. This integrated surveillance initiative is an example of One Health—a collaborative approach that engages an array of partners for the collection and analysis of information on WNV activity in humans, mosquitoes, wild birds and horses. The goal of the system is to reduce the risk of WNV infection in the human population and contribute to increased awareness of preventative measures. The WNV surveillance system meets the 2005 *International Health Regulations* obligations. The Public Health Agency of Canada, in collaboration with key partners, will continue to adapt and respond to the evolving nature of WNV and other mosquito-borne diseases.

Authors' statement

DT — Co-conceived manuscript idea, acquired information, researched and drafted the manuscript
MM, ACB, HZ — Co-conceived manuscript idea, participated in information acquisition and edited the manuscript
SG — Validated references and edited the manuscript
AS — Contributed to the manuscript draft, validated information and reviewed
SC — Created figures and validated information
MD — Contributed to the manuscript, validated information and reviewed
JP — Contributed to the manuscript, validated information and reviewed
MZ — Validated information and reviewed
LV, PB — Validated information, reviewed and edited the manuscript

Competing interests

None.

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References

1. Public Health Agency of Canada. Pathogen Safety Data Sheets: Infectious Substances - West Nile Virus (WNV). Ottawa (ON): PHAC; (updated 2018; accessed 2020-05-05). https://www.canada.ca/en/public-health/services/laboratory-biosafety-biosecurity/pathogen-safety-data-sheets-risk-assessment/west-nile-virus.html

2. Infection Prevention and Control Canada. West Nile Virus Resources. Winnipeg (MB); IPAC Canada (accessed 2020-05-05). https://ipac-canada.org/west-nile-virus-resources.php

3. Nash D, Mostashari F, Fine A, Miller J, O'Leary D, Murray K, Huang A, Rosenberg A, Greenberg A, Sherman M, Wong S, Layton M; 1999 West Nile Outbreak Response Working Group. The outbreak of West Nile virus infection in the New York City area in 1999. N Engl J Med 2001;344(24):1807–14. DOI PubMed

4. Blitvich BJ. Transmission dynamics and changing epidemiology of West Nile virus. Anim Health Res Rev 2008;9(1):71–86. DOI PubMed

5. Public Health Agency of Canada. Management of Patients with West Nile Virus: Guideline for Health Care Providers. Can Commun Dis Rep. 2005:3IS4:1-10. https://publications.gc.ca/collections/Collection/HP3-3-31S3E.pdf

6. Public Health Agency of Canada. Surveillance of West Nile virus. Ottawa (ON): PHAC; (updated 2022; accessed 2020-04-05). https://www.canada.ca/en/public-health/services/diseases/west-nile-virus/surveillance-west-nile-virus.html

7. Centers for Disease Control and Prevention. West Nile virus. Surveillance Resources. Atlanta (GA): CDC; 2021 (accessed 2021-08-13). https://www.cdc.gov/westnile/resourcepages/survResources.html

8. Drebot MA, Lindsay R, Barker IK, Buck PA, Fearon M, Hunter F, Sockett P, Artsob H. West Nile virus surveillance and diagnostics: A Canadian perspective. Can J Infect Dis 2003;14(2):105–14. DOI PubMed

9. Public Health Agency of Canada. History. Ottawa (ON): PHAC; (updated 2008; accessed 2020-02-03). https://www.canada.ca/en/public-health/corporate/mandate/about-agency/history.html

10. Venter A. West Nile virus reaches Canada. Trends Microbiol 2001;9(10):469. DOI PubMed

11. Gubler DJ. The continuing spread of West Nile virus in the western hemisphere. Clin Infect Dis 2007;45(8):1039–46. DOI PubMed

12. Giordano BV, Kaur S, Hunter FF. West Nile virus in Ontario, Canada: A twelve-year analysis of human case prevalence, mosquito surveillance, and climate data. PLoS One 2017;12(8):e0183568. DOI PubMed

13. Cruz-Pacheco G, Esteva L, Vargas C. Seasonality and outbreaks in West Nile virus infection. Bull Math Biol 2009;71(6):1378–93. DOI PubMed

14. Public Health Agency of Canada. National Case Definition: West Nile virus. Ottawa (ON): PHAC; 2008 (accessed 2021-05-05). https://www.canada.ca/en/public-health/services/diseases/west-nile-virus/health-professionals-treating-west-nile-virus/national-case-definition.html

15. World Health Organization. One Health. Geneva (CH): WHO; 2017 (accessed 2020-04-08). https://www.who.int/features/qa/one-health/en/

16. World Health Organization. Europe. International Health Regulations. Brussels (BE); WHO Europe; 2005 (accessed 2020-04-05). https://www.who.int/ihr/finalversion9Nov07.pdf

17. Cameron C, Reeves J, Antonishyn N, Tilley P, Alport T, Eurich B, Towns D, Lane D, Saldanha J. West Nile virus in Canadian blood donors. Transfusion 2005;45(4):487–91. DOI PubMed

18. O'Brien SF, Scalia V, Zuber E, Hawes G, Alport EC, Goldman M, Fearon MA. West Nile virus in 2006 and 2007: the Canadian Blood Services' experience. Transfusion 2010;50(5):1118–25. DOI PubMed

19. Canadian Blood Services. Transfusion: Clinical Guide. Chapter 6. Donor selection, donor testing and pathogen reduction (accessed 2021-08-13). https://professionaleducation.blood.ca/en/transfusion/clinical-guide/donor-selection-donor-testing-and-pathogen-reduction

20. Centres for Disease Control and Prevention. Division of Vector-Borne Diseases. West Nile Virus in the United States: Guidelines for Surveillance, Prevention and Control. Atlanta (GA): CDC; 2013 (accessed 2020-09-21). https://www.cdc.gov/westnile/resources/pdfs/wnvGuidelines.pdf

21. Canadian Wildlife Health Cooperative. West Nile Virus (accessed 2020-09-21). http://www.cwhc-rcsf.ca/wnv.php

22. Canadian Food Inspection Agency. West Nile Virus Fact Sheet. Ottawa (ON): CFIA; (updated 2018; accessed 2020-04-06). https://www.inspection.gc.ca/animal-health/terrestrial-animals/diseases/immediately-notifiable/west-nile-virus/fact-sheet/eng/1305853043399/1305853235540

23. Levasseur A, Arsenault J, Paré J. Surveillance of West Nile virus in horses in Canada: A retrospective study of cases reported to the Canadian Food Inspection Agency from 2003 to 2019. Can Vet J 2021;62(5):469–76. PubMed

24. Pan-Canadian Public Health Network. Blueprint for a Federated System for Public Health Surveillance in Canada. PHN; (updated 2017; accessed 2020-04-05). http://www.phn-rsp.ca/pubs/bfsph-psfsp-2016/index-eng.php

25. Public Health Agency of Canada. West Nile virus surveillance and monitoring. Ottawa (ON): PHAC; (updated 2021). https://www.canada.ca/en/public-health/services/diseases/west-nile-virus/surveillance-west-nile-virus/west-nile-virus-weekly-surveillance-monitoring.html

26. Drebot MA. Emerging mosquito-borne bunyaviruses in Canada. Can Commun Dis Rep 2015;41(6):117–23. DOI PubMed

Identification of an unusual cluster of human granulocytic anaplasmosis in the Estrie region, Québec, Canada in 2021

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Abstract

Background: Human granulocytic anaplasmosis (HGA) is a potentially severe tick-borne infection caused by the bacterium *Anaplasma phagocytophilum* (*A. phagocytophilum*) of the genus Rickettsia. Here, we describe the epidemiological and clinical characteristics of an unusual cluster of HGA cases detected in the Estrie region in Québec, Canada, during the 2021 transmission season.

Methods: Confirmed cases of HGA were defined as individuals with typical clinical manifestations and a positive polymerase chain reaction assay. The cases were interviewed using a structured questionnaire and clinical data was obtained from medical records.

Results: A total of 25 confirmed cases were identified during the 2021 transmission season, thus constituting the largest known cluster of HGA in Canada. The most common symptoms reported were fever, fatigue and headaches. Laboratory investigations found that 20 (80%) of the patients had thrombocytopenia and 18 (72%) had leukopenia at presentation. Almost half of the patients required hospitalization (n=11, 44%), with a median duration of four days (interquartile range [IQR] 2.5–5 days), including one patient who required intensive care. No deaths were recorded during the study. Epidemiological investigation found that all cases were domestically acquired, and yard maintenance was the most prevalent at-risk activity identified. Only seven (28%) cases had been aware of a tick bite in the previous two weeks.

Conclusion: Detection of this unusual cluster of HGA cases provides further evidence that *A. phagocytophilum* may now be established along the southern border of Québec. Clinicians should consider HGA when assessing patients with typical symptoms and recent exposure to high-risk environments for tick bite.

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Keywords: *Anaplasma phagocytophilum*, human granulocytic anaplasmosis, tick-borne disease, zoonosis

Introduction

Human granulocytic anaplasmosis (HGA) is a tick-borne infection caused by the bacterium *Anaplasma phagocytophilum* (*A. phagocytophilum*) of the genus Rickettsia. In Northeastern America, the main vector of the disease is Ixodes scapularis (1), commonly known as the blacklegged tick, that also transmits *Borrelia burgdorferi*, the causative agent for Lyme disease (LD). Individuals usually develop nonspecific symptoms such as fever, chills, myalgias, malaise, severe headaches and gastrointestinal symptoms one to two weeks after exposure (2). While the illness can be severe and possibly life threatening if left untreated, antimicrobial treatment generally leads to resolution of symptoms within 48 hours (3).

Human granulocytic anaplasmosis is primarily endemic in the upper Midwestern and Northeastern United States (4), but *A. phagocytophilum* has been detected in tick populations of all Canadian provinces in recent years. Nonetheless, data on HGA infections among humans in the Canadian context are

limited because Manitoba and Québec are the only provinces where HGA is a reportable disease. Between 2015 and 2019, 37 confirmed cases were reported in Manitoba (5). In Québec, three confirmed cases have been reported to public health since the disease became subject to mandatory reporting for laboratories in 2019. This included one case in the Estrie region, which is located along the southern border of eastern Québec (*personal communication, Institut national de santé publique du Québec* [*INSPQ*]). Here, we describe the epidemiological and clinical characteristics of an unusual cluster of HGA infections reported in the Estrie region during the 2021 transmission season.

Methods

Study setting, population, and design

We conducted a retrospective case series analysis in the Estrie region, Québec, Canada that has a total population of 489,479 (6). This region accounts for the majority of LD cases in the province and shares its southern border with three of the eight states in the United States with the highest incidence of HGA: Vermont; New Hampshire; and Maine (4). Our study sample included all confirmed cases of anaplasmosis in this region from May 1, 2021, to November 20, 2021. A confirmed HGA case was defined as an individual with typical clinical manifestations and a positive polymerase chain reaction (PCR) assay (7). As anaplasmosis is a notifiable disease in Québec, the list of patients with positive PCR results was extracted from the regional notifiable diseases database of the *Direction de la santé publique de l'Estrie*.

Laboratory methods for detection of tick-borne infections

All the diagnostic and confirmatory microbiological tests for *Anaplasma phagocytophlum* and other potential coinfections were performed either at the National Microbiology *Laboratory in Winnipeg, Manitoba, at the Laboratoire de santé publique du Québec* in Sainte-Anne de Bellevue, Québec, or at the National Reference Center for Parasitology in Montréal, Québec. Detailed laboratory testing methods are available in **Annex**.

Data collection

One infectious disease fellow and one field epidemiologist in collaboration with the Communicable Disease team at the *Direction de la santé publique de l'Estrie*, performed chart reviews in three different acute care hospitals within the *Centre intégré universitaire de santé et service sociaux de l'Estrie – Centre hospitalier universitaire de Sherbrooke* (*CIUSSS de l'Estrie – CHUS*), where the confirmed cases were evaluated and treated. A standardized data abstraction form, which was developed by our research team after an initial literature review and pre-tested on one patient, was used for data collection. Past medical history was collected to calculate the Charlson Comorbidity Index (8), along with demographic, microbiological, and treatment data. Data on symptoms, clinical signs, and laboratory findings were also collected. A standardized questionnaire to assess history of tick bite and possible exposure sources, including the location, the activities undertaken and their frequency, was built and all patients underwent a phone interview. Activities undertaken by the cases in the two weeks prior to symptom onset were considered at-risk if they took place in an area known to be endemic for LD and the environment was suitable for ticks (e.g. grassy, brushy or wooded areas). If a case practiced multiple at-risk activities during the time period, all activities were included in the descriptive analysis.

Geographic information and data visualization

Spatial data was uploaded to a geographic information software (QGIS 3.10.9) to develop a map of the location of residence of cases.

Statistical analysis

Data cleaning and descriptive analyses were performed using Excel 2016 and Stata version 15.1 (StataCorp, College Station, Texas, United States).

Ethics approval

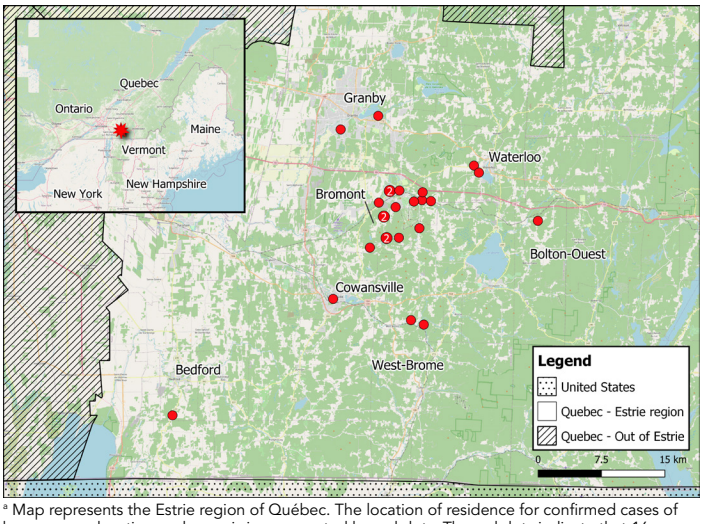
The *Comité d'éthique clinique et organisationnelle* (institutional review board) of the CIUSSS de l'Estrie-CHUS approved this study (Project #2022-4465).

Results

During the study period, 25 confirmed cases were identified in the Estrie region (**Figure 1**). The patients' demographic and clinical characteristics are summarized in **Table 1**. The majority of cases were male (n=15, 60%) and the median age was 65 years. All cases were either permanent or seasonal residents of the regions of La Pommeraie or Haute-Yamaska at the time of exposure, with a majority of cases residing in the town of Bromont (n=16, 64%). None of the cases reported out-of-province travel in the previous two months. The activity most often reported by cases was yard maintenance (n=22, 88%), which included gardening, lawn mowing and wood chopping. Additionally, 48% (n=12) of the cases reported outdoor recreational activities such as walking, mountain biking and shooting practice, whereas five (20%) cases reported potential exposure while taking care of farm animals or visiting a farm. Overall, 28% (n=7) of the cases had observed a tick attached to their skin in the two weeks prior to symptom onset

Most patients developed symptoms in either June (n=9) or July (n=11) (**Figure 2**). All cases experienced fever and reported symptoms such as fatigue (n=24; 96%), headaches (n=22; 88%), myalgia (n=20; 80%) and sweating (n=17; 68%). A significant proportion of patients presented gastrointestinal symptoms such as vomiting (n=11; 44%), diarrhea (n=9; 36%) and abdominal pain (n=8; 32%). Two cases (8%) reported a

Figure 1: Location of residence of confirmed cases of human granulocytic anaplasmosis in the Estrie region[a], 2021



[a] Map represents the Estrie region of Québec. The location of residence for confirmed cases of human granulocytic anaplasmosis is represented by red dots. The red dots indicate that 16 cases are located in proximity to the town of Bromont. The other municipalities included in the map are Bedford, Bolton-Ouest, Cowansville, Granby, Waterloo and West-Brome, with one or two confirmed cases residing in each

Table 1: Characteristics of confirmed human granulocytic anaplasmosis cases

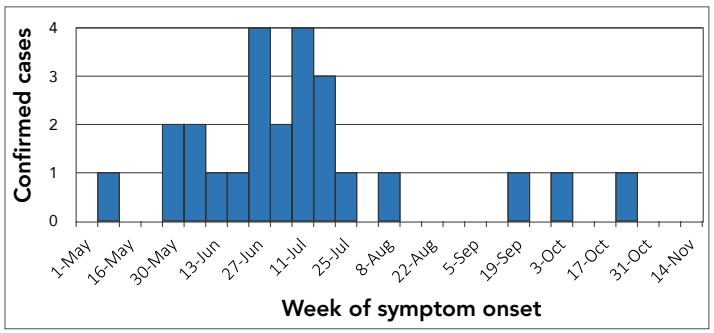
Characteristic	n=25	
	n	%
Sex		
Female	10	40
Male	15	60
Age		
Years, median (IQR)	65	53–70
Municipality of residence		
Bedford	1	4
West Bolton	1	4
Bromont	16	64
Cowansville	1	4
Granby	2	8
Waterloo	2	8
West Brome	2	8
At-risk activities reported[a]		
Yard maintenance	22	88
Outdoor recreational activity	12	48
Farm visit or animal care	5	20
Recent out-of-province travel	0	0
Tick bite ≤2 weeks preceding symptom onset	7	28
Charlson comorbidity index		
0	21	84
1	2	8
≥2	2	8

Table 1: Characteristics of confirmed human granulocytic anaplasmosis cases (*continued*)

Characteristic	n=25	
	n	%
Symptoms and clinical signs		
Fever[b]	25	100
Duration of fever in days (median [IQR])[c]	4	2–5
Sweating	17	68
Fatigue	24	96
Myalgia	20	80
Arthralgia	12	48
Vomiting	11	44
Diarrhea	9	36
Abdominal pain	8	32
Headache	22	88
Cough	5	20
Dyspnea	5	20
Erythema migrans	0	0
Nonspecific rash	2	8
Outcome		
Hospitalization	11	44
Duration of hospitalization in days (median [IQR])	4	2.5–5
Intensive care unit	1	4
Death	0	0
Immunosuppression[d]	3	12

Abbreviation: IQR, interquartile range
[a] Non-mutually exclusive categories
[b] 23 out of 25 patients had objective fever and two had subjective sensation of fever without measurement confirmation
[c] Data missing for two patients
[d] Two patients were using immunosuppressing drugs (one using ustekinumab and one using prednisone) and one patient had HIV (but virologically controlled and on antiretroviral therapy)

Figure 2: Confirmed cases of human granulocytic anaplasmosis in the Estrie region by week of symptom onset, Québec, 2021



rash; in both cases the rashes were less than 5 cm in diameter and, therefore, not characteristic of erythema migrans. The detailed hematologic and biochemical laboratory findings are listed in **Table 2**. The most frequent laboratory anomalies were leukopenia (n=18/25; 72%), thrombocytopenia (n=20/25; 80%) and mildly elevated alanine aminotransferase levels (n=14/24; 58%).

Table 2: Hematologic and biochemical laboratory findings

Hematologic and biochemical findings	n=25	
	Median	IQR
Leucocytes (1x10⁹/L)		
Count upon presentation	3.3	2.5–5.2
Lowest count	2.9	2.1–3.4
Neutrophiles (1x10⁹/L)		
Count upon presentation	2.4	1.4–3.9
Lowest count	1.4	0.9–1.7
Lymphocytes (1x10⁹/L)		
Count upon presentation	0.7	0.2–1.0
Lowest count	0.6	0.2–1.0
Highest count	2.5	1.5–3.7
Platelets (1x10⁹/L)		
Count upon presentation	114	72–141
Lowest count	76	61–123
Anemia[a] (n, [%])	9	36%
Alanine aminotransferase (IU/L)		
Upon presentation	61.5	36.8–122.8
Maximum value	80	58.5–224.5
C-reactive protein (mg/L)		
Upon presentation	82	35.5–171
Maximum value	94.5	35.8–184.5
Acute kidney injury[b]	3	12%

Abbreviation: IQR, interquartile range
[a] Anemia was defined as hemoglobin levels below 130 g/L for men and 120 g/L for women, as per local laboratory guidelines
[b] Acute kidney injury was defined as increase of ≥1.5 × compared to baseline creatinine or increase of ≥27 mmol/L over baseline creatinine

Almost half of the patients required hospitalization (n=11; 44%), with a median duration of 4 days (interquartile range [IQR] 2.5–5 days), including one patient who required intensive care. Hospitalized patients were slightly older than those who did not require hospitalization, but this difference was not statistically significant (67.0 vs 61.3 years old; p=0.2). None of the patients died during the study period. All patients were treated with doxycycline for a median duration of 14 days (IQR 14–16 days).

The findings of the diagnostic tests for anaplasmosis and other potential coinfections are listed in Table 3. *Anaplasma phagocytophilum* species serology (indirect immunofluorescence assay) was performed for 21 patients during the acute phase of infection and antibodies were detected in four patients. Convalescent-phase repeated testing was performed in two patients; none showed a four-fold increase in antibody titers. Interestingly, among patients with positive serology (n=4), the time between the start of symptoms and serology was significantly longer compared to patients with negative serology (median of 18.5 days vs 4.0 days), and an indeterminate serology result was obtained in a patient whose blood was drawn seven days after symptom onset. Three patients had peripheral smears showing morulae in the neutrophils in addition to positive PCR results. For other coinfections, 11 patients out of 23 tested positive using enzyme immunoassay (EIA) for Lyme serology, of whom seven were positive for isolated line blot IgM in the confirmatory test. The other four patients were positive for Lyme western blot IgG.

Table 3: Results from diagnostic tests for anaplasmosis and other potential coinfections

Pathogen	Diagnostic test (positive results/total tests performed)		
	Polymerase chain reaction	Serology	Blood smear
Anaplasma phagocytophilum	25/25	4/21[a]	3/4[b]
Borrelia burgdorferi	0/1	EIA: 11/23[c] Western blot IgG: 4/11 Line blot IgM[d]: 7/7	N/A
Babesia microti	0/19	0/14	0/18

Abbreviations: EIA, enzyme immunoassay; N/A, not applicable
[a] Dilution range: 1/64-1/2048
[b] Was found in two patients in routine blood smear
[c] EIA positive tests were sent for western blot IgG
[d] IgM line blot was performed only if the western blot IgG was negative

Discussion

This report describes the epidemiological and clinical features of a cluster of HGA cases in the Estrie region, located along the southern border of Québec. A total of 25 cases have been confirmed in 2021, thus constituting the largest reported cluster of confirmed HGA cases identified during a transmission season in Canada. Since the first reported case of HGA in Canada in 2009 (9), surveillance data shows that HGA seroprevalence has increased among the populations of Manitoba and Ontario (10,11). Nonetheless, an article describing three cases in Manitoba is the only other publicly available case series that describes a cluster of confirmed HGA cases in Canada (10).

Our data also provides further evidence that *A. phagocytophilum* may now be established in blacklegged tick populations in

the Estrie region, as previously indicated by acarological surveillance programs (12). These findings are also consistent with a recent study that suggests an expansion of the suitable geographic areas for tick reservoirs and hosts, such as mice and deer, resulting in the emergence of tick-borne diseases in new areas (13). Before 2021, only three confirmed cases of human anaplasmosis had been reported to public health in Québec, including one in the Estrie region (14).

In this study, most cases were observed in males, which is consistent with previous findings indicating that men are more likely to adopt behaviors that put them at risk of tick bites (15,16). Only four patients were younger than 50 years old; however, this could be partly due to an increased likelihood of asymptomatic infections among younger individuals. Yard maintenance was the most common at-risk activity reported by cases during their exposure period. This is consistent with similar finding by Porter et al., which found that yard work was the most common activity practiced during tick encounters in a sample of individuals who submitted ticks through a passive tick surveillance system in the Northeastern United States (17).

Most cases had nonspecific symptoms such as fever, headaches and fatigue. Digestive symptoms were also prevalent in our case series. Laboratory abnormalities, including leukopenia, thrombocytopenia and elevated hepatic transaminase levels, were present in majority of patients. These data are consistent with the clinical and paraclinical presentations reported recently (1,18). The proportion of hospitalized patients seen in our sample was marginally higher than that reported in the national surveillance data in the United States from 2008 to 2012 (44% vs 31%) (3); however, the higher hospitalization rates were probably because HGA is not yet a well-recognized disease in our region and physicians may be less likely to identify HGA in outpatient settings.

It has been reported that among patients with positive *Anaplasma phagocytophilum* serology, 4%–36% show positive serology for either *Borrelia burgdorferi* or *Babesia microti* (1). Interestingly, almost half of our patients had positive Lyme serology, but only two reported a nonspecific rash, which is not indicative of classic erythema migrans. Among those with positive EIA (n=11), four were positive for IgG (determined by western blot); this methodology was in line with the two-tier testing approach currently used in Canada. For those with positive EIA and negative IgG, IgM positivity was shown in all (using the line blot method). Although IgM titers are classically known to indicate a recent infection, there are limitations to the test. IgM can be falsely positive and can remain positive for months or years after the initial infection (1). Therefore, even if a high proportion of the patients in our case series were IgM positive, it is difficult to conclude that all patients had a coinfection, especially without the manifestation of erythema migrans. Convalescent serology would have helped the confirmation of early coinfection with LD if IgG developed afterward, but these results were not available at the time of manuscript submission. No coinfection with *Babesia microti* was diagnosed in our series; this was expected since this parasite is not commonly found in ticks in the region according to acarological surveillance programs (12).

Future directions

While HGA is a nationally reportable condition in the United States (19), it is only reported in the provinces of Manitoba and Québec in Canada. As suggested elsewhere (2,20), a nationally reportable disease status would improve epidemiologic monitoring, which is especially important in identifying other newly endemic areas. Mandatory reporting would also increase physician awareness of this emerging infection, facilitating early diagnosis and treatment. Early antimicrobial treatment of HGA is critical as it reduces the risk of severe complications and may be lifesaving for individuals at higher risk of death, such as immunocompromised and elderly patients (10). The adoption of multiplex tests for tick-borne diseases should also be considered to facilitate the identification of emerging pathogens in areas where LD is already endemic (21).

Improvements to current acarological surveillance strategies are also needed to preemptively identify regions where *A. phagocytophilum* is most likely to occur. This was highlighted in the conclusions of the federal framework on LD in Canada (14), which identified the development of a national tick-borne diseases surveillance system as a priority action item. This system would incorporate region-specific data on the distribution of vectors and the prevalence of disease-causing pathogens to improve the monitoring of the distribution of ticks capable of transmitting LD, HGA and other infections.

Furthermore, the primary prevention method for tick-borne diseases, including HGA, remains the adoption of preventive behaviors that reduce the risk of tick encounters. Existing LD health promotion efforts should be reinforced and, in regions where *A. phagocytophilum* has been detected, tailored to incorporate HGA. A multi-sectoral and multidisciplinary approach that involves both human and animal health stakeholders should also be emphasized to help identify prevention strategies that leverage the One Health approach, as well as to better understand the role of tick vectors, such as deer and mice, in the emergence of new risk areas for HGA (22).

Limitations of the study

Our study was limited by its observational design, as it included only cases reported to the public health department. Even if our definition of confirmed cases was based on a very specific and reliable assay (PCR), our data certainly underestimated the true burden of HGA in the region. Subclinical cases are likely to remain undetected and since this disease has only recently emerged in the area, physicians are likely to miss diagnoses due to lack of awareness. Another limitation of our study is that it was not possible to attribute the acquisition of HGA to a specific at-risk activity when multiple exposures took place in the two

weeks prior to symptom onset; therefore, all activities were listed.

Conclusion

Human granulocytic anaplasmosis is a growing public health concern in the southern regions of Québec, Canada. A reportable disease status should be considered by provincial and federal jurisdictions, and health promotion efforts that aim to reduce the risk of tick encounters should be reinforced. Clinicians should consider the possibility of HGA when assessing patients with fever, leukopenia, thrombocytopenia, elevated hepatic transaminase levels and recent exposure to high-risk environments for tick bites. The initiation of empiric treatment with doxycycline should be considered prior to reception of PCR testing results when those results cannot be obtained in a timely manner.

Authors' statement

LC — Collected the data, analyzed the data, interpreted the results, drafted the manuscript
VR — Collected the data, analyzed the data, interpreted the results, drafted the manuscript
AC — Analyzed the data, interpreted the results, drafted the manuscript
GP — Drafted the manuscript
GB — Drafted the manuscript
JB — Drafted the manuscript

All authors participated in designing the study methodology. All authors reviewed the results and approved the final version of the manuscript.

Competing interests

None.

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References

1. Dumler JS, Walker DH. Ehrlichia chaffeensis (Human Monocytotropic Ehrlichiosis), Anaplasma phagocytophilum (Human Granulocytotropic Anaplasmosis), and Other Anaplasmataceae. Mandell, Douglas, and Bennett's Principles and Practice of Infectious Diseases. 2014;2:2227-33.e3. http://www.scopus.com/inward/record.url?scp=84944627061&partnerID=8YFLogxK

2. Edginton S, Guan TH, Evans G, Srivastava S. Human granulocytic anaplasmosis acquired from a blacklegged tick in Ontario. CMAJ 2018;190(12):E363–6. DOI PubMed

3. Dahlgren FS, Heitman KN, Drexler NA, Massung RF, Behravesh CB. Human granulocytic anaplasmosis in the United States from 2008 to 2012: a summary of national surveillance data. Am J Trop Med Hyg 2015;93(1):66–72. DOI PubMed

4. Center for Disease Control and Prevention. Anaplasmosis: Epidemiology and Statistics. Atlanta (GA): CDC; 2021 (accessed 2022-01-25). https://www.cdc.gov/anaplasmosis/stats/index.html

5. Government of Manitoba. Manitoba Health. Tick-Borne Diseases (accessed 2022-01-25). https://www.gov.mb.ca/health/publichealth/cdc/tickborne/index.html

6. Institut de la statistique du Québec. Main indicators on Québec and its regions. ISQ; 2022 (accessed 2022-01-25). https://statistique.quebec.ca/en/vitrine/region

7. Ministère de la Santé et des Services sociaux. Surveillance des maladies à déclaration obligatoire au Québec. Maladies d'origine infectieuse: Définitions nosologiques (12e édition). MSSS; 2019. https://publications.msss.gouv.qc.ca/msss/fichiers/2019/19-268-05W.pdf

8. Charlson ME, Pompei P, Ales KL, MacKenzie CR. A new method of classifying prognostic comorbidity in longitudinal studies: development and validation. J Chronic Dis 1987;40(5):373–83. DOI PubMed

9. Parkins MD, Church DL, Jiang XY, Gregson DB. Human granulocytic anaplasmosis: first reported case in Canada. Can J Infect Dis Med Microbiol 2009;20(3):e100–2. DOI PubMed

10. Uminski K, Kadkhoda K, Houston BL, Lopez A, MacKenzie LJ, Lindsay R, Walkty A, Embil J, Zarychanski R. Anaplasmosis: an emerging tick-borne disease of importance in Canada. IDCases 2018;14:e00472. DOI PubMed

11. Nelder MP, Russell CB, Lindsay LR, Dibernardo A, Brandon NC, Pritchard J, Johnson S, Cronin K, Patel SN. Recent Emergence of Anaplasma phagocytophilum in Ontario, Canada: Early Serological and Entomological Indicators. Am J Trop Med Hyg 2019;101(6):1249–58. DOI PubMed

12. Institut national de santé publique du Québec. Résultats de surveillance de la maladie de Lyme : année 2019. INSPQ; 2020 (accessed 2022-01-25). https://www.inspq.qc.ca/zoonoses/maladie-de-lyme/resultats-de-surveillance-2019

13. Bouchard C, Dibernardo A, Koffi J, Wood H, Leighton PA, Lindsay LR. N Increased risk of tick-borne diseases with climate and environmental changes. Can Commun Dis Rep 2019 Apr;45(4):83–9. DOI PubMed

14. Public Health Agency of Canada. Lyme Disease in Canada - A Federal Framework. Ottawa (ON): PHAC; 2017 (accessed 2022-01-25). https://www.canada.ca/en/public-health/services/publications/diseases-conditions/lyme-disease-canada-federal-framework.html

15. Russell A, Prusinski M, Sommer J, O'Connor C, White J, Falco R, Kokas J, Vinci V, Gall W, Tober K, Haight J, Oliver J, Meehan L, Sporn LA, Brisson D, Backenson PB. Epidemiology and Spatial Emergence of Anaplasmosis, New York, USA, 2010–2018. Emerg Infect Dis 2021;27(8):2154–62. DOI PubMed

16. Omodior O, Kianersi S, Luetke M. Prevalence of Risk and Protective Factors for Tick Exposure and Tick-Borne Disease Among Residents of Indiana. J Public Health Manag Pract 2021;27(6):E210–9. DOI PubMed

17. Porter WT, Motyka PJ, Wachara J, Barrand ZA, Hmood Z, McLaughlin M, Pemberton K, Nieto NC. Citizen science informs human-tick exposure in the Northeastern United States. Int J Health Geogr 2019;18(1):9. DOI PubMed

18. Sexton DJ, McClain MT. Human ehrlichiosis and anaplasmosis. UpToDate.com (accessed 2022-01-25). https://www.uptodate.com/contents/human-ehrlichiosis-and-anaplasmosis/print

19. Centers for Disease Control and Prevention. Anaplasmosis: Information for public health officials. Atlanta (GA): CDC; 2020 (accessed 2022-01-25). https://www.cdc.gov/anaplasmosis/info/index.html

20. Kulkarni MA, Berrang-Ford L, Buck PA, Drebot MA, Lindsay LR, Ogden NH. Major emerging vector-borne zoonotic diseases of public health importance in Canada. Emerg Microbes Infect 2015;4(6):e33. DOI PubMed

21. Tokarz R, Mishra N, Tagliafierro T, Sameroff S, Caciula A, Chauhan L, Patel J, Sullivan E, Gucwa A, Fallon B, Golightly M, Molins C, Schriefer M, Marques A, Briese T, Lipkin WI. A multiplex serologic platform for diagnosis of tick-borne diseases. Sci Rep 2018;8(1):3158. DOI PubMed

22. Atif FA. Anaplasma marginale and Anaplasma phagocytophilum: rickettsiales pathogens of veterinary and public health significance. Parasitol Res 2015;114(11):3941–57. DOI PubMed

23. Government of Canada. Molecular detection of Anaplasma phagocytophilum in clinical specimens 2021 (updated 2022-01-13). https://cnphi.canada.ca/gts/reference-diagnostic-test/4165?labId=1019

24. Government of Canada. Detection of IgG antibodies to Anaplasma phagocytophilum by IFA (updated 2022-01-13). https://cnphi.canada.ca/gts/reference-diagnostic-test/4168?labId=1019

25. Government of Canada. Molecular detection of Babesia species including but not limited to B. microti, B. duncani and B. divergens in clinical specimen (updated 2022-01-13). https://cnphi.canada.ca/gts/reference-diagnostic-test/4189?labId=1019

26. National Reference Centre for Parasitology. Tests Information 2021 (updated 2022-01-13). http://www.nrcp.ca/test-information.html

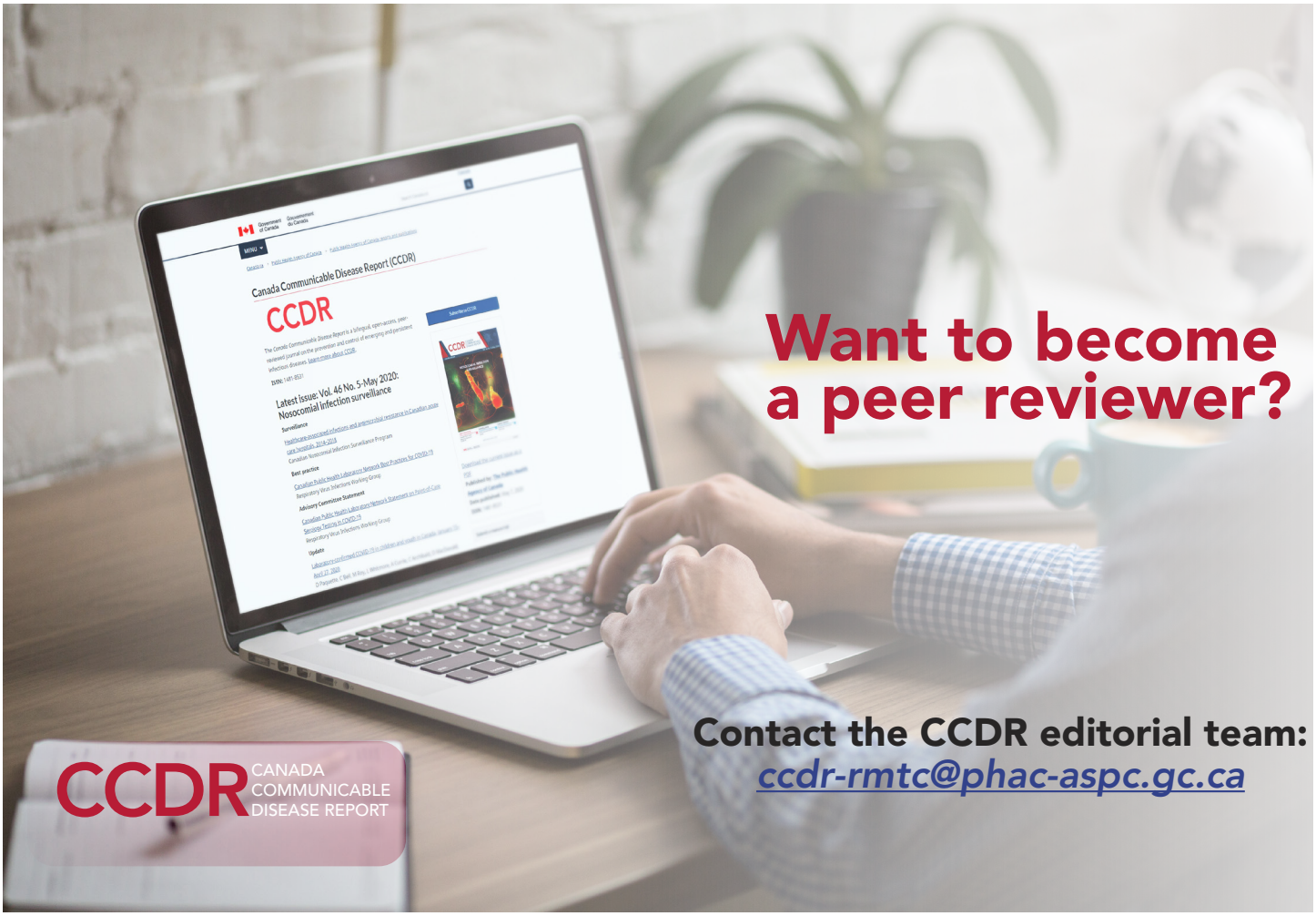
27. Institut national de santé publique du Québec. Borrelia burgdorferi (Lyme); détection (anticorps) sur sérum (updated 2022-01-30). https://www.inspq.qc.ca/lspq/repertoire-des-analyses/borrelia-burgdorferi-lyme-detection-anticorps-sur-serum

Annex: Laboratory methods for detection of tick-borne infections

For *Anaplasma phagocytophilum*, the molecular detection is realized with an in-house real-time polymerase chain reaction (RT-PCR) targeting the msp2 gene. If positive, a conventional PCR and sequencing are performed to confirm and further characterize the strain of *A. phagocytophilum* (23). The National Microbiology Laboratory (NML) performed an indirect immunofluorescence assay (IFA) using the Focus *A. phagocytophilum* IFA IgG kit (DiaSorin Molecular, Cypress, California, United States), according to the manufacturer's instructions (24).

For molecular detection of *Babesia* spp., amplification of the 18s rRNA gene common to all *Babesia* species is first performed. If positive, specific-species RT-PCR, melted-curve analysis, conventional PCR and sequencing are completed to establish species (25). Testing for antibody to *Babesia microti* was performed using a manual indirect immunofluorescent antibody (immunoglobulin G) assay (Imugen, Norwood, Massachusetts, United States) (26).

For Lyme disease, a first serological assay is performed at the *Laboratoire de santé publique du Québec* with a commercial enzyme immunoassay (ELISA Borrelia VlsE1/pepC10 IgG/IgM, Zeus Scientific, Branchburg, New Jersey, United States). If positive, the specimen is sent to the NML for confirmatory Western Blot (WB) for IgG antibodies against *Borrelia burgdorferi* (Anti-B. burgdorferi US EUROLINE IgG, Euroimmun, Lübeck, Germany). If the WB is negative, a Line Blot (LB) to detect IgM is executed (Anti-Borrelia EUROLINE-RN-AT-adv IgM, Euroimmun, Lübeck, Germany) (27).



A meteorological-based forecasting model for predicting minimal infection rates in *Culex pipiens-restuans* complex using Québec's West Nile virus integrated surveillance system

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Abstract

Background: *The ministère de la Santé et des Services sociaux* (MSSS) du Québec (Québec's health authority) has expressed an interest in the development of an early warning tool to identify seasonal human outbreaks of West Nile virus infection in order to modulate public health interventions. The objective of this study was to determine if a user-friendly meteorological-based forecasting tool could be used to predict minimal infection rates for the *Culex pipiens-restuans* complex—a proxy of human risk—ahead of mosquito season.

Methods: Annual minimal infection rate (number of positive pools/number of mosquitoes) was calculated for 856 mosquito traps set from 2003 to 2006 and 2013 to 2018 throughout the south of Québec's. Coefficient of determination (R^2) were estimated using the validation dataset (one third of the database by random selection) with generalized estimation equations, which were prior fitted backwards with polynomial terms using the training dataset (two thirds of the database), in order to minimize the Bayesian information criteria. Mean temperatures and precipitation were grouped at five temporal scales (by month, by season and by 4, 6 and 10-months groupings).

Results: Mean temperatures and cumulative precipitation from the previous months of March (R^2=0.37), May (R^2=0.36), December (R^2=0.35) and the autumn season (R^2=0.38) accounted for ~40% of *Cx. pipiens-restuans* annual minimal infection rates variations. Including the "year of sampling" variable in all regression models increased the predictive abilities (R^2 between 0.42 and 0.57).

Conclusion: All regression models explored have too weak predictive abilities to be useful as a public health tool. Other factors implicated in the epidemiology of the West Nile virus need to be incorporated in a meteorological-based early warning model for it to be useful to the provincial health authorities.

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Keywords: epidemiology, outbreaks, forecasting tool, Québec, West Nile virus

Introduction

West Nile virus (WNV) has been the most important mosquito-borne infection in Québec for the past two decades (1). A provincial surveillance program specific for this arbovirus has been put in place since 2000 (2), one year after its first detection in North America following an outbreak of neuro-invasive diseases in the state of New York, United States (US) (3). It was composed of an enhanced passive surveillance of humans, of sick or dead wild birds (which act as reservoirs or accidental hosts) and active mosquito surveillance (4).The surveillance system confirmed WNV's introduction in Québec in 2002 with the

first WNV-positive birds and locally-acquired human cases (5,6). Neurological cases of WNV-infections typically represent a very small proportion (~1%) of infected individuals since 70% to 80% of infections remain asymptomatic, while the rest have unspecific symptoms (i.e. influenza-like illness) (3). Between 2003 and 2018, a total of 541 cases (n=24 deaths) were reported in Québec with the following clinical presentation: neurological impairment (70%); non-neurological (23%); asymptomatic (6%); and unknown (1%) (1). Since then, two peaks of reported cases have been observed in 2012 (n=134; 30% of cases from across Canada) and 2018 (n=200; 46% of cases from across Canada) (1,7).Yearly fluctuations in the number of human cases are observed in other regions (8,9) and appeared to be associated with phenomena occurring at different geographic and temporal scales (10) (i.e. according to local interactions between mosquitoes, birds and humans, environmental factors and large-scale climatic fluctuations such as the El Niño-Southern Oscillation) (11–14).

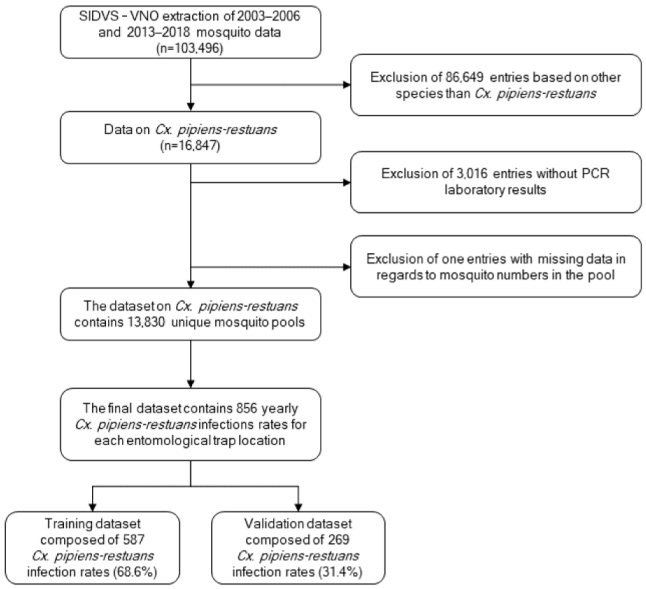
Scientists are still working to understand and identify factors influencing outbreaks of WNV infections, and to develop models that would be able to predict when and where these outbreaks could potentially occur. The provincial health authority (*Ministère de la Santé et des Services sociaux*) expressed an interest in the development of an early warning tool to identify outbreak years in advance, and to use this information to mitigate risk and decrease human exposure by modulating their interventions. Such tools are generally based on meteorological data in order to predict a potential outbreak with a delay ranging from a few weeks to a few months before the surveillance system confirms that WNV is circulating (15). Temperature and precipitation are the most commonly used WNV predictors (16). The main goal of this project is to determine if a meteorological-based early warning tool could predict WNV infection rates in mosquitoes.

Methods

The history of Québec's WNV integrated (using human, animal and entomological components) surveillance system is fully described elsewhere (17). Background screening of the scientific literature was used to build a directed acyclic graph (DAG) (**Figure A1**) to conceptualize relationships between potential drivers of WNV and identify important variables to include in models, using the DAGitty tool (18).

Data from 13,830 mosquito pools of the *Culex pipiens-restuans* complex, these two species espèces (*Cx. pipiens* and *Cx. restuans*) cannot be differentiate morphologically (19), were extracted from the *Système intégrée des données de vigie sanitaire du virus du Nil occidental* (20) to calculate annual minimal infection rate (MIR) (number of positive pools/number of mosquitoes in each pool) (**Figure 1**). The MIRs were calculated for each of the 856 mosquito pools, which were grouped for each trap deployed per year (i.e. mosquito trap-year) and distanced by greater or equal to 1 km^2 radius, since it represents the average travel distance of *Cx. pipiens-restuans* (21) and the spatial resolution of the meteorological data (1 km^2). Mosquito surveillance was carried out inconsistently in 12 out of 18 Public Health Units (PHU), with a greater number of mosquito pools tested for Montreal and Montérégie (**Table 1**), except since 2017 where 49 traps are deployed annually in the same seven PHU (Montréal=5, Laval=4, Montérégie=5, Outaouais=7, Lanaudière=7, Mauricie-Centre-du-Québec=7 et Capitale-Nationale=14).

Figure 1: Flow chart of the entomological data extracted from Québec's *Système intégrée des données de vigie sanitaire du virus du Nil occidental*



Abbreviations: *Cx. pipiens-restuans*, *Culex pipiens-restuans*; PCR, polymerase chain reaction; SIDVS-VNO, *Système intégrée des données de vigie sanitaire du virus du Nil occidental*

Explanatory variables included the mean daily temperatures ($T_{mean}=T_{maximal}+T_{minimal}/2$) (°C) and daily precipitation (mm) extracted from the Oak Ridge National Laboratory Distributed Active Archive Center (http://daymet.ornl.gov/) according to the Global Positioning System (GPS) coordinates of each trap-year (latitude and longitude). Mean daily temperature and sum of precipitation were grouped according to five different temporal scales: 1) previous months; 2) previous seasons: summer (June and July), spring (March to May), winter (December to February) and autumn (September to November); 3) previous four-months (November of the year before to February of the same year); 4) previous six-months (September of the year before to February of the same year); and 5) previous ten-months (September of the previous year to July of the current year) groupings, based on the literature suggesting that meteorological conditions impact WNV transmission months ahead (11,22). Meteorological data from the closest neighboring traps were assigned to eight mosquito traps with missing data, with half of these traps being separated by more than one kilometer from their matched trap. To consider variations in the geographical and temporal mosquito sampling, two new "sampling strengths" variables were created for each

Table 1: Descriptions of *Culex pipiens-restuans* minimal infection rates and meteorological data at different geographical and temporal scales

Spatio-temporal variables	Number of data entry	Minimal infection rate per 1,000 mosquitoes		Mean temperatures at mosquito traps		Mean precipitation at mosquito traps	
		n	95% CI	n	min; max	n	min; max
Province of Québec	856	3.1[a]	2.2; 4.0[a]	6.3	2.1; 8.2	3.0	2.2; 4.3
Public Health Units							
01 – Bas Saint-Laurent	0	–	–	–	–	–	–
02 – Saguenay – Lac Saint-Jean	6	0	0; 45.9	2.5	2.1; 2.9	2.6	2.4; 2.8
03 – Capitale Nationale	40	4.4	1.5; 7.3	5.0	3.5; 7.8	3.5	2.9; 4.3
04 – Mauricie et Centre-du-Québec	28	1.6	0; 4.0	5.4	4.4; 7.2	3.1	2.3; 3.5
05 – Estrie	8	0	0; 36.9	5.8	5.0; 7.0	3.5	3.0; 3.8
06 – Montréal	265	3.1	2.2; 3.9	6.4	5.7; 8.2	3.0	2.4; 3.9
07 – Outaouais	47	3.1	0; 7.3	6.0	3.5; 7.8	2.9	2.2; 3.9
08 – Abitibi-Témiscamingue	3	0	0; 70.8	3.2	3.1; 3.3	2.7	2.7; 2.8
09 – Côte-Nord	0	–	–	–	–	–	–
10 – Nord-du-Québec	0	–	–	–	–	–	–
11 – Gaspésie-îles-de-la-Madeleine	0	–	–	–	–	–	–
12 – Chaudières-Appalaches	8	0	0; 36.9	4.6	3.7; 6.2	3.1	2.7; 3.6
13 – Laval	82	4.9	3.1; 6.7	6.5	5.7; 8.0	3.0	2.5; 4.0
14 – Lanaudière	36	3.5	0.6; 6.5	6.7	5.4; 7.8	3.1	2.3; 4.0
15 – Laurentides	70	4.8	2.0; 7.7	6.4	5.3; 8.0	3.2	2.6; 4.2
16 – Montérégie	263	3.9	2.9; 5.0	6.5	5.3; 8.1	2.9	2.4; 3.9
17 – Nunavik	0	–	–	–	–	–	–
18 – Terres-Cries-de-la-Baie-James	0	–	–	–	–	–	–
Type 3 global analysis: Chi-square (*p*-value)[b]	–	9.9	0.5	23.3	0.02	17.2	0.1
Year							
2003	118	3.0	1.7; 4.4	5.5	3.1; 6.3	2.6	2.3; 3.4
2004	86	0.9	0; 2.1	5.7	2.1; 6.5	3.1	2.4; 3.8
2005	146	3.4	2.0; 4.8	6.5	3.7; 7.0	3.1	2.4; 4.3
2006	65	0.2	0; 0.4	7.5	6.8; 7.9	3.8	3.1; 4.2
2007	0	–	–	–	–	–	–
2008	0	–	–	–	–	–	–
2009	0	–	–	–	–	–	–
2010	0	–	–	–	–	–	–
2011	0	–	–	–	–	–	–
2012	0	–	–	–	–	–	–
2013	63	5.5	3.2; 7.8	7.1	6.4; 7.5	2.8	2.4; 3.1
2014	199	4.2	2.7; 5.6	6.0	5.7; 6.2	3.0	2.8; 3.2
2015	45	5.6	2.6; 8.7	6.2	4.5; 6.5	2.7	2.2; 3.4
2016	47[c]	5.6	2.3; 9.0	7.0	3.1; 8.2	3.0	2.5; 3.8
2017	46[c]	5.4	3.2; 7.7	6.5	5.1; 7.7	3.5	3.2; 3.9
2018	41[c]	11.8	0; 91.1	6.2	4.7; 7.5	3.1	2.6; 3.5
Type 3 global analysis: Chi-square (*p*-value)[b]	–	28.5	0.008	61.1	<0.0001	53.9	<0.0001
Month[d]							
January	0	–	–	-10.8	−19.7; −4.2	2.0	0.6; 5.3
February	0	–	–	-8.8	−16.9; −4.1	2.1	0.9; 5.4
March	0	–	–	-3.8	−7.3; 0.5	2.0	0.8; 5.0
April	0	–	–	5.4	−3.0; 7.8	3.6	0.2; 7.4
May	96	0	0; 37.7	13.4	7.5; 16.6	3.2	0.7; 6.8
June	1,518	0	0; 0.1	18.7	13.1; 21.4	4.2	1.5; 7.6
July	3,611	0.8	0.4; 1.2	21.1	18.0; 23.5	3.2	1.6; 7.2
August	4,688	5.5	4.3; 6.7	20.1	16.4; 22.3	3.5	1.7; 6.2
September	3,675	6.0	4.4; 7.5	16.1	12.4; 18.6	2.9	0.8; 7.7

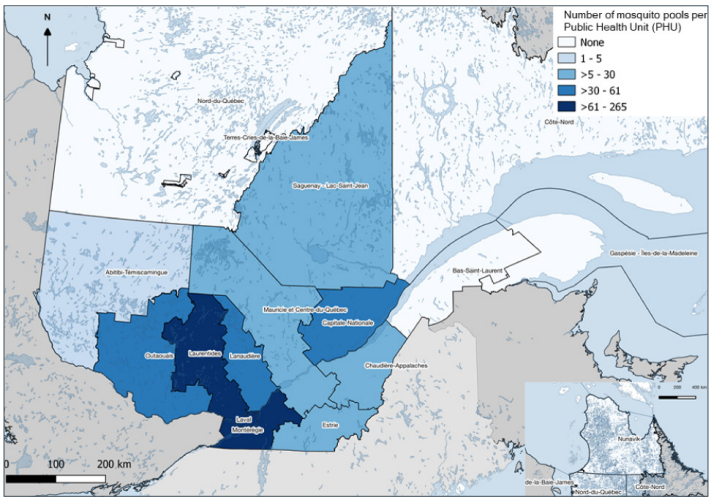
Table 1: Description of *Culex pipiens-restuans* minimal infection rates and meteorological data at different geographical and temporal scales (*continued*)

Spatio-temporal variables	Number of data entry	Minimal infection rate per 1,000 mosquitoes		Mean temperatures at mosquito traps		Mean precipitation at mosquito traps	
		n	95% CI	n	min; max	n	min; max
Month[d] (*continued*)							
October	242	1.9	0; 4.4	9.0	3,4; 12.9	3.4	1.2; 6.8
November	0	–	–	1.4	−2.3; 4.4	3.0	0.3; 5.6
December	0	–	–	−6.5	−11.8; 1.8	3.2	0.6; 7.1
Type 3 global analysis: Chi-square (*p*-value)[b]	–	15.6	<0.0001	N/A[e]	N/A[e]	N/A[e]	N/A[e]

Abbreviations: CI, confidence interval; N/A, not applicable; –, no information is available
[a] Minimal infection rates using mosquitoes trapped during the month of August and September was 5.0 (95% CI; 2.6–7.4)
[b] Using a linear regression model with a repeated measure on the mosquito trap name
[c] Monthly minimal infection rates were calculated using the dataset containing the 13,830 mosquito pools while the mean monthly temperatures and precipitation were calculated using the 856 mosquito pools grouped by unique trap-year
[d] These numbers are lower than the fixed number of 49 mosquito traps that have been deployed since 2017, because entries from traps within a 1 km² radius were merged together
[e] Not available because of multicollinearity (VIF>2.5) in the models

PHU (**Figure 2**) based on the number of tested mosquito pool: 1) annually; and 2) during the 2003–2018 period (Table 1).

Figure 2: Map of the 18 Public Health Units in the province of Québec according to the number of mosquito pools tested between 2003–2006 and 2013–2018



Note: Created on the 19th of May 2021 with QGIS. Projection NAD83 / MTQ Lambert. Data downloaded from https://donneesquebec.ca/ and https://publications.msss.gouv.qc.ca/msss/document-001647/

Bivariate analysis between *Cx. pipiens-restuans* annual MIR (outcome) and explanatory variables (PHU, year and month) were performed using a linear regression model; an auto-regressive working covariance matrix with mosquito traps in the same city were nested within each PHU. Then multivariate regression models evaluated the predictive ability of each temperature and precipitation temporal scale to estimate MIRs, with observations randomly separated into training (n=2/3) and validation (n=1/3) datasets. A backward variable selection with a maximum of four polynomial terms to obtain the lowest Bayesian information criteria using the training dataset was fitted back into a Poisson regression model using the validation dataset (23). MIRs were obtained using the number of positive *Cx. pipiens-restuans* pools on the logarithm of the number of mosquitoes tested, while mosquito traps in the same city were nested within each PHU to account for correlated data using an auto-regressive working covariance matrix. The methodology of sensitivity and post hoc analyses are described in the Annex material. The SAS macro (%RsquareV) was used to calculate the coefficient of determination (R^2), reflecting the proportion of the variance explained by the predictors (24). Only $R^2 \geq 0.30$ are highlighted in the text. The 95% confidence intervals (CI) and *p*-values are presented, and all postulates associated with the regression models were visually inspected (25). Statistical analysis were performed using version 9.4 of SAS/STAT™ software (SAS Institute, Cary, North Carolina, US).

Results

Since 2003, 172,094 *Cx. pipiens-restuans* mosquitoes were analyzed by polymerase chain reaction (PCR), resulting in a mean MIR of 3.1 per 1,000 mosquitoes (95% CI; 2.2–4.0), when data were grouped under the 856 mosquito trap-years, which varied according to the sampling year (χ^2=28.5; *p*=0.0008) and month (χ^2=5.6; *p*<0.0001) but not across the PHU (χ^2=9.9; *p*=0.5) (Table 1). For the studied period, mean monthly temperatures near mosquito traps varied from 23.5°C (July) to −19.7°C

(January) while monthly cumulative precipitation varied from 0.3 mm (November) to 7.7 mm (September).

The predictive ability of the previous mean temperatures and precipitation to predict the seasonal MIRs was the highest using the previous months of March (R^2=0.37), May (R^2=0.36) and December (R^2=0.35) as well as the previous autumn season (R^2=0.38), with all other coefficients of determination below 0.30 (**Table 2**). The results of all the sensitivity and post hoc analysis are fully described in the Annex material. Briefly, including the year of sampling variable in the main regression models increased all R^2 (range: 0.42 to 0.57) while the increased was less

Table 2: The ability of meteorological variables to predict *Culex pipiens-restuans* minimal infection rates, at different temporal grouping scales for the meteorological data

	Regression models and equations from the training dataset	Coefficient of determination of the validation dataset (*Penalised R^2*)
A) By previous month		
July	$MIR = -915.67 + 130.81Temp - 6.45Temp^2 + 0.11Temp^3 + 35.05Prec - 14.65Prec^2 + 2.58Prec^3 - 0.17Prec^4 + \varepsilon$	0.28
June[a]	$MIR = -40.79 + 3.54Temp - 0.10Temp^2 + 0.95Prec - 0.09Prec^2 + \varepsilon$	0.15
May[a]	$MIR = 13.60 - 2.13Temp + 0.09Temp^2 - 7.98Prec + 2.48Prec^2 - 0.24Prec^3 + \varepsilon$	0.36
April	$MIR = -7.64 - 0.27Temp + 2.47Prec - 0.69Prec^2 + 0.08Prec^3 - 0.003Prec^4 + \varepsilon$	0.19
March	$MIR = -22.03 - 4.28Temp - 2.31Temp^2 - 0.44Temp^3 - 0.03Temp^4 + 30.83Prec - 22.71Prec^2 + 6.79Prec^3 - 0.70Prec^4 + \varepsilon$	0.37
February	$MIR = -2.85 + 2.38Temp + 0.20Temp^2 - 0.01Temp^3 + \varepsilon$	0.10
January	$MIR = -47.75 - 17.42Temp - 2.65Temp^2 - 0.18Temp^3 - 0.004Temp^4 + 0.34Prec - 0.04Prec^2 + \varepsilon$	0.24
December	$MIR = -6.93 + 0.21Temp - 0.05Temp^2 - 0.01Temp^3 + 2.67Prec - 0.79Prec^2 - 0.06Prec^3 + \varepsilon$	0.35
November	$MIR = -4.74 - 0.07Temp - 0.46Temp^2 + 0.12Temp^3 + 2.61Prec + 2.74Prec^2 - 0.65Prec^3 + 0.09Prec^4 + \varepsilon$	0.18
October	$MIR = -7.48 + 0.20Temp - 0.83Prec + 0.47Prec^2 + 0.06Prec^3 + \varepsilon$	0.28
September	$MIR = -6.02 + 0.16Temp - 1.75Prec + 0.26Prec^2 + \varepsilon$	0.28
August	$MIR = -13.09 + 0.40Temp - 0.24Prec + \varepsilon$	0.08
B) By season[b]		
Summer[a]	$MIR = -45.53 + 4.37Temp - 0.11Temp^2 - 3.25Prec + 0.46Prec^2 + \varepsilon$	0.15
Spring[c]	$MIR = -206.81 + 84.33Temp - 25.56Temp^2 + 3.36Temp^3 - 0.16Temp^4 + 132.67Prec - 64.01Prec^2 + 13.26Prec^3 - 1.00Prec^4 + \varepsilon$	0.09
Winter	$MIR = 2.31 + 0.89Temp + 0.05Temp^2 - 6.40Prec + 3.04Prec^2 - 0.46Prec^3 + \varepsilon$	0.24
Autumn	$MIR = -438.86 + 153.19Temp - 17.32Temp^2 + 0.65Temp^3 - 15.35Prec + 4.79Prec^2 - 0.50Prec^3 + \varepsilon$	0.38
C) From November of the previous year to February of the same year		
Four months grouped together	$MIR = -48.07 - 2.87Temp - 1.24Temp^2 - 0.18Temp^3 - 0.01Temp^4 + 54.97Prec - 26.15Prec^2 + 15.35Prec^3 - 0.41Prec^4 + \varepsilon$	0.24
D) From September of the previous year to February of the same year		
Six months grouped together	$MIR = 9.37 + 0.48Temp - 0.23Prec + 13.46Prec^2 - 3.51Prec^3 + 0.33Prec^4 + \varepsilon$	0.27
E) From September of the previous year to July of the same year[c]		
Ten months grouped together	$MIR = -119.02 - 113.69Temp - 41.82Temp^2 + 6.68Temp^3 - 0.39Temp^4 + \varepsilon$	0.12

Abbreviations: MIR, minimal infection rates; Prec, precipitations; Temp, temperature

[a] A polynomial equation with three terms was used as the model did not converge with four

[b] Summer represents the months of June and July; Spring represents the months of March to May; Winter represents the months of December to February; Autumn represents the months of September to October

[c] The repeated measure was limited to each mosquito pool to allow the model to converge as it was not possible to nest mosquito traps from the same city within each Public Health Unit to account for their proximity

substantial when including the PHU variable (range: 0.18 to 0.46) (**Table A1**).

Discussion

This is the first time that a meteorological-based early warning tool to predict *Cx. pipiens-restuans* annual MIRs in Québec has been investigated using the province's own WNV surveillance data. The ability of mean temperatures and precipitation to predict MIRs was highest when the data were grouped under the previous months of March, December and May, and previous autumn season (September to November of the previous year). However, the predictive capacity of the model is probably too weak to be useful for an early warning system. The fact that only ~40% of the variance in *Cx. pipiens-restuans* annual MIRs can be explained by mean temperature and precipitation suggests that others factors are implicated in the epidemiology of WNV and that these factors need to be incorporated into this kind of predictive tool (15).

Many early warning or forecasting systems that are primarily or solely based on meteorological data have been developed to predict other mosquito-borne diseases (i.e. chikungunya, dengue, malaria, yellow fever, Zika) to anticipate vector control responses (24). Our results suggest that presently these models yield insufficient predicting abilities to be useful in real life for Quebec's public health authority. The epidemiology of WNV is known to be complex and adding variables such as environmental drivers (habitat suitability or distribution of vectors and reservoirs, vegetation index, land use) and data on avian hosts (abundance, migrations) usually improve predictions (15). However, the necessity of integrating data from the ongoing surveillance system and refining the geographical scale leads to less user-friendly tools, for public health authorities (26).

Strengths and limitations

One of the strengths of this project is that the geographical proximity of mosquito traps was accounted for in most of the regression models, as this can bias results. Additionally, multiple sensitivity and post hoc analyses brought robustness to our results. The polynomial equations accounted for non-linear associations between meteorological variables and MIRs, allowing for a better representation of their relationship and a better model fit, while the backward selection of variables proved to be as effective as the visual inspection of generalized additive models. Because MIRs are low numerical values, an attempt to increase the statistical power was made by calculating annual MIRs using mosquitoes trapped during August and September. Though the mean annual MIRs increased for most positive mosquito pools, the coefficient of determination for most regression models decreased unexpectedly; possibly as a consequence of a smaller sample size when including only August and September, since 13 mosquito traps had no mosquitoes captured, which decreased statistical power.

Based on our conceptual framework, it is unknown if an over adjustment bias occurred when adjusting for "year of sampling" in the regression models (27). Despite multiple sensitivity analysis with potential confounding variables, a residual confounding effect cannot be discarded (28). Because mosquito pools were grouped for each trap-year, it was not possible to account for the different types of traps that were employed. This limitation has probably a marginal effect, since 85.2% of mosquitoes were captured by the CDC light traps. It was not possible to account for the use of larvicides during the 2003–2005 and 2013–2014 seasons, which might have influenced the estimates. Because mosquito PCR testing is done independently from mosquito trapping, if a measurement bias was to be present, a decrease in the association would also be suspected.

A selection bias could influence our results because of the geographical distribution of traps which is linked to 1) past human WNV incidence and 2) the influence of weather on human physical activity and exposure to mosquitoes (29,30). Additionally, the fixed location of mosquitoes traps since 2017 comes at the expense of detecting WNV emergence in the less densely populated PHU situated at more northern latitudes. The limited number of mosquito traps on such a huge territory and the absence of mosquito surveillance during the colder months reduces the statistical power. Hence, a higher number of traps distributed over a wider geographical area would provide a wider range of meteorological data and increase statistical power. Since WNV vectors vary according to regions, and transmission pathways seem to be influenced environmental and geographical variables at a finer scale then the PHU results of this project may not be transferable to other situations. Despite these limitations, Québec's WNV surveillance data will be explored further. The next steps will be to directly predict human WNV incidence using meteorological data and bypass the gap that occurred in entomological data between 2007 and 2012 and to explore the development of an early detection system tool.

Conclusion

All regression models explored have too weak predictive abilities to be useful as a public health tool. Other factors implicated in the epidemiology of the West Nile virus need to be incorporated in a meteorological-based early warning model for it to be useful to the provincial health authorities.

Authors' statement

KFB, NO, AL and AIC — Conceptualized the project
ESL — Performed database management and statistical analysis
JD — Conceptualized the project, performed database management and statistical analysis, interpretation of results, wrote original draft

All coauthors reviewed and edited the text.

Competing interests

None.

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References

1. Ouhoummane N, Ducrocq J, Irace-Cima A. Portrait de l'infection par le virus du Nil occidental au Québec: 2003 - 2018. Montréal (QC): INSPQ; 2021. https://www.inspq.qc.ca/sites/default/files/publications/2809-portrait-infection-virus-nil-occidental.pdf

2. Alain L, Bolduc D, Couillard M, Deschênes L, Douville-Fradet M, Lacoursière D. Groupe de travail sur la prévention de l'encéphalite causée par le virus du Nil occidental - Secteur santé - Rapport des activités - année 2000. Ministère de la Santé et des Services sociaux. 2001.

3. Mostashari F, Bunning ML, Kitsutani PT, Singer DA, Nash D, Cooper MJ, Katz N, Liljebjelke KA, Biggerstaff BJ, Fine AD, Layton MC, Mullin SM, Johnson AJ, Martin DA, Hayes EB, Campbell GL. Epidemic West Nile encephalitis, New York, 1999: results of a household-based seroepidemiological survey. Lancet 2001;358(9278):261–4. DOI PubMed

4. Dallaire A, Sareault V. Rapport d'activités du Centre québécois sur la santé des animaux sauvages du 1er janvier 2000 au 3 décembre 2000. Saint-Hyacinthe: Faculté de médecine vétérinaire, Université de Montréal. 2000.

5. Brown KD, Dallaire A. Surveillance pour la détection précoce de l'infection par le virus du Nil Occidental chez les oiseaux sauvages au Québec: Saison 2002. Centre Québécois sur la Santé des Animaux Sauvages. Université de Montréal; 2002.

6. Direction de la santé publique de la Montérégie. Résumé des signalements pour le virus du Nil: Montérégie, saison 2002 (Internal document). 2002.

7. Government of Canada. Surveillance of West Nile virus. Government of Canada; 2021. https://www.canada.ca/en/public-health/services/diseases/west-nile-virus/surveillance-west-nile-virus.html

8. Sambri V, Capobianchi M, Charrel R, Fyodorova M, Gaibani P, Gould E, Niedrig M, Papa A, Pierro A, Rossini G, Varani S, Vocale C, Landini MP. West Nile virus in Europe: emergence, epidemiology, diagnosis, treatment, and prevention. Clin Microbiol Infect 2013;19(8):699–704. DOI PubMed

9. McDonald E, Mathis S, Martin SW, Staples JE, Fischer M, Lindsey NP. Surveillance for West Nile virus disease – United States, 2009-2018. MMWR Surveill Summ 2021;70(1):1–15. DOI PubMed

10. Uelmen JA, Irwin P, Bartlett D, Brown W, Karki S, Ruiz MO, Fraterrigo J, Li B, Smith RL. Effects of scale on modeling West Nile virus disease risk. Am J Trop Med Hyg 2021;104(1):151–65. DOI PubMed

11. Poh KC, Chaves LF, Reyna-Nava M, Roberts CM, Fredregill C, Bueno R Jr, Debboun M, Hamer GL. The influence of weather and weather variability on mosquito abundance and infection with West Nile virus in Harris County, Texas, USA. Sci Total Environ 2019;675:260–72. DOI PubMed

12. Hess A, Davis JK, Wimberly MC. Identifying environmental risk factors and mapping the distribution of West Nile virus in an endemic region of North America. Geohealth 2018;2(12):395–409. DOI PubMed

13. Kain MP, Bolker BM. Predicting West Nile virus transmission in North American bird communities using phylogenetic mixed effects models and eBird citizen science data. Parasit Vectors 2019;12(1):395. DOI PubMed

14. García-Carrasco JM, Muñoz AR, Olivero J, Segura M, Real R. Predicting the spatio-temporal spread of West Nile virus in Europe. PLoS Negl Trop Dis 2021;15(1):e0009022. DOI PubMed

15. Barker CM. Models and surveillance systems to detect and predict West Nile virus outbreaks. J Med Entomol 2019;56(6):1508–15. DOI PubMed

16. Forest-Bérard K. Utilisation d'indicateurs météorologiques de la présence de vecteurs du virus du Nil occidental (VNO). INSPQ; 2019. https://www.inspq.qc.ca/sites/default/files/publications/2537_temperature_precipitations_indicateurs_meteorologiques_vecteurs_vno.pdf

17. Ducrocq J, Pelletier R, Turcotte ME. Proposition d'un plan de surveillance intégrée des virus transmis par les moustiques au Québec, 2020-2025. INSPQ; 2019. https://www.inspq.qc.ca/sites/default/files/publications/2614_plan_surveillance_virus_moustiques.pdf

18. Textor J, van der Zander B, Gilthorpe MS, Liśkiewicz M, Ellison GT. Robust causal inference using directed acyclic graphs: the R package 'dagitty'. Int J Epidemiol 2016;45(6):1887–94. DOI PubMed

19. Harrington LC, Poulson RL. Considerations for accurate identification of adult Culex restuans (Diptera: Culicidae) in field studies. J Med Entomol 2008;45(1):1–8. DOI PubMed

20. Gosselin P, Lebel G, Rivest S, Douville-Fradet M. The Integrated System for Public Health Monitoring of West Nile Virus (ISPHM-WNV): a real-time GIS for surveillance and decision-making. Int J Health Geogr 2005;4:21. DOI PubMed

21. Hamer GL, Anderson TK, Donovan DJ, Brawn JD, Krebs BL, Gardner AM, Ruiz MO, Brown WM, Kitron UD, Newman CM, Goldberg TL, Walker ED. Dispersal of adult culex mosquitoes in an urban west nile virus hotspot: a mark-capture study incorporating stable isotope enrichment of natural larval habitats. PLoS Negl Trop Dis 2014;8(3):e2768. DOI PubMed

22. Paz S. Climate change impacts on West Nile virus transmission in a global context. Philos Trans R Soc London B Biol Sci. 2015;370(1665):20130561. DOI

23. Zou GY, Donner A. Extension of the modified Poisson regression model to prospective studies with correlated binary data. Stat Methods Med Res 2013;22(6):661–70. DOI PubMed

24. Zhang D. A Coefficient of Determination for Generalized Linear Models. Am Stat 2018;71(4):310–6. DOI

25. Vittinghoff E, Glidden DV, Shiboski SC, McCulloch CE. Regression Methods in Biostatistics. Linear, Logistic, Survival, and Repeated Measures Models. New York (NY): Springer; 2012.

26. Hussain-Alkhateeb L, Rivera Ramírez T, Kroeger A, Gozzer E, Runge-Ranzinger S. Early warning systems (EWSs) for chikungunya, dengue, malaria, yellow fever, and Zika outbreaks: what is the evidence? A scoping review. PLoS Negl Trop Dis 2021;15(9):e0009686. DOI PubMed

27. Schisterman EF, Cole SR, Platt RW. Overadjustment bias and unnecessary adjustment in epidemiologic studies. Epidemiology 2009;20(4):488–95. DOI PubMed

28. Liang W, Zhao Y, Lee AH. An investigation of the significance of residual confounding effect. BioMed Res Int 2014;2014:658056. DOI PubMed

29. Chan CB, Ryan DA. Assessing the effects of weather conditions on physical activity participation using objective measures. Int J Environ Res Public Health 2009;6(10):2639–54. DOI PubMed

30. Hernán MA, Hernández-Díaz S, Robins JM. A structural approach to selection bias. Epidemiology 2004;15(5):615–25. DOI PubMed

31. Greenland S. Invited commentary: variable selection versus shrinkage in the control of multiple confounders. Am J Epidemiol 2008;167(5):523–9. DOI PubMed

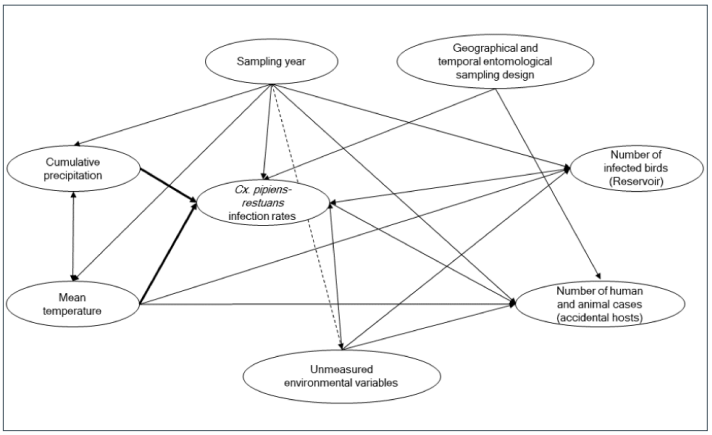
Annex

Methods

Because human cases of West Nile virus (WNV) infection are usually reported at the beginning of August (1) and that the objective is to develop an early alert tool able to predict these human cases a couple of months before they occur, temperatures and precipitation during August have not been included in our analysis.

Background screening of the scientific literature was used to build a directed acyclic graph (DAG) (**Figure A1**) to conceptualize relationships between potential drivers of WNV and identify the variables that need to be adjusted for in the model using the DAGitty tool.

Figure A1: Conceptual framework using a directed acyclic graph between meteorological variables and the main outcomes of Québec's West Nile virus integrated surveillance system



Notes: The darker arrows represent the associations evaluated in this project. To estimate the associations between mean temperatures and precipitations and *Cx. pipiens-restuans* complex minimal infection rates the model needs to be minimally adjusted for the "sampling year" variable. However, since the database already represents the seasonal minimal infection rate for each mosquito trap-year, this variable has not been directly included in the regression models of the principal analysis. Its inclusion was rather evaluated using a sensitivity analysis

Sensitivity and post hoc analysis

Seven sensitivity analyses were carried out as follows:
1) regression models were fitted using visual inspection of graphs generated by a generalized additive model with a maximum of four degree of smoothing performed by generalized cross validation; 2) the main models were reanalyzed without the data from the four mosquito traps (LAV 034, LAV 904, SHA 002 and WEN 001) that inherited meteorological data of their closest neighbour with a radius superior to 1 km^2; 3) by including the Public Health Units (PHU) 2003–2018 sampling strength variable; 4) by including the annual sampling strength by PHU; 5) by attributing the minimal infection rate of mosquitoes trapped only during the month of August and September instead of during the whole summer; 6) by adding the year of sampling in the model; and 7) by adding the PHU in the model instead of in the repeated measure. Following results from the 6th sensitivity analysis, year of sampling was used as a proxy for unmeasured confounders. An post hoc Poisson analyses was performed by modeling directly the MIR using the year of sampling (categorical) as the explanatory variable. To measure if the meteorological variables were confounders of this association, the year of sampling was included as a continuous variable to facilitate the calculation and interpretation of the difference and ratio between both estimates ($\beta_{\text{Year of sampling}}$). Confounding was present based on a difference and/or ratio of estimates superior to 0.1 decimal or 10% (31). Four additional bivariate analysis were carried out with the year of sampling as an explanatory continuous variable and respectively, the mean annual temperatures, mean annual precipitation, annual sampling strength and PHU sampling strength as the main outcome. Specifying a normal distribution, an "identity" link and an auto-regressive working covariance matrix with mosquito traps in the same city nested within each PHU, yielded estimates representing differences in minimal infection rates (MIRs).

Results

Sensitivity analysis

Fitting regression models after a visual inspection of the generalized additive model graphs led to similar results of the main analysis, except for the month of February (R^2 increased to 0.22) and August (R^2 increased to 0.24) as well as the ten-month grouped (R^2 increased to 0.18), while all other comparisons had difference within five decimal units (Table A1). Excluding the four entomological traps with meteorological data borrowed from the closest neighboring trap influenced the results for the months of May (R^2 decreased to 0.19) and September (R^2 increased to 0.38), summer (R^2 increased to 0.29) and winter (R^2 decreased to 0.16) (Table A1). When including the PHU sampling strength variable, all R^2 were within five decimals of the main results (Table A1). Including the variable reflecting the annual strength of sampling, increased the predictive abilities of at least five decimals for nine temporal groupings (June, April, February, November, August; summer and spring; the six and ten-months groupings). Using the minimal infection rates of *Cx. pipiens-restuans* trapped in August and September instead of the whole summer, influenced the R^2 for 14 temporal groupings (decreased for May, April, December, November, September, summer, winter, autumn, four and six-months grouping and increased for June, October, August and spring). When including the year of sampling in the main regression models, all coefficient of determination increased between 0.42 and 0.57. Including the PHU variable in the main regression models increased the predictive ability of at least five decimals for all temporal groupings except July, May and autumn.

Post hoc analysis

When modelling directly the MIR using only the "year of sampling" variable, the R^2 was 0.53. The estimate associated with the year of sampling on a continuous linear scale and as the only explanatory variable of *Cx. pipiens-restuans* MIRs was 1.09 (95%

Table A1: Penalized coefficients of determination (Penalized R^2 for all seven sensitivity analyses)

Regression models	Sensitivity analyses[a]						
	Using generalized additive models for model specifications	Without the four entomological traps	Including the PHU strength of sampling variable	Including the annual sampling strength variable	Using the August and September MIR	Adding the year of sampling in the main model	Adding the PHU vairable in the main model
A) By previous month							
July	0.28	0.28	0.27	0.30	0.31	0.56↑	0.29
June[b]	0.18	0.15	0.17	0.21↑	0.24↑	0.53↑	0.24↑
May[b]	0.36	0.19↓	0.35	0.39	0.30↓	0.53↑	0.35
April	0.23	0.19	0.19	0.31↑	0.13↓	0.55↑	0.31↑
March	0.37	0.37	0.38	0.34	0.41	0.53↑	0.46↑
February	0.22↑	0.22↑	0.10	0.20↑	0.09	0.53↑	0.22↑
January	0.26	0.24	0.24	0.27	0.21	0.57↑	0.30↑
December	0.33	0.34	0.37	0.36	0.29↓	0.53↑	0.41↑
November	0.18	0.18	0.19	0.33↑	0.04↓	0.54↑	0.36↑
October	0.28	0.28	0.27	0.30	0.34↑	0.51↑	0.41↑
September[b]	0.29	0.38↑	0.30	0.35↑	0.21↓	0.57↑	0.38↑
August	0.24↑	0.11	0.09	0.23↑	0.24↑	0.48↑	0.20↑
B) By season[c]							
Summer	0.14	0.29↑	0.15	0.24[d]↑	0.02↓	0.55↑	0.27[e]↑
Spring	0.09	0.09	0.09	0.18↑	0.15[e]↑	0.53↑	0.23[e]↑
Winter	0.20	0.16↓	0.23	0.26	0.08↓	0.51↑	0.32↑
Autumn	0.38	0.38	0.38	0.40	0.27↓	0.53↑	0.41
C) Four months grouping							
From November of the year before to February of the same year	0.26	0.24	0.24	0.23	0.14↓	0.57↑	0.35↑
D) Six months grouping							
From September of the year before to February of the same year	0.27	0.26	0.29	0.34↑	0.19↓	0.56↑	0.36↑
E) Ten months grouped together[b,d]							
From September of the year before to July of the same year	0.18↑	0.12[e]	0.13[e]	0.20↑	0.17	0.42↑	0.18↑

Abbreviations: MIR, minimal infection rates; PHU, public health unit
[a] Arrows indicate the direction of change above and below five decimal units compared to results of the main analysis in Table 2
[b] A polynomial equation with three terms was used as the model did not converge with four
[c] Summer represents the months of June and July; Spring represents the months of March to May; Winter represents the months of December to February; Autumn represents the months of September to October
[d] The repeated measure was limited to each mosquito pool to allow the model to converge as it was not possible to nest mosquito traps from the same city within each Public Health Unit
[e] No repeated measure was employed for this model to converge

CI; 1.06–1.11; $p<0.0001$) while yearly fluctuations are observed when treated on the categorical scale (results not shown). The results of the estimates obtained in all the main regression models using the meteorological variables and year of sampling varied between 1.06 and 1.15, with very low confounding effects on the difference and ratio scales (**Table A2**). When comparing MIRs between years and using 2018 as the reference, all anterior sampling years had lower values except for 2016 since the upper 95% CI of the estimate overlaps the null value (**Table A3**). When the year of sampling is treated on a continuous scale, the number of mosquito traps decreased linearly from 2003 to 2018 (β=−1.13 [−1.45–−0.81; $p<0.0001$]). Therefore, the number of mosquito traps and MIRs are inversely correlated between 2003 and 2018 with an increase of 2% in MIRs for each less mosquito trap in time (β=0.98 [0.98–0.99; $p<0.0001$]). At the level of each mosquito trap location in Québec, mean annual temperatures increased (β=0.04 [0.02–0.06; $p=0.0003$]) while mean annual precipitation decreased (β=−0.008 [−0.02–0.006; $p=0.07$]) from 2003 to 2018.

Table A2: Differences and ratios between estimates for sampling year in the model, with and without meteorological data using the 2003–2018 entomological dataset

Regression models	Estimate for the sampling year as a continuous variable with meteorological data		*p*-value	Difference in estimates[a]	Ratio in estimates for the sampling year[b]
	n	95% CI			
A) By previous month					
July	1.08	1.04–1.12	<0.0001	0.01	1.01
June[c]	1.11	1.07–1.15	<0.0001	−0.02	0.98
May[c]	1.09	1.06–1.12	<0.0001	0.00	1.00
April	1.07	1.04–1.11	0.0001	0.02	1.02
March	1.15	1.12–1.18	<0.0001	−0.06	0.95
February	1.08	1.05–1.11	<0.0001	0.01	1.01
January	1.14	1.10–1.18	<0.0001	−0.05	0.96
December	1.11	1.06–1.14	0.0007	−0.02	0.98
November	1.06	1.03–1.09	0.0003	0.03	1.03
October	1.08	1.04–1.13	<0.0001	0.01	1.01
September	1.09	1.06–1.13	<0.0001	0.00	1.00
August	1.09	1.07–1.12	<0.0001	0.00	1.00
B) By season[d]					
Summer[c]	1.12	1.10–1.15	<0.0001	−0.03	0.97
Spring[e]	1.09	1.06–1.1	<0.0001	0.00	1.00
Winter	1.12	1.07–1.16	<0.0001	−0.03	0.97
Autumn	1.08	1.05–1.11	<0.0001	0.01	1.01
C) Four months grouping					
From November of the year before to February of the same year	1.09	1.05–1.13	<0.0001	0.00	1.00
D) Six months grouping					
From September of the year before to February of the same year	1.09	1.06–1.11	<0.0001	0.00	1.00
E) Ten months grouping[f]					
From September of the year before to July of the same year	1.08	1.06–1.10	<0.0001	0.01	1.01

[a] β without meteorological data equivalent to 1.09 (95% CI; 1.06–1.12; *p*-value <0.0001) – β with meteorological data
[b] β without meteorological data equivalent to 1.09 (95% CI; 1.06–1.12; *p*-value <0.0001) / β with meteorological data
[c] A polynomial equation with three terms was used as the model did not converge with four
[d] Summer represents the months of June and July; Spring represents the months of March to May; Winter represents the months of December to February; Autumn represents the months of September to October
[e] The repeated measure was limited to each mosquito pool to allow the model to converge as it was not possible to nest mosquito traps from the same city within each Public Health Unit
[f] No repeated measure was employed for models to converge

Table A3: Results of the post hoc regression model using the year of sampling to predict *Cx. pipiens-restuans* minimal infection rates using the 2003–2018 entomological dataset

Year of sampling	*Cx. pipiens-restuans* minimal infection rates per 1,000 mosquitoes		Minimal infection rate ratio		*p*–value
	n	Rate	n	Rate	
2003	3.0	1.7–4.4	0.24	0.16–0.34	<0.0001[a]
2004	0.9	0–2.1	0.06	0.04–0.10	<0.0001[a]
2005	3.4	2.0–4.8	0.21	0.12–0.36	<0.0001[a]
2006	0.2	0–0.4	0.05	0.03–0.10	<0.0001[a]
2013	5.5	3.2–7.8	0.41	0.26–0.66	0.0002[a]
2014	4.2	2.7–5.6	0.31	0.20–0.46	<0.0001[a]
2015	5.6	2.6–8.7	0.36	0.21–0.65	0.0005[a]
2016	5.6	2.3–9.0	0.50	0.22–1.13	0.1
2017	5.4	3.2–7.7	0.53	0.35–0.80	0.002[a]
2018 (Reference)	11.8	0–91.1	1.00	1.00	–
Type 3 global analysis (with 9 degree of liberty)	–	–	χ^2=17.98	χ^2=17.98	0.04

Abbreviation: –, information not available
[a] Statistically significant after the Bonferroni correction for nine comparisons using a threshold of 0.006 (corresponding to 0.05/9)

Surveillance for *Ixodes scapularis* and *Ixodes pacificus* ticks and their associated pathogens in Canada, 2019

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Abstract

Background: The primary vectors of the agent of Lyme disease in Canada are *Ixodes scapularis* and *Ixodes pacificus* ticks. Surveillance for ticks and the pathogens they can transmit can inform local tick-borne disease risk and guide public health interventions. The objective of this article is to characterize passive and active surveillance of the main Lyme disease tick vectors in Canada in 2019 and the tick-borne pathogens they carry.

Methods: Passive surveillance data were compiled from the National Microbiology Laboratory Branch and provincial public health data sources. Active surveillance was conducted in selected sentinel sites in all provinces. Descriptive analysis of ticks submitted and infection prevalence of tick-borne pathogens are presented. Seasonal and spatial trends are also described.

Results: In passive surveillance, specimens of *I. scapularis* (n=9,858) were submitted from all provinces except British Columbia and *I. pacificus* (n=691) were submitted in British Columbia and Alberta. No ticks were submitted from the territories. The seasonal distribution pattern was bimodal for *I. scapularis* adults, but unimodal for *I. pacificus* adults. *Borrelia burgdorferi* was the most prevalent pathogen in *I. scapularis* (18.8%) and *I. pacificus* (0.3%). In active surveillance, *B. burgdorferi* was identified in 26.2% of *I. scapularis*; *Anaplasma phagocytophilum* in 3.4% of *I. scapularis*, and *Borrelia miyamotoi* and Powassan virus in 0.5% or fewer of *I. scapularis*. These same tick-borne pathogens were not found in the small number of *I. pacificus* tested.

Conclusion: This surveillance article provides a snapshot of the main Lyme disease vectors in Canada and their associated pathogens, which can be used to monitor emerging risk areas for exposure to tick-borne pathogens.

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Keywords: *Ixodes scapularis*, *Ixodes pacificus*, surveillance, *Borrelia*, *Anaplasma*, *Babesia*

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Introduction

Ixodes scapularis and *Ixodes pacificus* are tick vectors capable of transmitting several bacterial, viral and protozoan pathogens to humans (1). *Ixodes scapularis* populations are increasing in number and distribution in southern central and eastern Canada (2–4). Climate (e.g. increasing temperatures, changes in precipitation) and environmental factors (e.g. changes in land use) contribute to the geographic range expansion of ticks, which can enhance exposure to tick-borne diseases (TBD) (1,5–7). These changes can also create longer seasons for adventitious ticks to become established in new areas and increase

human-tick interactions (1,4,6–8). Continued expansion of the range of ticks in Canada presents a public health challenge, as awareness of TBD risks and capacity for surveillance and testing must also expand to these areas (1).

Lyme disease (LD) is the most commonly reported vector-borne disease in Canada, and incidence of reported cases has increased more than 17-fold from 2009 through 2019 (9,10). The causative agent of LD, *Borrelia burgdorferi*, is transmitted by *I. scapularis* in central and eastern Canada and by *I. pacificus* in British Columbia. Beyond LD, other TBD including anaplasmosis (caused by the bacterium *Anaplasma phagocytophilum*), babesiosis (caused by the parasite *Babesia microti*), hard tick-borne relapsing fever (caused by the bacterium *Borrelia miyamotoi*) and Powassan virus (POWV) disease are emerging as diseases locally acquired within Canada (1,11–15).

Passive surveillance began in the early 1990s in Canada to detect the occurrence of *I. scapularis* and *I. pacificus* tick vectors and their infection with *B. burgdorferi* (16). Active surveillance has been ongoing since the 2000s to identify areas where vector tick populations are establishing and, as a result, where LD may become endemic (LD risk areas) (17,18). This is the first edition of a pan-Canadian annual article summarizing the findings of both passive and active vector surveillance and updating estimates of infection prevalence in ticks. A previous study by Guillot *et al.* (19) summarized results of a pan-Canadian study on tick surveillance; however, that study only included active tick surveillance from sentinel sites.

The objective of this surveillance article is to provide an epidemiologic summary of the main LD vectors in Canada, *I. scapularis* and *I. pacificus*, and their associated pathogens, collected through active and passive surveillance systems in 2019. This article will also summarize the prevalence and spatial distribution of tick-borne pathogens.

Methods

Data sources

This article uses two types of surveillance data from six different sources: 1) passive tick surveillance data from the National Microbiology Laboratory (NML) Branch of the Public Health Agency of Canada, the British Columbia Centre for Disease Control and Alberta Health (20); and 2) active tick surveillance data from the Canadian Lyme Sentinel Network (CaLSeN), the New Brunswick Department of Health and the University of Ottawa.

Passive tick surveillance

In passive tick surveillance, ticks are collected by the public and submitted to medical clinics, veterinary clinics, or directly to a provincial public health laboratory or other institution (e.g. university laboratory) for species identification (16). Location of acquisition, history of travel in the past two weeks, date of collection, level of engorgement, tick instar and host are recorded.

This article focuses on *I. scapularis* and *I. pacificus* ticks collected in Canada, although several other tick species were also collected. Ticks with an international location of acquisition, an imprecise location within Canada that could not be geocoded (e.g. province listed only, multiple locations listed) or history of travel were excluded to create a dataset of locally acquired ticks. Over the years, passive tick surveillance programs have been discontinued in different jurisdictions, i.e. Nova Scotia, southwestern Québec (Montérégie) and eastern Ontario; however, the public continues to submit a relatively small number of ticks acquired in these jurisdictions directly to NML.

In 2019, Saskatchewan, Manitoba, Ontario, Québec, Newfoundland and Labrador, New Brunswick, Nova Scotia and Prince Edward Island sent ticks to NML for testing of tick-borne pathogens (*A. phagocytophilum*, *B. burgdorferi* and *B. microti*) using methods described previously (21,22). Ticks could be submitted singly or in groups of two or more (multiple submission). For laboratory testing, ticks from the same multiple submission were pooled and tested together. In British Columbia (23) and Alberta (24), testing was done at provincially funded laboratories on individual ticks for only *B. burgdorferi*. Ticks are rarely encountered in northern Canada and as a result, formal passive tick surveillance programs for *I. scapularis* or *I. pacificus* are not established in the Yukon, Northwest Territories or Nunavut.

Active tick surveillance

Active surveillance involves collection of ticks in the environment through drag sampling or through capture of host mammals that are examined for ticks. This method aims to identify where emerging tick populations are establishing (4,18). For this article, only *I. scapularis* and *I. pacificus* collected by drag sampling were included for analysis, although several other tick species were also collected.

This article collates data from CaLSeN, the New Brunswick Department of Health and the University of Ottawa. The CaLSeN used standardized methods to conduct dragging in 96 sites across all provinces (19). The New Brunswick Department of Health and the University of Ottawa used similar dragging methods to visit 73 and 15 sites, respectively (25). Visit date, location of collection (latitude and longitude), tick species and tick instar were recorded for all ticks collected.

Nymphs and adult *I. scapularis* and *I. pacificus* were tested for tick-borne pathogens. Ticks collected by CaLSeN and by the province of New Brunswick were tested for *A. phagocytophilum*, *B. microti*, *B. burgdorferi*, *B. miyamotoi* and POWV (CaLSeN ticks only) at NML using methods previously described (19,21,22). Ticks collected by the University of Ottawa were tested for *A. phagocytophilum*, *B. burgdorferi* and *B. miyamotoi* with quantitative polymerase chain reaction (qPCR) assays

described previously (25) using the *flaB* gene for *B. miyamotoi* and including a confirmatory assay targeting *msp2* in *A. phagocytophilum*. Testing for *B. microti* used a qPCR assay targeted towards the *cctη* gene (21).

Analysis

Tick characteristics

For passive tick surveillance, we calculated descriptive statistics for province of acquisition, tick species, instar (larva, nymph, adult male or adult female), level of engorgement (unfed, partially engorged or fully engorged), host (human, dog, cat or other) and month of collection. For active tick surveillance, we calculated descriptive statistics for province of acquisition, tick species and instar (larva, nymph or adult). The probable location of acquisition for ticks was mapped using QGIS (version 3.8.1).

Infection prevalence

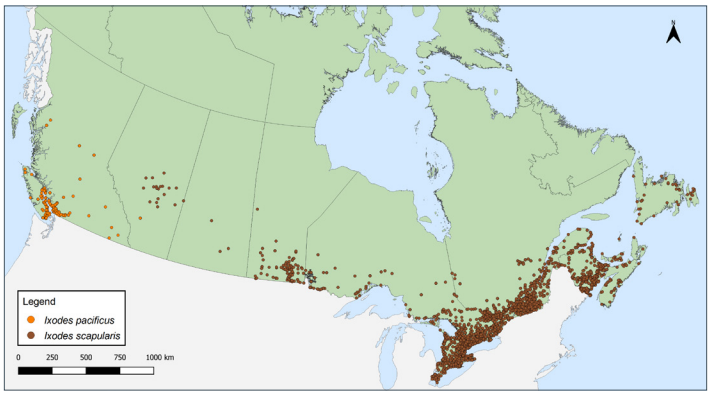
For ticks submitted through passive surveillance, maximum likelihood estimates (MLE) of prevalence with 95% confidence intervals (CI) were calculated in Excel (version 16.0) using the PooledInfRate add-in (version 4.0) to account for pooled testing (26,27). Co-infection prevalence was assessed among single submissions only to ensure they were true co-infections (two or more pathogens in the same tick). The prevalence of co-infections was calculated as the number of co-infected ticks divided by the total number of ticks tested. Prevalence in active surveillance was calculated in the same manner as all ticks were tested individually.

Results

Passive surveillance tick characteristics

In 2019, there were 10,549 *I. pacificus* and *I. scapularis* ticks submitted from all provinces through passive surveillance (**Table 1**). The majority of ticks (90.0%) were submitted from three provinces: Ontario, Québec, and New Brunswick (**Figure 1**). The majority of ticks (94.0%) were single submissions, but there were 242 multiple submissions (range: 2–8 ticks). Nova Scotia had the highest proportion of multiple submissions (13.7%; n=7/51).

Figure 1: *Ixodes pacificus* and *Ixodes scapularis* ticks submitted through passive tick surveillance, Canada, 2019[a,b]



[a] Each dot represents the probable location of acquisition for an *I. pacificus* (n=691) or *I. scapularis* (n=9,858) tick submitted through passive surveillance
[b] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions

Table 1: Number of *Ixodes scapularis* and *Ixodes pacificus* ticks and submissions collected through passive surveillance by province, Canada, 2019[a]

Province	Number of ticks			Number of single submissions[b]	Multiple submissions[b]		
	Ixodes scapularis	*Ixodes pacificus*	Total		Number of submissions	Median number of ticks per submission	
						n	Range
British Columbia	0	690	690	690	N/A[c]	N/A[c]	N/A[c]
Alberta	55	1	56	56	N/A[c]	N/A[c]	N/A[c]
Saskatchewan	3	0	3	3	0	N/A	N/A
Manitoba	175	0	175	149	8	3	2–7
Ontario[d]	6,857	0	6,857	6,436	167	2	2–8
Québec[d]	1,697	0	1,697	1,618	31	2	2–7
Newfoundland and Labrador	44	0	44	42	1	2	2
New Brunswick	941	0	941	868	28	2	2–8
Nova Scotia[e]	72	0	72	44	7	5	2–5
Prince Edward Island	14	0	14	14	0	N/A	N/A
Total	9,858	691	10,549	9,920	242	2	2–8

Abbreviation: N/A, not applicable
[a] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks
[b] Single submissions consist of one tick; multiple submissions consist of two or more ticks submitted together by the same person
[c] Province did not report whether ticks were from single or multiple submissions
[d] Passive tick surveillance has been discontinued in some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch
[e] Passive tick surveillance has been discontinued in the entire province of Nova Scotia; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch

Data on tick instar, level of engorgement and host were available for 99.9%, 0% and 100% of *I. pacificus*, respectively. Data on tick instar, level of engorgement and host were available for 99.4%, 99.3% and 99.6% of *I. scapularis*, respectively. Adult ticks were submitted most frequently, of which most were female (*I. scapularis*: 89.0%; *I. pacificus*: 93.8%) (**Table 2**). Larvae (0.3%; 0.4%) and nymphs (8.1%; 3.3%) were submitted less frequently. Overall, 44.0% of *I. scapularis* were partially or fully engorged. Humans were the most common host among *I. scapularis* and *I. pacificus* (90.3%, 94.4%, respectively), followed by dogs (7.7%, 5.4%, respectively).

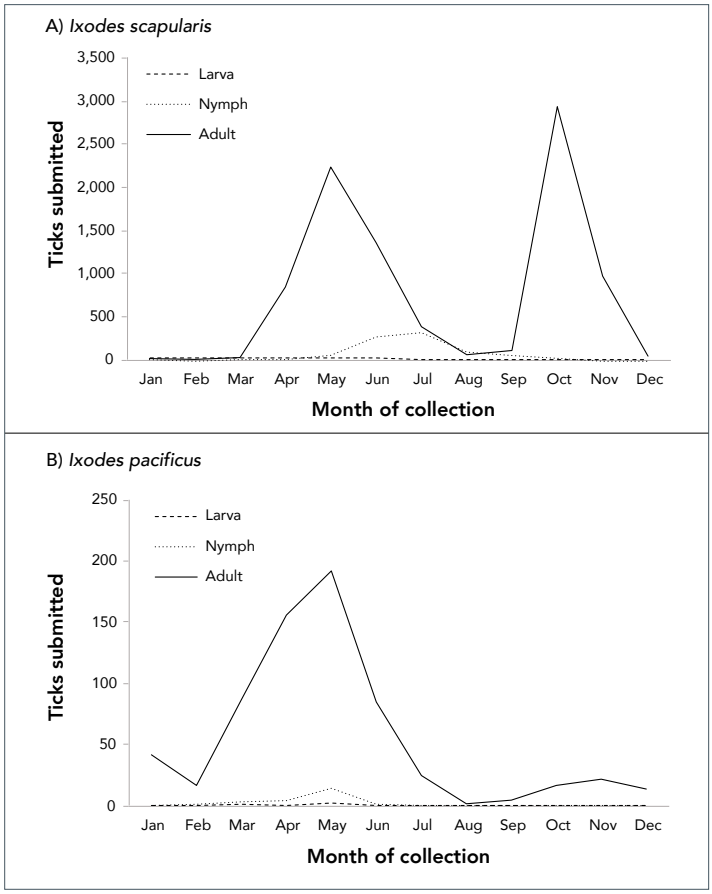
Table 2: Instar, level of engorgement and host of *Ixodes scapularis* and *Ixodes pacificus* ticks submitted through passive surveillance, Canada, 2019[a,b]

Characteristic	Tick species			
	Ixodes scapularis		*Ixodes pacificus*	
	n	%	n	%
Instar				
Larva	27	0.3	3	0.4
Nymph	795	8.1	23	3.3
Adult female	8,719	89.0	647	93.8
Adult male	256	2.6	17	2.5
Total	9,797	100	690	100
Level of engorgement[c]				
Fully engorged	113	1.2	N/A	N/A
Partially engorged	4,188	42.8	N/A	N/A
Unfed	5,485	56.0	N/A	N/A
Total	9,786	100	N/A	N/A
Host				
Human	8,870	90.3	652	94.4
Dog	761	7.7	37	5.4
Cat	119	1.2	1	0.1
Other[d]	72	0.7	1	0.1
Total	9,822	100	691	100

Abbreviation: N/A, not applicable
[a] Data are presented for all ticks where available, regardless of whether the tick was part of a single or a multiple submission
[b] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions
[c] Level of engorgement was not reported for *I. pacificus*
[d] Includes environment, horse, rabbit, deer, skunk and other unspecified animal

Month of acquisition was available for 99.9% of *I. pacificus* and 99.4% of *I. scapularis*. Locally acquired ticks were submitted in every month of the year (**Figure 2**). Submissions of *I. scapularis* adults peaked in May and October, while there was a single peak for *I. pacificus* adults in May. *Ixodes scapularis* nymph submissions peaked in June and July, while *I. pacificus* nymph submissions peaked in May.

Figure 2: Number of *Ixodes scapularis* and *Ixodes pacificus* ticks submitted through passive surveillance, by month and tick instar, Canada, 2019[a,b]



[a] Data are presented for *I. scapularis* (n=9,797) and *I. pacificus* (n=690) ticks submitted through passive surveillance. Month of submission or tick instar was not available for *I. scapularis* (n=61) and *I. pacificus* (n=1)
[b] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions

Passive surveillance infection prevalence

Data on laboratory testing were available for 97.4% of *I. pacificus* and 99.0%–99.5% of *I. scapularis*, depending on the pathogen. The most prevalent tick-borne pathogen was *B. burgdorferi*, found in 18.8% of *I. scapularis* (95% CI: 18.00–19.55), but only 0.3% of *I. pacificus* (95% CI: 0.05–0.97). Other tick-borne pathogens and co-infections were less prevalent (**Table 3**).

Prevalence of *B. burgdorferi* was higher in *I. scapularis* from multiple submissions (24.5%, 95% CI: 20.64–28.69) than from single submissions (18.5%, 95% CI: 17.71–19.29) (**Table 4**). Prevalence did not significantly differ by submission type for any other pathogens.

Ixodes scapularis submitted from human hosts had higher prevalence of *B. burgdorferi* infection (19.2%, 95% CI: 18.39–20.04) than those submitted from non-human

Table 3: Prevalence of *Borrelia burgdorferi*, *Anaplasma phagocytophilum* and *Babesia microti* infection in *Ixodes pacificus* and *Ixodes scapularis* ticks submitted through passive surveillance, Canada, 2019[a,b]

Pathogen	Infection prevalence			
	Ixodes pacificus		*Ixodes scapularis*	
Single agent	Maximum likelihood estimate[c]			
	%	95% CI	%	95% CI
Borrelia burgdorferi	0.3	0.05–0.97	18.8	18.00–19.55
Anaplasma phagocytophilum	N/A	N/A	1.4	1.22–1.70
Babesia microti	N/A	N/A	0.1	0.07–0.22
Any of above	0.3	0.05–0.97	20.0	19.23–20.83
Co-infection	Co-infection rate[d]			
	%	Number co-infected ticks/number ticks tested	%	Number co-infected ticks/number ticks tested
Borrelia burgdorferi + *Anaplasma phagocytophilum*	N/A	N/A	0.28	26/9,171
Borrelia burgdorferi + *Babesia microti*	N/A	N/A	0.02	2/9,171
Anaplasma phagocytophilum + *Babesia microti*	N/A	N/A	0.01	1/9,171
Any co-infection	N/A	N/A	0.32	29/9,171

Abbreviations: CI, confidence interval; N/A, not tested
[a] All *I. pacificus* (n=691) and all *I. scapularis* from Alberta (n=55) were not tested for *A. phagocytophilum* and *B. microti*
[b] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions
[c] Maximum likelihood estimates of infection prevalence were used to account for pooled testing
[d] Co-infection rate was calculated only among single submissions of ticks

Table 4: Prevalence of *Borrelia burgdorferi*, *Anaplasma phagocytophilum* and *Babesia microti* infections in *Ixodes scapularis* ticks submitted through passive surveillance by submission type and host, Canada, 2019[a]

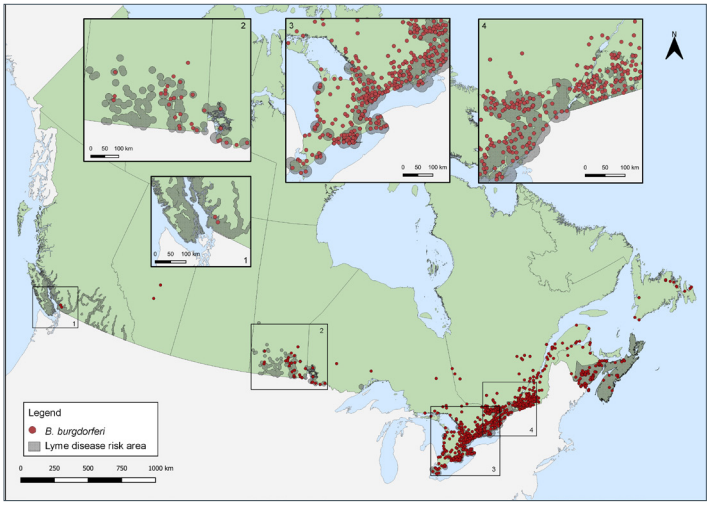
Characteristic	Infection prevalence Maximum likelihood estimate							
	Borrelia burgdorferi		*Anaplasma phagocytophilum*		*Babesia microti*		Any of above	
	%	95% CI	%	95% CI	%	95% CI	%	95% CI
Submission type[b]								
Single	18.5	17.71–19.29	1.4	1.20–1.69	0.1	0.07–0.22	19.7	18.92–20.55
Multiple	24.5	20.64–28.69	1.7	0.89–3.06	0.2	0.01–0.82	26.3	22.31–30.70
Host[c]								
Human	19.2	18.39–20.04	1.3	1.11–1.59	0.1	0.07–0.23	20.4	19.54–21.23
Non-human[d]	14.7	12.44–17.13	2.6	1.68–3.85	0.1	0.01–0.57	16.7	14.31–19.29

Abbreviation: CI, confidence interval
[a] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions
[b] Single submissions consist of one tick. Multiple submissions consist of two or more ticks submitted together by the same person. All *I. scapularis* from Alberta were considered single submissions
[c] Excludes *I. scapularis* where host is unknown or missing (n=43)
[d] Non-human hosts include dog, cat, environment, horse, rabbit, deer, skunk or other unspecified animal

hosts (14.7%, 95% CI: 12.44–17.13) (Table 4). However, *I. scapularis* submitted from non-human hosts had higher prevalence of *A. phagocytophilum* infection (2.6%, 95% CI: 1.68–3.85) than those submitted from human hosts (1.3%, 95% CI: 1.11–1.59). Both *B. burgdorferi*-infected *I. pacificus* ticks were from human hosts.

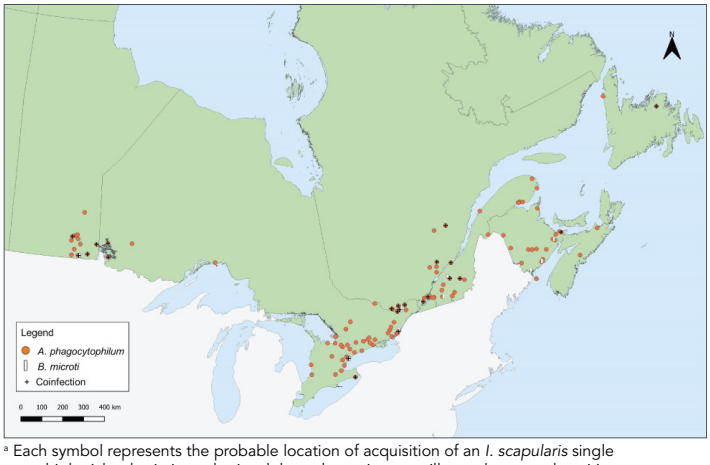
Tick-borne pathogens were commonly found in ticks submitted from southern Manitoba, northwestern Ontario, southern and eastern Ontario, southern Québec and southern New Brunswick (**Figure 3** and **Figure 4**). Over two-thirds of *B. burgdorferi*-infected tick submissions were within previously identified LD risk areas (72.1%; n=1,313/1,821) (Figure 3).

Figure 3: *Ixodes pacificus* and *Ixodes scapularis* ticks submitted through passive surveillance that were infected with *Borrelia burgdorferi*, Canada, 2019[a,b,c]



[a] Each dot represents the probable location of acquisition of at least one *I. pacificus* (n=2) or *I. scapularis* (n=1,819) single or multiple tick submission submitted through passive surveillance that was infected with *B. burgdorferi*
[b] Lyme disease risk areas are identified by the provinces as of 2020 using the methods described in the 2016 national Lyme disease case definition (28)
[c] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions

Figure 4: *Ixodes scapularis* ticks submitted through passive surveillance that were infected with *Anaplasma phagocytophilum*, *Babesia microti* and co-infections, Canada, 2019[a,b]



[a] Each symbol represents the probable location of acquisition of an *I. scapularis* single or multiple tick submission submitted through passive surveillance that tested positive for *A. phagocytophilum* (n=141), *B. microti* (n=13) or a co-infection (n=29). Co-infections were limited to only single submissions of *I. scapularis*, and include *B. burgdorferi* + *A. phagocytophilum* (n=26), *B. burgdorferi* + *B. microti* (n=2) and *A. phagocytophilum* + *B. microti* (n=1)
[b] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions

The majority of multiple submissions came from LD risk areas (76.9%; n=186/242), of which approximately half were infected with *B. burgdorferi* (51.4%; n=90/175). Newfoundland and Labrador, Nova Scotia and Québec all had higher infection prevalence of *B. burgdorferi* than the national average for *I. scapularis* (**Table 5**). Manitoba had the highest prevalence of *A. phagocytophilum* and *B. microti* infection among all provinces.

Active surveillance tick characteristics

In active surveillance, *I. scapularis* and *I. pacificus* were found at 78 of 184 surveillance sites (range of ticks found: n=0–130). *Ixodes scapularis* (n=1,156) were found in Manitoba, Ontario, Québec, New Brunswick, Nova Scotia and Prince Edward Island, while *I. pacificus* (n=10) were found in British Columbia. Regarding the instar, 51.5% (n=601/1,166) of ticks were identified as nymphs, 29.5% (n=344/1,166) were adults and 19.0% (n=221/1,166) were larvae.

Active surveillance infection prevalence

Data on laboratory testing were available for 100% of *I. pacificus* collected and 73.8%–98.3% of *I. scapularis* nymphs and adults collected, depending on the pathogen. No tick-borne pathogens were found in *I. pacificus* (**Table 6**). In *I. scapularis*, *B. burgdorferi* was identified in 26.2% of ticks tested and in four provinces: Ontario, Québec, New Brunswick, and Nova Scotia. *Anaplasma phagocytophilum* was identified in the same four provinces in 3.4% of *I. scapularis*. *Borrelia miyamotoi* and POWV were found in 0.5% or fewer. **Figure 5** shows the locations of ticks with tick-borne pathogens collected in active surveillance.

Table 5: Prevalence of *Borrelia burgdorferi*, *Anaplasma phagocytophilum* and *Babesia microti* infection in *Ixodes scapularis* and *Ixodes pacificus* ticks submitted through passive surveillance, by province, Canada, 2019[a]

Province	Infection prevalence Maximum likelihood estimate					
	Borrelia burgdorferi		*Anaplasma phagocytophilum*		*Babesia microti*	
	%	95% CI	%	95% CI	%	95% CI
Ixodes pacificus						
British Columbia	0.3	0.05–0.97	N/A	N/A	N/A	N/A
Ixodes scapularis						
Alberta[b]	5.5	1.45–14.01	N/A	N/A	N/A	N/A
Saskatchewan	0.0	0–56.15	0.0	0–56.15	0.0	0–56.15
Manitoba	18.3	12.94–24.68	10.4	6.38–15.81	2.4	0.78–5.63
Ontario	18.3	17.37–19.22	0.9	0.73–1.18	0.1	0.02–0.14
Québec	24.2	22.18–26.30	1.9	1.32–2.63	0.1	0.02–0.39
Newfoundland and Labrador	29.5	17.63–44.01	4.6	0.82–14.28	0.0	0–8.02
New Brunswick	12.8	10.80–15.10	2.6	1.70–3.74	0.3	0.08–0.87
Nova Scotia	26.2	15.38–39.82	3.9	0.70–12.31	0.0	0–6.82
Prince Edward Island	0.0	0–21.53	0.0	0–21.53	0.0	0–21.53
Total	18.8	18.00–19.55	1.5	1.22–1.70	0.1	0.07–0.22

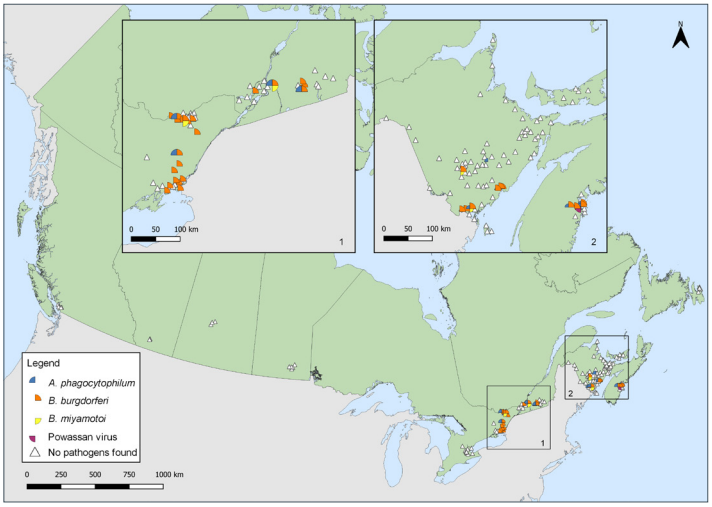
Abbreviations: CI, confidence interval; N/A, not tested
[a] No passive surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. Passive tick surveillance has been discontinued in the entire province of Nova Scotia, and some regions of Ontario and Québec; however, individuals could submit ticks directly to the National Microbiology Laboratory Branch from these jurisdictions
[b] Excludes *I. pacificus* found in the province (n=1) which tested negative for *B. burgdorferi*

Table 6: Infection prevalence of *Ixodes scapularis* and *Ixodes pacificus* ticks collected in active surveillance, by province, Canada, 2019[a,b]

Province	Infection prevalence									
	Anaplasma phagocytophilum		*Babesia microti*		*Borrelia burgdorferi*		*Borrelia miyamotoi*		Powassan virus	
	Number positive tick/number tick tested	%	Number positive tick/number tick tested	%	Number positive tick/number tick tested	%	Number positive tick/number tick tested	%	Number positive tick/number tick tested	%
Ixodes pacificus										
British Columbia	0/10	0	0/10	0	0/10	0	0/10	0	0/10	0
Ixodes scapularis										
Manitoba	0/3	0	0/3	0	0/3	0	0/3	0	0/3	0
Ontario	14/406	3.5	0/397	0	126/410	30.7	1/410	0.2	0/188	0
Québec	2/141	1.4	0/141	0	28/141	19.8	1/141	0.7	0/141	0
New Brunswick	8/194	4.1	0/194	0	41/194	21.1	3/194	1.6	0/194	0
Nova Scotia	7/169	4.1	0/169	0	46/169	27.2	0/169	0	1/169	0.6
Prince Edward Island	0/2	0	0/2	0	0/2	0	0/2	0	0/2	0
Total	31/915	3.4	0/906	0	241/919	26.2	5/919	0.5	1/697	0.1

[a] No *I. scapularis* or *I. pacificus* ticks were collected or tested in Alberta, Saskatchewan or Newfoundland and Labrador through active surveillance. No active surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks
[b] Infection prevalence is influenced by varying level of effort of active surveillance between provinces and seasonal variation when active surveillance took place. Infection prevalence should be interpreted with caution as not all active surveillance conducted in 2019 in Canada is included

Figure 5: *Ixodes scapularis* and *Ixodes pacificus* ticks with associated pathogens collected through active surveillance, Canada, 2019[a,b]



[a] Each symbol represents an active surveillance site where *B. burgdorferi* (n=38), *A. phagocytophilum* (n=12), *B. miyamotoi* (n=4), or Powassan virus (n=1) were found in *I. scapularis ticks*. There were 142 sites where no tick-borne pathogens were identified in ticks, including sites where no *I. scapularis* or *I. pacificus* were found (n=108). No active surveillance was conducted in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus* ticks. The presence or absence of infected *I. scapularis* ticks is influenced by varying level of effort of active surveillance between provinces and seasonal variation when active surveillance took place. Infection prevalence should be interpreted with caution as not all active surveillance conducted in 2019 in Canada is included

[b] Number of ticks tested: British Columbia (n=10), Alberta n=(0), Saskatchewan (n=0), Manitoba (n=3), Ontario (n=188–406 depending on pathogen), Québec (n=141), Newfoundland and Labrador (n=0), New Brunswick (n=194), Nova Scotia (n=169) and Prince Edward Island (n=2)

Discussion

In 2019, 9,858 *I. scapularis* and 691 *I. pacificus* were submitted in passive surveillance in eight provinces. Of these, 20.0% of *I. scapularis* and 0.3% of *I. pacificus* were infected with at least one of the tick-borne pathogens tested, including *B. burgdorferi*, *A. phagocytophilum* or *B. microti*. Active surveillance identified four tick-borne pathogens among *I. scapularis* collected in four provinces, and no tick-borne pathogens among the few *I. pacificus* collected.

In passive surveillance, one *I. pacificus* with no travel history was identified in Alberta, outside of British Columbia where reproducing populations are known to be established. *Ixodes pacificus* have been found in the province before on migratory birds (29), or from human or animal hosts mostly associated with travel (20).

Ticks were submitted through passive surveillance in every month, highlighting the potential year-round risk (depending on location and weather) of exposure to ticks, which may or may not be infected with tick-borne pathogen(s). *Ixodes* spp. ticks, for example, were often found in western Canada in the winter but were rarely infected (23). The single peak of *I. pacificus* tick submissions in the spring has historically been observed in British Columbia (23) and in the western United States (30), as nymphs and adults are both active during the cooler spring months (31). Bimodal peaks for adult *I. scapularis* in late spring and autumn have been previously observed in central and eastern Canada (3,16,32), and are consistent with adult *I. scapularis* activity in a 3 to 4-year lifecycle extended, in part, by cooler spring temperatures (31,33). Nymphs of both species, which are most implicated in LD transmission (34), peak during the late spring to summer months when LD onset in humans also peaks (9).

Compared to most recent estimates, infection prevalence of *B. burgdorferi* among *I. pacificus* ticks in British Columbia (0.3%) was consistent with annual rates from 2002 to 2018 between 0.1 and 0.4% (23). In Manitoba, infection prevalence among *I. scapularis* was lower (18.3%) than the 2018 minimum infection rate of 20.7% (35). In Ontario, infection prevalence among *I. scapularis* increased to 18.3% from the 2011–2017 rate of 15.8% (36). In Québec, infection prevalence also increased to 24.2% from 17.6% in *I. scapularis* adults from 2009 to 2015 (37). Inter and intra-provincial variability in annual prevalence is influenced, however, by annual variation in weather, effort of surveillance, history of established vector populations and habitat suitability.

Prevalence of *I. scapularis* being infected with at least one of the tick-borne pathogens tested was higher in multiple submissions than single submissions. As multiple submissions are indicators of tick establishment in a given area (38), this suggests higher infection prevalence among established tick populations.

Over two-thirds of *B. burgdorferi*-infected ticks had probable locations of acquisition within LD risk areas. The LD risk areas are identified by the provinces using the methods described in the 2016 national LD case definition (28) and are regularly updated to incorporate new surveillance data. *Borrelia burgdorferi*-infected ticks collected outside of these known LD risk areas may be adventitious ticks, brought to these areas by migratory birds or terrestrial hosts (18). Public health authorities and clinicians should be aware that risk of exposure to infected ticks exists outside of known LD risk areas. Increasing the collaborative effort of active surveillance can support the timely recognition of new LD risk areas. Promptly identifying and removing ticks, regardless of their locality of acquisition, can prevent transmission of tick-borne pathogens.

In active surveillance, there was geographic variability in infection prevalence, similar to findings from passive surveillance. Conducting standardized and consistent active surveillance across the country can help identify new LD-risk areas and detect other emerging tick-borne pathogens in known LD-risk areas, thereby informing local risk of exposure to TBD.

While *B. burgdorferi* was the most prevalent tick-borne pathogen in both passive and active surveillance, *A. phagocytophilum*, *B. microti*, *B. miyamotoi* and POWV were also detected. All provinces, however, had lower infection prevalence than hyper-endemic areas in the northeastern United States. For example, *I. scapularis* adults collected in Maine through

passive surveillance had *B. burgdorferi*, *A. phagocytophilum* and *B. microti* infection prevalence of 42.4%, 11.1% and 6.5%, respectively (39).

Ongoing climate and environmental changes affect TBD risk in a variety of ways, by altering populations of ticks and their animal hosts, as well as increasing human exposure to ticks (1). As current projections predict an increased risk of TBD from expansion of *Ixodes* spp. habitat in the future (1,5,40), continued surveillance can monitor changes in tick distribution and infection prevalence. More studies are also needed to understand the emergence and ecology of other tick-borne pathogens across Canada, which may differ from *B. burgdorferi*, for example, in their enzootic transmission cycles (41).

Strengths and limitations

This inaugural article combining active and passive tick surveillance presents a national snapshot of tick vectors and their emerging associated pathogens. By integrating the two types of surveillance, the strengths and weaknesses of the individual systems are complemented. Whereas active surveillance is resource-intensive and therefore limited in geographic scope, passive surveillance programs can be implemented on a larger geographic scale; however, passive surveillance lacks specificity as it often collects adventitious ticks seeded by migratory birds, especially ticks collected from companion animal hosts which readily acquire ticks from the environment (18,38).

There are several limitations to this study. Provincial passive surveillance programs, and the effort and timing of active surveillance, vary across Canada due to resource limitations or logistics. Passive tick surveillance has been discontinued or limited to specific hosts in several regions. Further, passive tick surveillance can be limited by public awareness, and geographic or host-specific biases in tick submissions (3,42,43). Not all active surveillance conducted in Canada in 2019 was included in this study; data from the many groups that conduct active surveillance, which includes university researchers, Indigenous communities and local or provincial public health units, was not all available. These limitations lead to underestimating the number of ticks, which affects the accuracy of infection prevalence. Lastly, it may be inappropriate to pool data from multiple active and passive surveillance systems due to differences in methodology between sources.

Conclusion

Passive and active surveillance identified both *I. scapularis* and *I. pacificus* across Canada in varying amounts depending on location, including some ticks which were infected with tick-borne pathogen(s). Both passive and active tick surveillance have utility in signalling and confirming new LD risk areas, which can be used to inform public health authorities where environmental risk for LD occurs. This information is used to communicate the local risk of LD and TBD to the public as well as to healthcare workers. Continued surveillance will be crucial for monitoring any expansion of areas at risk of exposure to ticks and tick-borne pathogens, and to appropriately target public health interventions such as education and awareness campaigns towards at-risk areas.

Authors' statement

CW — Formal analysis, visualization, writing–original draft, writing–review and editing
SG, AB, JK — Conceptualization, supervision, writing–review and editing
JB, NC, MK, ML, PL, RL, MM, CS — Writing–review and editing

Competing interests

None.

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References

1. Bouchard C, Dibernardo A, Koffi J, Wood H, Leighton PA, Lindsay LR. N Increased risk of tick-borne diseases with climate and environmental changes. Can Commun Dis Rep 2019;45(4):83–9. DOI PubMed

2. Ogden NH, Lindsay LR, Morshed M, Sockett PN, Artsob H. The emergence of Lyme disease in Canada. CMAJ 2009;180(12):1221–4. DOI PubMed

3. Nelder MP, Russell C, Lindsay LR, Dhar B, Patel SN, Johnson S, Moore S, Kristjanson E, Li Y, Ralevski F. Population-based passive tick surveillance and detection of expanding foci of blacklegged ticks Ixodes scapularis and the Lyme disease agent Borrelia burgdorferi in Ontario, Canada. PLoS One 2014;9(8):e105358. DOI PubMed

4. Ogden NH, Koffi JK, Pelcat Y, Lindsay LR. Environmental risk from Lyme disease in central and eastern Canada: a summary of recent surveillance information. Can Commun Dis Rep 2014;40(5):74–82. DOI PubMed

5. Leighton PA, Koffi JK, Pelcat Y, Lindsay LR, Ogden NH. Predicting the speed of tick invasion: an empirical model of range expansion for the Lyme disease vector Ixodes scapularis in Canada. J Appl Ecol 2012;49(2):457–64. DOI

6. Ogden NH, Ben Beard C, Ginsberg HS, Tsao JI. Possible effects of climate change on Ixodid ticks and the pathogens they transmit: predictions and observations. J Med Entomol 2021;58(4):1536–45. DOI PubMed

7. Ogden NH, Mechai S, Margos G. Changing geographic ranges of ticks and tick-borne pathogens: drivers, mechanisms and consequences for pathogen diversity. Front Cell Infect Microbiol 2013;3:46. DOI PubMed

8. Ogden NH, Lindsay LR. Effects of climate and climate change on vectors and vector-borne diseases: ticks are different. Trends Parasitol 2016;32(8):646–56. DOI PubMed

9. Gasmi S, Ogden NH, Lindsay LR, Burns S, Fleming S, Badcock J, Hanan S, Gaulin C, Leblanc MA, Russell C, Nelder M, Hobbs L, Graham-Derham S, Lachance L, Scott AN, Galanis E, Koffi JK. Surveillance for Lyme disease in Canada: 2009-2015. Can Commun Dis Rep 2017;43(10):194–9. DOI PubMed

10. Public Health Agency of Canada. Lyme disease surveillance in Canada: Preliminary annual report 2019. Ottawa, ON: PHAC; 2022 (accessed 2022-03-30). https://www.canada.ca/en/public-health/services/publications/diseases-conditions/lyme-disease-surveillance-report-2019.html

11. Kulkarni MA, Berrang-Ford L, Buck PA, Drebot MA, Lindsay LR, Ogden NH. Major emerging vector-borne zoonotic diseases of public health importance in Canada. Emerg Microbes Infect 2015;4:e33. DOI PubMed

12. Nelder MP, Russell CB, Lindsay LR, Dibernardo A, Brandon NC, Pritchard J, Johnson S, Cronin K, Patel SN. Recent emergence of Anaplasma phagocytophilum in Ontario, Canada: early serological and entomological indicators. Am J Trop Med Hyg 2019;101(6):1249–58. DOI PubMed

13. Bullard JM, Ahsanuddin AN, Perry AM, Lindsay LR, Iranpour M, Dibernardo A, Van Caeseele PG. The first case of locally acquired tick-borne Babesia microti infection in Canada. Can J Infect Dis Med Microbiol 2014;25(6):e87–9. DOI PubMed

14. Kadkhoda K, Dumouchel C, Brancato J, Gretchen A, Krause PJ. Human seroprevalence of Borrelia miyamotoi in Manitoba, Canada, in 2011-2014: a cross-sectional study. CMAJ Open 2017;5(3):E690–3. DOI PubMed

15. Bogaty C, Drebot M. Powassan virus - an emerging public health concern. CMAJ 2018;190(15):E472. DOI PubMed

16. Ogden NH, Trudel L, Artsob H, Barker IK, Beauchamp G, Charron DF, Drebot MA, Galloway TD, O'Handley R, Thompson RA, Lindsay LR. Ixodes scapularis ticks collected by passive surveillance in Canada: analysis of geographic distribution and infection with Lyme borreliosis agent Borrelia burgdorferi. J Med Entomol 2006;43(3):600–9. DOI PubMed

17. Bouchard C, Leonard E, Koffi JK, Pelcat Y, Peregrine A, Chilton N, Rochon K, Lysyk T, Lindsay LR, Ogden NH. The increasing risk of Lyme disease in Canada. Can Vet J 2015;56(7):693–9. PubMed

18. Ogden NH, Bouchard C, Kurtenbach K, Margos G, Lindsay LR, Trudel L, Nguon S, Milord F. Active and passive surveillance and phylogenetic analysis of Borrelia burgdorferi elucidate the process of Lyme disease risk emergence in Canada. Environ Health Perspect 2010;118(7):909–14. DOI PubMed

19. Guillot C, Badcock J, Clow K, Cram J, Dergousoff S, Dibernardo A, Evason M, Fraser E, Galanis E, Gasmi S, German GJ, Howse DT, Jardine C, Jenkins E, Koffi J, Kulkarni M, Lindsay LR, Lumsden G, McKay R, Moore K, Morshed M, Munn D, Nelder M, Nocera J, Ripoche M, Rochon K, Russell C, Slatculescu A, Talbot B, Thivierge K, Voordouw M, Bouchard C, Leighton P. Sentinel surveillance of Lyme disease risk in Canada, 2019: Results from the first year of the Canadian Lyme Sentinel Network (CaLSeN). Can Commun Dis Rep 2020;46(10):354–61. DOI PubMed

20. Government of Alberta. Tick surveillance - Interactive map. Tableau Public; 2020 (accessed 2021-07-15). https://public.tableau.com/app/profile/ellehojpublic/viz/Ticks_in_AB/AlbertaTicks

21. Schillberg E, Lunny D, Lindsay LR, Nelder MP, Russell C, Mackie M, Coats D, Berry A, Young Hoon KN. Distribution of Ixodes scapularis in northwestern Ontario: results from active and passive surveillance activities in the Northwestern Health Unit catchment area. Int J Environ Res Public Health 2018;15(10):2225. DOI PubMed

22. Dibernardo A, Cote T, Ogden NH, Lindsay LR. The prevalence of Borrelia miyamotoi infection, and co-infections with other Borrelia spp. in Ixodes scapularis ticks collected in Canada. Parasit Vectors 2014;7:183. DOI PubMed

23. Morshed MG, Lee MK, Boyd E, Mak S, Fraser E, Nguyen J, Dykstra EA, Otterstatter M, Henry B, Galanis E. Passive tick surveillance and detection of Borrelia species in ticks from British Columbia, Canada: 2002-2018. Vector Borne Zoonotic Dis 2021;21(7):490–7. DOI PubMed

24. Government of Alberta. Tick surveillance 2019: Summary. Edmonton, AB: Government of Alberta; 2020 (accessed 2021-09-15). https://open.alberta.ca/dataset/f0b7698f-03d4-4d32-858f-141ec7c3c108/resource/91920d4a-96df-4796-93f2-91262d748c68/download/health-tick-surveillance-2019-summary-report.pdf

25. Burrows H, Talbot B, McKay R, Slatculescu A, Logan J, Thickstun C, Lindsay LR, Dibernardo A, Koffi JK, Ogden NH, Kulkarni MA. A multi-year assessment of blacklegged tick (Ixodes scapularis) population establishment and Lyme disease risk areas in Ottawa, Canada, 2017-2019. PLoS One 2021;16(2):e0246484. DOI PubMed

26. Biggerstaff BJ. West Nile virus. Mosquito Surveillance Software. Atlanta (GA): CDC; 2009. https://www.cdc.gov/westnile/resourcepages/mosqSurvSoft.html

27. Walter SD, Hildreth SW, Beaty BJ. Estimation of infection rates in population of organisms using pools of variable size. Am J Epidemiol 1980;112(1):124–8. DOI PubMed

28. Public Health Agency of Canada. Lyme disease 2016 case definition. Ottawa, ON: PHAC; 2017 (accessed 2021-10-22). https://www.canada.ca/en/public-health/services/diseases/lyme-disease/surveillance-lyme-disease/case-definition.html

29. Morshed MG, Scott JD, Fernando K, Beati L, Mazerolle DF, Geddes G, Durden LA. Migratory songbirds disperse ticks across Canada, and first isolation of the Lyme disease spirochete, Borrelia burgdorferi, from the avian tick, Ixodes auritulus. J Parasitol 2005;91(4):780–90. DOI PubMed

30. Xu G, Pearson P, Dykstra E, Andrews ES, Rich SM. Human-biting Ixodes ticks and pathogen prevalence from California, Oregon, and Washington. Vector Borne Zoonotic Dis 2019;19(2):106–14. DOI PubMed

31. Eisen RJ, Eisen L, Ogden NH, Beard CB. Linkages of weather and climate with Ixodes scapularis and Ixodes pacificus (Acari: Ixodidae), enzootic transmission of Borrelia burgdorferi, and Lyme disease in North America. J Med Entomol 2016;53(2):250–61. DOI PubMed

32. Gasmi S, Ogden NH, Leighton PA, Lindsay LR, Thivierge K. Analysis of the human population bitten by Ixodes scapularis ticks in Quebec, Canada: increasing risk of Lyme disease. Ticks Tick Borne Dis 2016;7(6):1075–81. DOI PubMed

33. Ogden NH, Lindsay LR, Beauchamp G, Charron D, Maarouf A, O'Callaghan CJ, Waltner-Toews D, Barker IK. Investigation of relationships between temperature and developmental rates of tick Ixodes scapularis (Acari: Ixodidae) in the laboratory and field. J Med Entomol 2004;41(4):622–33. DOI PubMed

34. Mead PS. Epidemiology of Lyme disease. Infect Dis Clin North Am 2015 Jun;29(2):187–210. DOI PubMed

35. Government of Manitoba. Manitoba Health, Seniors and Active Living, Population Health Division, Population and Public Health Branch CDC. Manitoba Annual Tick-borne Disease Report 2018. Winnipeg, MB: Government of Manitoba; 2020 (accessed 2021-09-29). https://www.gov.mb.ca/health/publichealth/cdc/tickborne/docs/tbd_report2018.pdf

36. Nelder MP, Russell CB, Dibernardo A, Clow KM, Johnson S, Cronin K, Patel SN, Lindsay LR. Monitoring the patterns of submission and presence of tick-borne pathogens in Ixodes scapularis collected from humans and companion animals in Ontario, Canada (2011-2017). Parasit Vectors 2021;14(1):260. DOI PubMed

37. Gasmi S, Ogden NH, Ripoche M, Leighton PA, Lindsay RL, Nelder MP, Rees E, Bouchard C, Vrbova L, Rusk R, Russell C, Pelcat Y, Mechai S, Kotchi SO, Koffi JK. Detection of municipalities at-risk of Lyme disease using passive surveillance of Ixodes scapularis as an early signal: A province-specific indicator in Canada. PLoS One 2019;14(2):e0212637. DOI PubMed

38. Gasmi S, Bouchard C, Ogden NH, Adam-Poupart A, Pelcat Y, Rees EE, Milord F, Leighton PA, Lindsay RL, Koffi JK, Thivierge K. Evidence for increasing densities and geographic ranges of tick species of public health significance other than Ixodes scapularis in Québec, Canada. PLoS One 2018;13(8):e0201924. DOI PubMed

39. Rounsville TF, Dill GM, Bryant AM, Desjardins CC, Dill JF. Statewide passive surveillance of Ixodes scapularis and associated pathogens in Maine. Vector Borne Zoonotic Dis 2021;21(6):406–12. DOI PubMed

40. Koffi JK, Leighton PA, Pelcat Y, Trudel L, Lindsay LR, Milord F, Ogden NH. Passive surveillance for I. scapularis ticks: enhanced analysis for early detection of emerging Lyme disease risk. J Med Entomol 2012;49(2):400–9. DOI PubMed

41. Eisen RJ, Eisen L. The blacklegged tick, Ixodes scapularis: an increasing public health concern. Trends Parasitol 2018;34(4):295–309. DOI PubMed

42. Johnson JL, Ginsberg HS, Zhioua E, Whitworth UG Jr, Markowski D, Hyland KE, Hu R. Passive tick surveillance, dog seropositivity, and incidence of human lyme disease. Vector Borne Zoonotic Dis 2004;4(2):137–42. DOI PubMed

43. Ogden NH, Feil EJ, Leighton PA, Lindsay LR, Margos G, Mechai S, Michel P, Moriarty TJ. Evolutionary aspects of emerging Lyme disease in Canada. Appl Environ Microbiol 2015;81(21):7350–9. DOI PubMed

Surveillance for Lyme disease in Canada, 2009–2019

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Abstract

Background: Lyme disease (LD) is a multisystem infection that can affect the skin, heart, joints and nervous system. In Canada, the incidence of LD cases has increased over the past decade making this a disease of public health concern. The objective of this study is to summarize the epidemiology of LD cases reported in Canada from 2009 through 2019.

Methods: Incidence over time, case classification (confirmed and probable), seasonal and geographic distribution, demographic and clinical characteristics of reported LD cases were determined. Logistic regression was used to explore potential demographic risk factors for the occurrence of LD.

Results: During 2009–2019, a total of 10,150 LD cases were reported by the provinces to the Public Health Agency of Canada, of which 7,242 (71.3%) were confirmed and 2,908 (28.7%) were probable cases. The annual count increased from 144 in 2009 to 2,634 in 2019, mainly due to an increase in locally acquired infections, from 65.3% to 93.6%, respectively. The majority of cases (92.1%) were reported from three provinces: Ontario (46.0%); Nova Scotia (28.0%); and Québec (18.1%). Most of the locally acquired cases (74.0%) were reported in the summer months of June (20.0%), July (35.4%) and August (18.6%). The highest incidence rates (cases per 100,000 population) were in children aged 5–9 years (45.0) and in adults aged 65–69 years (74.3), with 57.3% of all reported cases occurring among males. The most common presenting symptoms were single erythema migrans rash (75.1%) and arthritis (34.1%). The frequency of reported clinical manifestations varied among age groups and seasons with erythema migrans and arthritis at presentation reported more frequently in children than older patients.

Conclusion: The results of this report highlight the continued emergence of LD in Canada and the need for further development and implementation of targeted awareness campaigns designed to minimize the burden of LD.

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Introduction

Lyme disease (LD) is the most commonly reported tick-borne zoonosis in North America and Europe. In Canada, LD is caused by the spirochete *Borrelia burgdorferi* (*B. burgdorferi*) *sensu stricto* and transmitted by *Ixodes pacificus* (*I. pacificus*) ticks in British Columbia and *Ixodes scapularis* (*I. scapularis*) in central and eastern Canada. Over the last decade, the warming climate as well as anthropogenic factors such as landscape changes, have contributed to tick and tick-borne diseases expanding their geographic range (1,2). As a result, the incidence of LD cases increased over the past decade (3) making this a disease of public health concern in Canada.

Lyme disease is a multisystem infection that can affect the skin, heart, joints and nervous system. Approximately 70% of people bitten by a *B. burgdorferi*-infected tick will develop a cutaneous rash, erythema migrans, which may be accompanied by flu-like symptoms (4). If left untreated, spirochetes disseminate throughout the body via the blood and may cause multiple secondary erythema migrans lesions, cardiac manifestations (carditis, atrioventricular heart block, arrhythmia and palpitations) and neurologic manifestations (facial paralysis—Bell's palsy—and meningitis). Months to years post-infection, late LD can manifest with single or recurrent joint arthritis episode(s). It is noteworthy that one death attributed to complications of Lyme carditis has been recorded in Canada in 2018 (5).

This report summarizes the epidemiology of LD cases reported in Canada from 2009 through 2019.

Methods

Case definition

Lyme disease became nationally notifiable in 2009. In 2016, the LD case definition (6) was revised to propose five methods to identify LD risk to simplify reporting by jurisdictions (**Table A1**).

Data sources

Information on reported LD cases from 2009 through 2019 was obtained from the provincial and territorial public health authorities via the Canadian Notifiable Disease Surveillance System (CNDSS) and the Lyme Disease Enhanced Surveillance (LDES) system of the Public Health Agency of Canada (PHAC). The CNDSS only collects demographic data, episode date and case classification from the provinces and territories. The LDES system captures additional data, including possible geographic location of exposure for both locally acquired and travel-related cases, clinical manifestations and results of laboratory testing. Public health units in the provinces and territories are responsible for investigating the cases reported by clinicians using a case management tool (7). They collect among other information, the most likely location of LD acquisition, whether in Canada or abroad, regardless of the stage of disease (8).

Analysis

Incidence rates per 100,000 population for reported cases were calculated by year, province, age group and sex using the census population estimates for July 1st of Statistics Canada data (9) for each year of the reporting period, 2009–2019. Seasonality was determined by the reported date of the symptom onset. Percentages of reported clinical manifestations of locally acquired infections were calculated for overall cases and by age group. The most likely geographic location for acquisition of LD infection was superimposed on a map of LD risk areas (6). Cases with a history of travel (within or outside of Canada) within 30 days of reporting were not included in the analysis of geographic distribution.

For locally acquired cases with no missing data, variations among age groups, sex, month of onset and reporting year were explored in multivariate logistic regression using Stata, version 15.1 (StataCorp, College Station, Texas, United States). In separate models, the binary outcome variable was the presence or absence of LD stage at presentation, for each of early localized (single erythema migrans), early disseminated (multiple erythema migrans, cardiac manifestations, Bell's palsy and other neurological manifestations) and late disseminated stage (arthritis) as classified by the Infectious Disease Society of America guidelines (10). For each model, explanatory variables were age group (10 and 15-year intervals), sex, month of symptom onset (in four categories for simplicity), year and province of reporting. The explanatory variable "province" was included in the analysis to account for possible variability in reporting between provinces. Explanatory variables were screened in bivariable logistic regression models, and those significant at the level of $p<0.1$ were included in multivariable models. The most parsimonious multivariate models were sought by backward elimination of non-significant variables until all factors in the model were significant ($p<0.05$).

Results

Incidence over time

From 2009 through 2019, 10,150 LD cases were reported in Canada. Of these 7,242 (71.3%) were confirmed and 2,908 (28.7%) were probable cases (**Table 1**). Overall, the annual number of reported cases increased from 144 in 2009 to 2,634 in 2019 (incidence rates per 100,000 population of 0.4 and 7.0, respectively); however, in 2014 and 2018 the number of cases decreased (**Table A2**). The number of cases acquired in Canada increased from 79 to 2,052 during the same period, representing 65.3% and 93.6%, respectively, of cases with known exposure location (**Figure 1**).

Among all reported cases, the majority (92.1%) were reported from three provinces: Ontario (46.0%); Nova Scotia (28.0%); and Québec (18.1%). In 2019, Nova Scotia reported a LD incidence that was twelve-fold greater than the LD incidence for Canada overall (85.6 versus 7.0 per 100,000 population) (**Table 2**).

During 2009–2019, data on history of travel was available for 83.2% (n=8,444) of all reported cases (n=10,150). Of the cases acquired during travel outside Canada, 363 (57.4%) were exposed in the United States and 261 (41.3%) in Europe.

Seasonal distribution

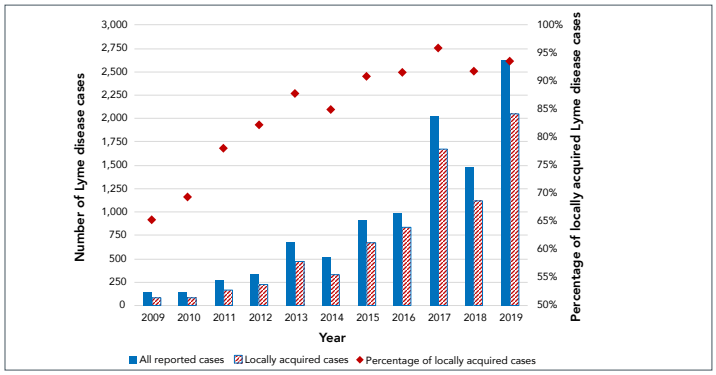
Over the study period, the month of illness onset for locally acquired cases was available for 6,278 cases (81.6%). Most cases (95.8%) were reported from May through November, with the majority reported in the summer months of June (20.0%), July (35.4%) and August (18.6%) (**Figure 2**).

Table 1: Classification (confirmed and probable) of reported Lyme disease cases[a], 2009–2019

Classification	Reported Lyme disease cases																							
	Year																							
	2009		2010		2011		2012		2013		2014		2015		2016		2017		2018		2019		Total	
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
All cases (n=10,150)																								
Confirmed	115	79.9	109	76.2	109	76.2	232	68.6	485	71.1	334	64.0	651	71.0	672	67.7	1,496	73.9	1,053	70.8	1,900	72.2	7,242	71.3
Probable	29	20.1	34	23.8	34	23.8	106	31.4	197	28.9	188	36.0	266	29.0	320	32.3	529	26.1	434	29.2	734	27.8	2,908	28.7
Total	144	100	143	100	143	100	338	100	682	100	522	100	917	100	992	100	2,025	100	1,487	100	2,634	100	10,150	100
Cases acquired in Canada (n=7,691)																								
Confirmed	56	70.9	56	65.1	56	65.1	129	58.1	286	61.1	198	59.5	467	70.0	542	64.8	1,204	72.0	751	67.2	1,410	68.7	5,195	67.5
Probable	23	29.1	30	34.9	30	34.9	93	41.9	182	38.9	135	40.5	200	30.0	294	35.2	467	28.0	366	32.8	642	31.3	2,496	32.5
Total	79	100	86	100	86	100	222	100	468	100	333	100	667	100	836	100	1,671	100	1,117	100	2,052	100	7,691	100

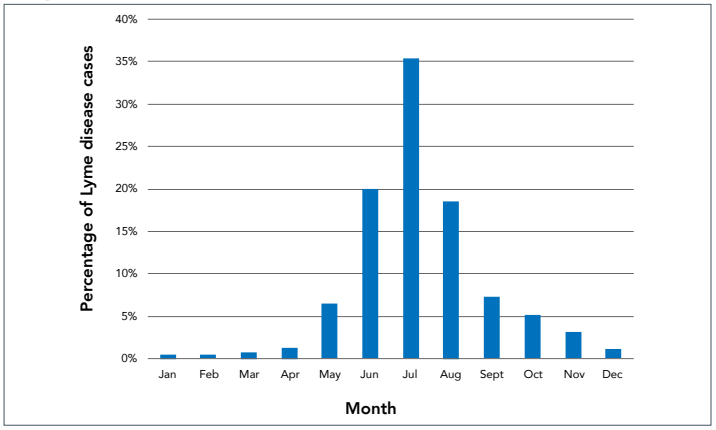
[a] Acquired in Canada: cases with no history of travel outside of Canada, within 30 days of reporting

Figure 1: Number and proportion of Lyme disease cases, all reported and locally acquired (percentage[a]) in Canada, 2009–2019



[a] Percentage of locally acquired cases among those cases with known location of probable acquisition in Canada

Figure 2: Month of illness onset[a] of Lyme disease cases acquired in Canada, 2009–2019



[a] Month of illness onset is the month of first symptoms seen

Table 2: Incidence per 100,000 population of Lyme disease cases reported by province and year in Canada[a], 2009–2019

Province	Incidence per 100,000 population										
	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
All cases (n=10,150)											
British Columbia	0.2	0.2	0.4	0.4	0.1	0.1	0.4	0.8	0.3	0.2	0.3
Alberta	0.0	0.0	0.2	0.2	0.5	0.2	0.3	0.2	0.3	0.3	0.3
Saskatchewan	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.1	0.3	0.2	0.1
Manitoba	0.4	1.0	1.0	1.5	2.3	2.7	2.4	3.9	3.2	4.0	4.7
Ontario	0.8	0.7	1.0	1.4	2.4	1.7	3.1	2.7	7.1	4.4	8.0
Québec	0.2	0.1	0.4	0.5	1.7	1.5	1.9	2.2	4.0	3.6	5.9
New Brunswick	0.0	0.3	0.7	0.9	0.7	0.7	1.7	1.4	3.9	2.6	4.6
Nova Scotia	1.7	1.8	5.7	5.4	16.2	12.1	26.1	34.6	61.2	47.0	85.6
Prince Edward Island	0.0	0.0	0.7	1.4	0.0	0.0	2.7	2.7	2.0	0.7	3.8
Newfoundland & Labrador	0.0	0.2	0.0	0.0	0.0	0.0	0.4	0.2	0.0	0.4	0.0
Canada	0.4	0.4	0.8	1.0	1.9	1.5	2.6	2.7	5.5	4.0	7.0
Cases acquired in the province of residency (n=7,200)											
British Columbia	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.1	0.1	0.0	0.0
Saskatchewan	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.0	0.1	0.0	0.0
Manitoba	0.3	0.6	0.6	1.0	2.0	2.4	2.3	2.4	2.9	3.5	4.1
Ontario	0.5	0.5	0.8	0.8	2.1	1.3	2.7	2.0	5.5	2.5	5.0
Québec	N/A	N/A	N/A	N/A	N/A	N/A	N/A	1.4	3.0	2.7	3.8
New Brunswick	0.0	0.3	0.4	0.7	0.7	0.5	1.5	0.8	3.5	2.5	3.1
Nova Scotia	1.5	1.5	5.2	5.3	16.1	12.1	26.1	25.4	55.2	34.8	79.2
Prince Edward Island	0.0	0.0	0.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Abbreviation: N/A, data on probable location of Lyme disease acquisition not available

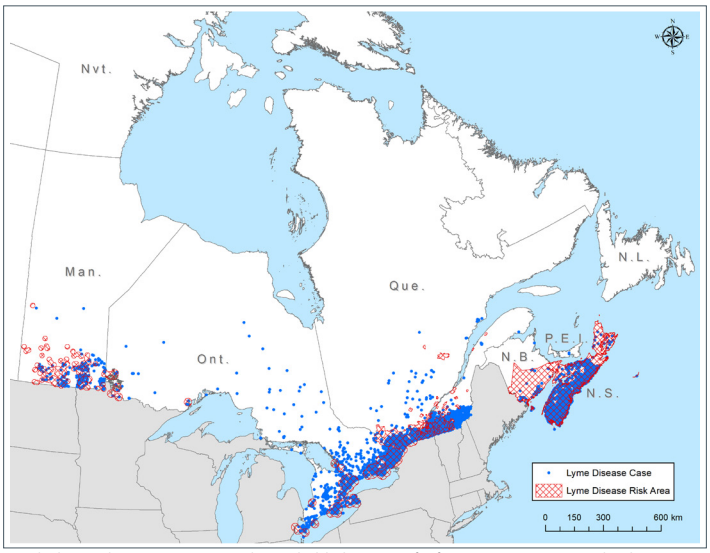
[a] No case has been reported from Yukon, Northwest Territories and Nunavut. All Lyme disease cases reported from Alberta and Newfoundland and Labrador were travel-related only. Data on location of acquisition were available for 83.2% (n=8,444) of all reported cases

Geographic distribution

Information on location of LD acquisition (at the sub-provincial level) was available for 93.5% (n=6,734) of the locally acquired cases. Most of the cases were concentrated in locations in southern Manitoba, south-central and south-eastern Ontario, southern Québec and New Brunswick and in Nova Scotia.

Some cases were likely acquired outside locations where populations of *I. scapularis* ticks are established (the hatched areas in the **Figure 3**).

Figure 3: Reported locations of Lyme disease acquisition[a], Canada, 2009–2019



[a] Each dot on the map represents the probable location of infection acquisition, randomly distributed at the census subdivision level for all provinces except: Québec (2016–2018) and Nova Scotia (2019) used the administrative region and forward sortation area (FSA) of residency, respectively. In 2018, all of Nova Scotia was declared at risk of Lyme disease, and since then, the probable location of acquisition was based on the FSA of residency for cases with no travel history outside the province. Data on location of acquisition was not available at sub-provincial level for British Columbia and Saskatchewan; Saskatchewan reported one locally acquired case in 2017. Cases reported by Alberta and Newfoundland & Labrador were travel-related only. Hatched areas indicate Lyme disease risk areas. These are locations where surveillance activities suggest that populations of the Lyme disease vector, *Ixodes scapularis* have been established and the likely transmission of *B. burgdorferi* is occurring

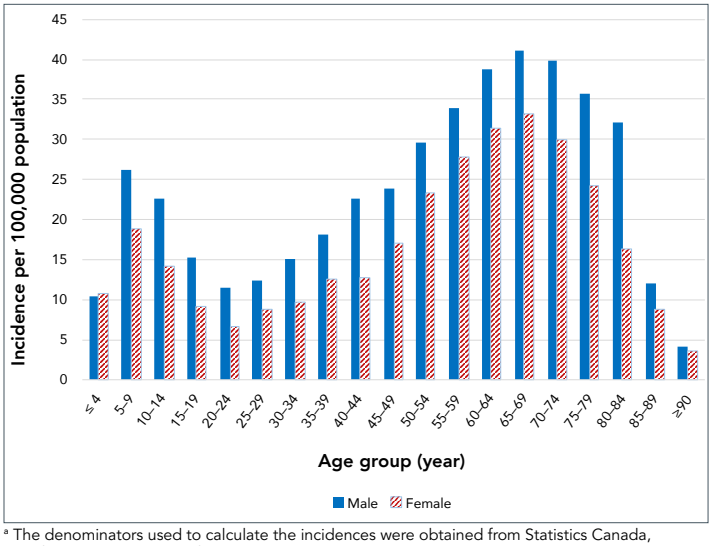
Demographic and clinical characteristics

Demographic information was available for 7,667 (99.7%) of reported locally acquired LD cases. The overall average age was 47.4 years (95% confidence interval (CI): 46.9–47.9).

The cumulative incidence per 100,000 population shows a bimodal pattern with peaks in children aged 5–9 years (45.0) and adults aged 65–69 years (74.3). Incidence was higher in adults aged 50–84 years, representing 57.0% of all reported cases (**Figure 4**).

Lyme disease cases were reported more often in males than females (57.3% versus 42.7%). In all age groups, incidence was higher among males than females, except for children under five years where the incidence was similar (Figure 4).

Figure 4: Cumulative incidence[a] per 100,000 population of Lyme disease cases by age group and sex, Canada, 2009–2019 (n=7,667)



[a] The denominators used to calculate the incidences were obtained from Statistics Canada, population estimates on July 1st

Information on clinical manifestations of LD cases was available for 4,961 (64.5%) of locally acquired infections. The most commonly reported manifestations were single erythema migrans rash (75.1%) and arthritis (34.1%). Cardiac manifestations, Bell's palsy and other neurologic manifestations were reported in 3.7%, 7.6% and 19.0% of cases, respectively. Among the 4,961 cases, 33.7% reported a combination of LD stages; 28.2% had early localized stage and early disseminated or late disseminated stage, and 5.5% had early and late disseminated stages.

In a multivariate analysis of the LD stages at presentation (**Table 3**), the odds of age groups 10–19, 20–29, 30–39 and 50–59 years for being diagnosed in early localized stage were respectively 0.56 (95% CI: 0.42–0.75), 0.63 (95% CI: 0.47–0.85), 0.60 (95% CI: 0.46–0.79) and 0.77 (95% CI: 0.61–0.97) times lower than the reference age group 0–9 years.

When the outcome was in the early disseminated stage, the odds of age groups 10–19, 20–29 and 60–69 years were, respectively, 1.56 (95% CI: 1.09–2.25), 1.76 (95% CI: 1.21–2.55) and 1.42 (95% CI: 1.04–1.94) times higher compared with the 0–9 years age group. In contrast, when the outcome was in late disseminated stage, the odds of age groups 60–74 and 75 years and older were respectively 0.78 (95% CI: 0.64–0.96) and 0.52 (95% CI: 0.38–0.78) times lower when compared to the reference age group, 0–14 years.

The number of cases with early localized stage was less likely to be reported from December–February versus June–August (odds ratio [OR]: 0.46; 95% CI: 0.30–0.69). Cases with early disseminated stage were less likely to be reported September–November (OR: 0.81; 95% CI: 0.66–0.99), December–February (OR: 0.51; 95% CI: 0.29–0.90) and March–May (OR: 0.62;

Table 3: Final multivariate binomial logistic regression models testing the factors that influence the occurrence of Lyme disease stages[a,b] of locally acquired cases, Canada, 2009–2019 (n=4,913)

Outcome	Explanatory variables	Odds ratio		Wald (*z* value)	*p*-value
		n	95% CI		
Early localized	10–19 years vs 0–9 years	0.56	0.42–0.75	-3.96	0.00
	20–29 years vs 0–9 years	0.63	0.47–0.85	-3.05	0.00
	30–39 years vs 0–9 years	0.60	0.46–0.79	-3.65	0.00
	50–59 years vs 0–9 years	0.77	0.61–0.97	-2.21	0.03
	Dec–Feb vs Jun–Aug	0.46	0.30–0.69	-3.77	0.00
Early disseminated	10–19 years vs 0–9 years	1.56	1.09–2.25	2.41	0.02
	20–29 years vs 0–9 years	1.76	1.21–2.55	2.98	0.00
	60–69 years vs 0–9 years	1.42	1.04–1.94	2.19	0.03
	Sep–Nov vs Jun–Aug	0.81	0.66–0.99	-2.08	0.04
	Dec–Feb vs Jun–Aug	0.51	0.29–0.90	-2.32	0.02
	Mar–May vs Jun–Aug	0.62	0.46–0.82	-3.32	0.00
Late disseminated	60–74 years vs 0–14 years	0.78	0.64–0.96	-2.36	0.02
	75 or more years vs 0–14 years	0.52	0.38–0.72	-4.04	0.00
	Male vs female	1.14	1.01–1.29	2.10	0.04
	Sep–Nov vs Jun–Aug	1.29	1.09–1.53	3.00	0.00
	Dec–Feb vs Jun–Aug	3.30	2.23–4.88	5.99	0.00
	Mar–May vs Jun–Aug	1.35	1.09–1.67	2.73	0.01

Abbreviations: CI, confidence intervals; vs, versus
[a] Clinical manifestations of Lyme disease classified as defined by the Infectious Disease Society of America guidelines (8)
[b] Early localized (single erythema migrans), early disseminated (multiple erythema migrans, cardiac manifestations, Bell's palsy and other neurological manifestations) and late disseminated (arthritis)

95% CI: 0.46−0.82) than in the summer months of June–August. Cases diagnosed in late disseminated stage were reported more often during September–November (OR: 1.29; 95% CI: 1.09−1.53), December−February (OR: 3.30; 95% CI: 2.23−4.88) and March−May (OR: 1.35; 95% CI: 1.09−1.67) when compared with June–August.

Males were more likely to be reported with late disseminated stage than females (OR: 1.14; 95% CI: 1.01−1.29).

Discussion

This report provides an update on the epidemiology of LD cases reported in Canada from 2009 through 2019. Over the 11-year period, the incidence of reported LD cases has increased dramatically in Canada, mainly due to an increase in the number of locally acquired infections. The vast majority of cases continued to be concentrated in southern Manitoba, south-central and south-eastern Ontario, southern Québec and New Brunswick and in Nova Scotia, which likely coincide in most cases with the areas where *I. scapularis* ticks carrying *B. burgdorferi* are established (11).

In these parts of the country, the tick vector is spreading northward as a result of climate warming that drives, in part, the growing suitable habitat for tick survival and establishment (12). Moreover, greater awareness among the public and healthcare providers and improvements to public health surveillance and notification may also have contributed to the increase in the number of reported cases.

It is important to note that the incidence in Nova Scotia during 2019 was twelve-fold higher than the national incidence. This is most likely a result of the increased number of established blacklegged tick populations; including the density, geographic range, *B. burgdorferi* infection prevalence (13), and the maritime climate that permits, during some warm spells in winter, tick activity in the absence of snow cover (14,15).

In contrast, in western Canada, where the predominant vector *I. pacificus* is distributed along the coast and southern region of British Columbia, the LD risk has remained relatively low and stable because of the low prevalence of infected ticks (16).

Lyme disease symptom onset was more likely reported from May to November, a pattern that corresponds to nymphal tick activity in the summer months (17); these time periods also overlap with when people are most engaged in outdoor activities that expose them to the risk of tick bites and *B. burgdorferi* transmission. However, some cases reported illness onset in winter months, which may be explained by 1) the occurrence of the late disseminated stage that appears months to years post-infection in untreated patients (18) or 2) advantageous weather that allows tick activity in British Columbia (19).

Consistent with previous studies, the age distribution of cases was bimodal in children and older adults. Among children, incidence peaked in those aged 5–9 years, which corroborates previous studies in Canada and the United States (20–22). However, we found that adults aged 50−84 years were at higher risk of LD compared with previous studies, which reported younger groups (range 50−64 years) to be the most at risk (20–23). The level of adoption of preventive behaviours toward LD or to the level of tick exposure could have contributed

to the observed discrepancy in the most at-risk age group for LD (24). Targeted education and awareness of preventive measures are needed for older persons in order to decrease the risk of tick bites and LD.

Erythema migrans and arthritis were the most commonly reported clinical manifestations in this study; consistent with findings reported previously in Canada and the United States (20–23). Lyme arthritis is a manifestation of late stage LD that usually appears in 51% of untreated patients (25), highlighting the importance of early detection and treatment.

Males were more likely to have LD than females across almost all age groups, similar to previous reports from Canada and the United States (20–22). Additionally, late disseminated stage was more common in males than females, although no significant differences were found for earlier disease stages. This apparent sex-based difference might be a result of higher risk of tick bites (26) and LD transmission; however, the reason why males are diagnosed more often than females with late Lyme arthritis may be due to a difference in immunologic response to *B. burgdorferi* infection (27) or simply to a delay in presenting for medical care. Further research is needed to elucidate this finding.

Across age categories, the percentage of reported clinical manifestations varied widely in children younger than 15 years. The percentage of cases with single erythema migrans (early localized stage) was higher in younger children and the proportion of arthritis (late disseminated stage) was higher in older children (**Figure A1**) which is consistent with a study from the Canadian Paediatric Surveillance Program (14). Furthermore, children are at higher risk of both early localized LD and Lyme arthritis than older patients. Studies have found that children are at higher risk of tick bites from vector ticks such as *I. scapularis* and *I. pacificus* (26,28,29); hence, efforts to enhance awareness of ticks and LD should target this at-risk age group and their parents and caregivers.

The LD stage at presentation varied significantly between seasons. Cases with early localized stage were more frequently reported in summer months (June–August) than winter months (December–February); and cases with arthritis were less frequently reported in summer months compared with the rest of the year. This is expected given that untreated patients have manifestations of the early localized stage that appear within 30 days of infection, and the late disseminated stage can appear months to years post infection (24). In contrast, cases with early disseminated stage were diagnosed more in the summer than other parts of the year. Given that early disseminated stage appears in untreated patients within three months post infection, this finding suggests it is likely that there is some underreporting of cases with cardiac and neurologic manifestations, which may go undetected or unreported outside of the summer months. This result underscores that prevention messages should not only be focused during the spring and summer months when nymphal and adult ticks are most active, but year-round.

Limitations

There are several limitations to the interpretation of the findings of this report. First, it is likely that the incidence rates over time are conservative estimates as some LD cases may be undiagnosed and probable cases may be underreported. Second, the 2016 LD case definition revision could have impacted the reporting of some cases. Third, clinical manifestations are reported voluntarily to the provincial public health organizations, which could have led to misclassification and underreporting. Fourth, information on whether the LD infection was locally acquired or travel-related is only an estimate because not all provinces provided these data. Finally, because of limited resources, field tick surveillance to detect the expansion of LD risk areas may not be up to date in many locations, which would affect the classification of cases.

Conclusion

The number of reported LD cases has continued to increase in Canada over the last decade, as did the geographic range of ticks that carry the LD bacterium. Continued surveillance, preventive strategies as well as early disease recognition and treatment will continue to minimize the impact of LD in Canada.

The key findings of this report highlight the need for further targeted awareness campaigns designed to minimize the burden of LD in Canada.

Authors' statement

SG — Data collection and curation, conceptualization, methodology, formal analysis, writing–original draft, writing–review and editing
JKK, ACB — Conceptualization, methodology, writing–review and editing, management
MPN, CR, SGD, CS, BA, JB, SB, BAB, BH, SJ, MS — Writing–review and editing

Competing interests

None.

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References

1. Ostfeld RS, Brunner JL. Climate change and Ixodes tick-borne diseases of humans. Phil Trans R Soc B. 2015;370(1665):20140051. DOI

2. Clow KM, Ogden NH, Lindsay LR, Michel P, Pearl DL, Jardine CM. Distribution of ticks and the risk of Lyme disease and other tick-borne pathogens of public health significance in Ontario, Canada. Vector Borne Zoonotic Dis 2016;16(4):215–22. DOI PubMed

3. Public Health Agency of Canada. Lyme disease surveillance report: Preliminary annual report 2018. Ottawa (ON): PHAC; 2021 (accessed 2021-02-22). https://www.canada.ca/en/public-health/services/publications/diseases-conditions/lyme-disease-surveillance-report-2018.html

4. Wormser GP, Dattwyler RJ, Shapiro ED, Halperin JJ, Steere AC, Klempner MS, Krause PJ, Bakken JS, Strle F, Stanek G, Bockenstedt L, Fish D, Dumler JS, Nadelman RB. The clinical assessment, treatment, and prevention of lyme disease, human granulocytic anaplasmosis, and babesiosis: clinical practice guidelines by the Infectious Diseases Society of America. Clin Infect Dis 2006;43(9):1089–134. DOI PubMed

5. Semproni M, Rusk R, Wuerz T. Fatal Lyme carditis presenting as fluctuating high-grade atrioventricular block. CMAJ 2020;192(21):E574–7. DOI PubMed

6. Public Health Agency of Canada. Lyme disease 2016 case definition. Ottawa (ON): PHAC; 2017 (accessed 2018-06-20). https://www.canada.ca/en/public-health/services/diseases/lyme-disease/surveillance-lyme-disease/case-definition.html

7. Johnson KO, Nelder MP, Russell C, Li Y, Badiani T, Sander B, Sider D, Patel SN. Clinical manifestations of reported Lyme disease cases in Ontario, Canada: 2005-2014. PLoS One 2018;13(6):e0198509. DOI PubMed

8. Institut National de Santé Publique du Québec. Portrait de la maladie de Lyme au Québec: 2006-2019. Québec (QC) : ISNPQ; 2022 (accessed 2022-03-12). https://www.inspq.qc.ca/publications/2844

9. Statistics Canada. Population estimates on July 1st, by age and sex. Ottawa (ON): StatCan; 2021 (accessed 2021-03-03). https://www150.statcan.gc.ca/t1/tbl1/en/tv.action?pid=1710000501

10. Sanchez E, Vannier E, Wormser GP, Hu LT. Diagnosis, treatment, and prevention of Lyme disease, human granulocytic anaplasmosis, and babesiosis: a review. JAMA 2016;315(16):1767–77. DOI PubMed

11. Ogden NH, Bouchard C, Kurtenbach K, Margos G, Lindsay LR, Trudel L, Nguon S, Milord F. Active and passive surveillance and phylogenetic analysis of Borrelia burgdorferi elucidate the process of Lyme disease risk emergence in Canada. Environ Health Perspect 2010;118(7):909–14. DOI PubMed

12. Ogden NH, Radojevic M, Wu X, Duvvuri VR, Leighton PA, Wu J. Estimated effects of projected climate change on the basic reproductive number of the Lyme disease vector Ixodes scapularis. Environ Health Perspect 2014;122(6):631–8. DOI PubMed

13. Hatchette TF, Johnston BL, Schleihauf E, Mask A, Haldane D, Drebot M, Baikie M, Cole TJ, Fleming S, Gould R, Lindsay R. Epidemiology of Lyme Disease, Nova Scotia, Canada, 2002-2013. Emerg Infect Dis 2015;21(10):1751–8. DOI PubMed

14. Ogden NH, Gasmi S, Koffi JK, Barton M, Lindsay LR, Langley JM. Lyme disease in children: Data from the Canadian Paediatric Surveillance Program. Ticks Tick Borne Dis 2020;11(2):101347. DOI PubMed

15. Environment and Natural Resources. 1981-2010 Canadian Climate Normals & Averages. Ottawa (ON): ENR; 2022 (accessed 2022-03-13). https://climate.weather.gc.ca/climate_normals/index_e.html

16. Morshed MG, Lee MK, Man S, Fernando K, Wong Q, Hojgaard A, Tang P, Mak S, Henry B, Patrick DM. Surveillance for Borrelia burgdorferi in Ixodes ticks and small rodents in British Columbia. Vector Borne Zoonotic Dis 2015;15(11):701–5. DOI PubMed

17. Kurtenbach K, Hanincová K, Tsao JI, Margos G, Fish D, Ogden NH. Fundamental processes in the evolutionary ecology of Lyme borreliosis. Nat Rev Microbiol 2006;4(9):660–9. DOI PubMed

18. Hatchette TF, Davis I, Johnston BL. Lyme disease: clinical diagnosis and treatment. Can Commun Dis Rep 2014;40(11):194–208. DOI PubMed

19. Salkeld DJ, Castro MB, Bonilla D, Kjemtrup A, Kramer VL, Lane RS, Padgett KA. Seasonal activity patterns of the western black-legged tick, Ixodes pacificus, in relation to onset of human Lyme disease in northwestern California. Ticks Tick Borne Dis 2014;5(6):790–6. DOI PubMed

20. Bacon RM, Kugeler KJ, Mead PS; Centers for Disease Control and Prevention (CDC). Surveillance for Lyme disease--United States, 1992-2006. MMWR Surveill Summ 2008;57(10):1–9. PubMed

21. Schwartz AM, Hinckley AF, Mead PS, Hook SA, Kugeler KJ. Surveillance for Lyme Disease - United States, 2008-2015. MMWR Surveill Summ 2017;66(22):1–12. DOI PubMed

22. Gasmi S, Ogden NH, Lindsay LR, Burns S, Fleming S, Badcock J, Hanan S, Gaulin C, Leblanc MA, Russell C, Nelder M, Hobbs L, Graham-Derham S, Lachance L, Scott AN, Galanis E, Koffi JK. Surveillance for Lyme disease in Canada: 2009-2015. Can Commun Dis Rep 2017;43(10):194–9. DOI PubMed

23. Ogden NH, Koffi JK, Lindsay LR, Fleming S, Mombourquette DC, Sanford C, Badcock J, Gad RR, Jain-Sheehan N, Moore S, Russell C, Hobbs L, Baydack R, Graham-Derham S, Lachance L, Simmonds K, Scott AN. Surveillance for Lyme disease in Canada, 2009 to 2012. Can Commun Dis Rep 2015;41(6):132–45. DOI PubMed

24. Aenishaenslin C, Bouchard C, Koffi JK, Ogden NH. Exposure and preventive behaviours toward ticks and Lyme disease in Canada: results from a first national survey. Ticks Tick Borne Dis 2017;8(1):112–8. DOI PubMed

25. Steere AC, Schoen RT, Taylor E. The clinical evolution of Lyme arthritis. Ann Intern Med 1987;107(5):725–31. DOI PubMed

26. Gasmi S, Ogden NH, Leighton PA, Lindsay LR, Thivierge K. Analysis of the human population bitten by Ixodes scapularis ticks in Quebec, Canada: increasing risk of Lyme disease. Ticks Tick Borne Dis 2016;7(6):1075–81. DOI PubMed

27. Schwarzwalder A, Schneider MF, Lydecker A, Aucott JN. Sex differences in the clinical and serologic presentation of early Lyme disease: results from a retrospective review. Gend Med 2010;7(4):320–9. DOI PubMed

28. Gasmi S, Bouchard C, Ogden NH, Adam-Poupart A, Pelcat Y, Rees EE, Milord F, Leighton PA, Lindsay RL, Koffi JK, Thivierge K. Evidence for increasing densities and geographic ranges of tick species of public health significance other than Ixodes scapularis in Québec, Canada. PLoS One 2018;13(8):e0201924. DOI PubMed

29. Xu G, Pearson P, Dykstra E, Andrews ES, Rich SM. Human-biting Ixodes ticks and pathogen prevalence from California, Oregon, and Washington. Vector Borne Zoonotic Dis 2019;19(2):106–14. DOI PubMed

30. Canadian Public Health Laboratory Network. The laboratory diagnosis of Lyme borreliosis: guidelines from the Canadian Public Health Laboratory Network. Can J Infect Dis Med Microbiol 2007;18(2):145–8. DOI PubMed

31. Centers for Disease Control and Prevention (CDC). Recommendations for test performance and interpretation from the Second National Conference on Serologic Diagnosis of Lyme Disease. MMWR Morb Mortal Wkly Rep 1995;44(31):590–1. PubMed

Annex

Table A1: 2016 Lyme disease case definition

Confirmed case	Probable case
Clinical evidence of illness with laboratory confirmation by one of the following methods: Isolation of *Borrelia burgdorferi* (*B. burgdorferi*) from a clinical specimen as specified by current guidelines (10,18,30) Detection of *B. burgdorferi* DNA by PCR testing on synovial fluid, cerebrospinal fluid, EM tissue biopsies or blood and by methods specified by current guidelines (10,18,30) OR Clinical evidence of illness with a history of residence in, or visit to, a Lyme disease risk area; and with laboratory evidence of infection in the form of a positive serologic test using the two-tiered approach. The two-tiered testing approach consists of a screening ELISA followed by an immunoblot assay. Immunoblots include traditional Western blots (30) or newer line blots, and both formats target an identical set of *B. burgdorferi* immunoreactive proteins (31)[a]	Clinical evidence of illness without a history of residence in, or visit to, a Lyme disease risk area; and with laboratory evidence of infection in the form of a positive serologic test as defined above under confirmed cases[a] OR Clinician-observed erythema migrans without laboratory evidence but with history of residence in, or visit to, a Lyme disease risk area

Abbreviations: DNA, deoxyribonucleic acid; ELISA, enzyme-linked immunosorbent assay; EM, erythema migrans; PCR, polymerase chain reaction

[a] Laboratory comments: Criteria for serologic testing are described by the guidelines of the Canadian Public Health Laboratory Network (26). Serologic evidence is confirmatory only in patients with objective clinical evidence of disseminated Lyme disease, and a history of residence in, or visit to, a Lyme disease risk area. Serologic testing is not recommended in patients with early localized Lyme disease with exposure from a Lyme disease risk area

Figure A1: Percentage of clinical manifestations by age group for locally acquired Lyme disease cases, in Canada, 2009–2019 (n=4,951)

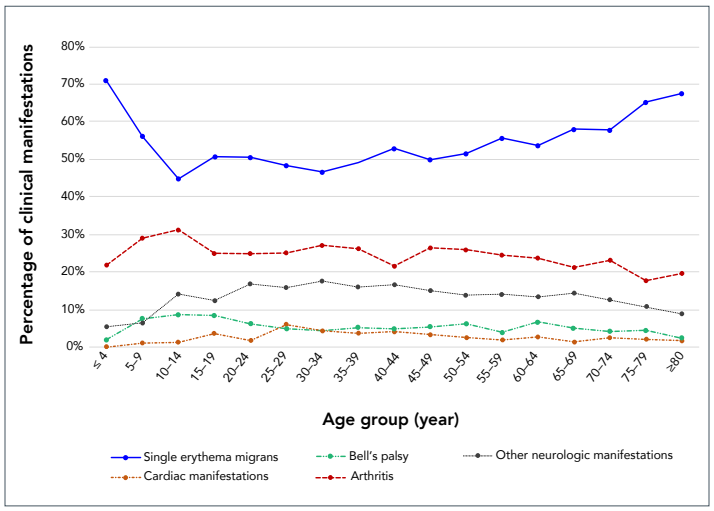

Table A2: Number of Lyme disease cases reported in Canada[a] by province and year, 2009–2019

Province	Lyme disease cases (n=10,150)											
	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	Total
British Columbia	9	7	20	18	6	5	21	40	17	9	14	166
Alberta	0	0	7	8	19	9	14	10	12	15	14	108
Saskatchewan	0	0	1	0	1	0	0	1	4	2	1	10
Manitoba	5	12	12	19	29	35	31	51	43	54	65	356
Ontario	100	93	134	191	327	229	426	371	1,005	628	1,168	4,672
Québec	14	11	32	42	142	125	160	177	329	305	500	1,837
New Brunswick	0	2	5	7	5	5	13	11	30	20	36	134
Nova Scotia	16	17	54	51	153	114	246	326	582	451	830	2,840
Prince Edward Island	0	0	1	2	0	0	4	4	3	1	6	21
Newfoundland & Labrador	0	1	0	0	0	0	2	1	0	2	0	6
Canada	144	143	266	338	682	522	917	992	2,025	1,487	2,634	10,150

[a] No case was reported from Yukon, Northwest Territories or Nunavut to the Canadian Notifiable Disease Surveillance System of the Public Health Agency of Canada, 2009–2019

Epidemiology of invasive meningococcal disease in Canada, 2012–2019

Myriam Saboui[1]*, Raymond SW Tsang[2], Robert MacTavish[1], Amisha Agarwal[1], Y Anita Li[1], Marina I Salvadori[1], Susan G Squires[1]

Abstract

Background: A variety of routine childhood and adolescent meningococcal vaccination programs using monovalent (serogroup C) and quadrivalent (A, C, Y, W) conjugate vaccines have been implemented in Canada since 2002, resulting in a decrease in invasive meningococcal disease (IMD) incidence, particularly in serogroup C. Meningococcal vaccines have also been used for outbreak response, including the multicomponent vaccine serogroup B vaccine. This report describes the epidemiology of IMD in Canada from 2012 to 2019.

Methods: Case data were obtained from the National Enhanced IMD Surveillance System between January 1, 2012 and December 31, 2019. Isolates were sent to the National Microbiology Laboratory for confirmation of serogroup and further studies including phenotype and clonal complex identification.

Results: A total of 983 cases of IMD were reported between 2012 and 2019. Overall, the age-adjusted incidence of IMD from 2012 to 2019 was 0.34 cases per 100,000 population per year when standardized to the Canadian 2011 population age distribution (95% CI: 0.32–0.36). Infants younger than one year of age had the highest average age-specific incidence rate (3.6 cases per 100,000 population per year, 95% CI: 2.8–4.3). The highest age-adjusted incidence rate was associated with serogroup B (0.17 cases per 100, 000 population per year, 95% CI: 0.16–0.19). Prior to 2015, most invasive serogroup W isolates were identified as clonal complex 22 (ST-22 CC) and the increase in serogroup W in Canada in recent years has been associated with the replacement of the endemic ST-22 CC with the hyper-virulent ST-11 CC.

Conclusion: Invasive meningococcal disease is a rare but severe infection in Canada that mostly affects the very young. Serogroup B continues to account for the greatest proportion of disease. Serogroup W associated with ST-11 CC is becoming a growing contributor of disease in all age groups not protected by serogroup W-containing vaccines.

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Keywords: epidemiology, meningococcal, invasive meningococcal disease, Canada

Introduction

Invasive meningococcal disease (IMD) is a serious illness caused by the bacterium *Neisseria meningitidis* (1). High-risk groups for contracting infection include travellers to endemic areas including the sub-Saharan African meningitis belt, young children, adolescents and individuals living in crowded quarters (2). Invasive meningococcal disease caused by some serogroups is vaccine preventable and endemic in Canada, with increased activity occurring periodically in the winter months. Since the early 2000s, a variety of routine childhood and adolescent vaccination programs using monovalent (serogroup C) and quadravalent (serogroup A, C, Y and W-135) meningococcal conjugate vaccines have been implemented in Canada (3). This has resulted in a decrease in IMD incidence, particularly for serogroup C. In the last decade, the multicomponent meningococcal B vaccine (4CMenB) has been used to control outbreaks (3) but has not been used in routine vaccination programs across the country. During the period covered in this report, the schedule of publicly funded vaccination programs has remained constant.

The last national IMD surveillance report described the epidemiology of IMD in Canada from 2006 to 2011. This article focuses on recent IMD data from 2012 to 2019 and explores trends over time, seasonality, spatial distribution and clinical presentation of cases and mortality.

Methods

Data

National enhanced case-based surveillance has been conducted in Canada since 1995 through the Public Health Agency of Canada's Enhanced Invasive Meningococcal Disease Surveillance System (eIMDSS). Provincial and territorial health departments voluntarily reported non-nominal epidemiologic data on confirmed IMD cases on an annual basis. Deterministic matching was conducted to retrospectively link epidemiologic and laboratory data. This article is based on IMD data extracted from eIMDSS, with disease onset between January 1, 2012, and December 31, 2019. See **Annex** for the national case definition.

Laboratory methods

Isolates were routinely sent to the National Microbiology Laboratory (NML) for confirmation of serogroup and further strain characterization. Serogrouping was done by bacterial agglutination test and confirmed by polymerase chain reaction (PCR) when necessary; serosubtypes of isolates were determined by whole cell enzyme-linked immunosorbent assay using monoclonal antibodies, while clonal analysis was done by multi-locus sequence typing as previously described (4).

Statistical analysis

The demographic, temporal and spatial distribution of IMD cases were examined, in addition to case manifestation, vaccination history, disease outcome and isolate characteristics. Incidence rates were calculated per 100,000 population using annual July 1st population estimates by province/territory, age and sex, which were obtained from Statistics Canada (5). The direct method was used for calculating age-standardized rates based on the 2011 Canadian census. Cases with missing age were excluded from the age standardization and all age-related analyses. Confidence intervals (CIs) for incidence rates were calculated at the 95% confidence level. The CIs of age-standardized rates were calculated according to the method based on the gamma distribution. All analyses were conducted using Microsoft Excel 2010, SAS 9.4, and R version 4.0.2 (R Foundation for Statistical Computing, Vienna, Austria).

Results

Trends over time

A total of 983 cases of IMD were reported between 2012 and 2019. Seven cases were excluded from age-specific analyses as the age was missing. The yearly number of reported cases ranged from 98 in 2016 to 154 in 2012 (**Figure 1**). Overall, the age-adjusted incidence of IMD from 2012 to 2019 was 0.34 cases per 100,000 population per year (95% CI: 0.32–0.36). As shown in **Table 1**, those patients 40 years of age and older accounted for 42% of all IMD cases between 2012 and 2019, followed by those 15–19 years (12%), 1–4 years (12%) and younger than one year of age (11%). Among serogroup B cases, children 1–4 years of age accounted for the largest proportion of cases (n=90/487, 18%), although those younger than one year of age and 60 years and older followed closely behind (15% of total cases for each age group). Adults over 40 years of age accounted for the majority of cases associated with serogroups C, W-135 and Y (55%, 56% and 63%, respectively).

The highest incidence rate observed was associated with serogroup B in 2012 (0.32 cases per 100,000, 95% CI: 0.26–0.38) (**Table 2**); since then, the rate has declined. The incidence rate for serogroups C and Y has remained low and stable throughout 2012–2019. In more recent years, the incidence rate was highest for serogroup W-135 (0.15 cases per 100,000, 95% CI: 0.11–0.19 in 2018 and 0.12 cases per 100,000, 95% CI: 0.09–0.16 in 2019).

Figure 1: Number of invasive meningococcal disease cases and overall incidence rates (per 100,000 population) in Canada by year, 2012–2019

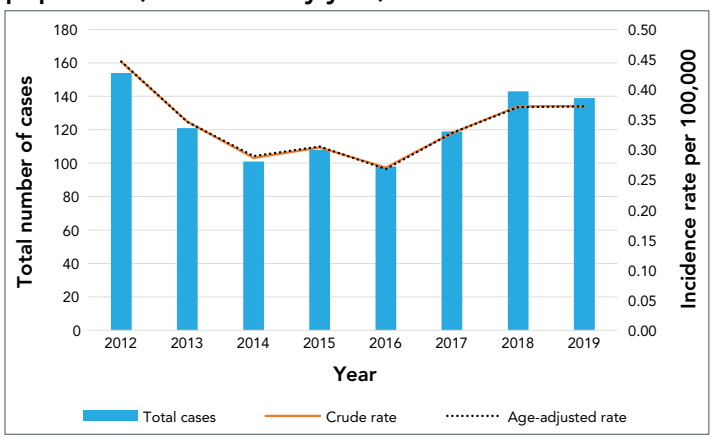


Table 1: Number and proportion of invasive meningococcal disease cases in Canada for each serogroup by age group, 2012–2019 (N=983 cases)

Age group (years)	Number and proportion of invasive meningococcal disease cases															
	Serogroup								Non-groupable		Other[a]		Unknown[b]		Total	
	B		C		W-135		Y									
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
<1	73	15	4	7	18	10	5	3	0	0	0	0	9	17	109	11
1–4	90	18	2	4	11	6	3	2	0	0	0	0	9	17	115	12
5–9	18	4	2	4	2	1	2	1	0	0	2	18	2	4	28	3
10–14	20	4	2	4	2	1	3	2	0	0	1	9	2	4	30	3
15–19	69	14	4	7	13	8	26	13	1	25	1	9	6	11	120	12
20–24	36	7	4	7	11	6	19	10	0	0	4	36	3	6	77	8
25–29	21	4	0	0	7	4	6	3	0	0	1	9	2	4	37	4
30–39	23	5	7	13	7	4	8	4	1	25	0	0	4	8	50	5
40–59	62	13	13	23	33	19	44	22	1	25	2	18	10	19	165	17
60+	75	15	18	32	63	37	82	41	1	25	0	0	6	11	245	25
Unknown	0	0	0	0	5	3	2	1	0	0	0	0	0	0	7	1
Total	487	–	56	–	172	–	200	–	4	–	11	–	53	–	983	–

Abbreviation: –, not obtained
[a] Other are those cases with the serogroup noted as: A, E, Z, 29E and non-encapsulated
[b] Unknown are those cases missing serogroup information

Table 2: Age-standardized incidence rates (per 100,000 population) and 95% CI of invasive meningococcal disease in Canada by serogroup and year, 2012–2019 (N=976 cases[a])

Serogroup	Age-standardized incidence rates (per 100,000 population)															
	2012		2013		2014		2015		2016		2017		2018		2019	
	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
B	0.32	0.26–0.38	0.23	0.18–0.29	0.16	0.12–0.20	0.18	0.14–0.23	0.13	0.09–0.17	0.14	0.10–0.18	0.12	0.08–0.16	0.12	0.09–0.16
C	0.04	0.02–0.06	0.02	0.01–0.04	0.03	0.01–0.05	0.01	0.0–0.03	0.01	0.0–0.02	0.02	0.01–0.05	0.02	0.01–0.04	0.01	0.0–0.03
W-135	0.01	0.0–0.03	0.01	0.0–0.03	0.02	0.01–0.04	0.03	0.01–0.05	0.04	0.02–0.06	0.08	0.05–0.11	0.15	0.11–0.19	0.12	0.09–0.16
Y	0.05	0.03–0.08	0.07	0.04–0.10	0.08	0.06–0.12	0.07	0.05–0.10	0.07	0.04–0.10	0.06	0.03–0.09	0.07	0.05–0.11	0.08	0.05–0.11
Non-groupable	–	–	–	–	–	–	0.01	0.0–0.02	–	–	–	–	–	–	0.01	0.0–0.02
Other[b]	–	–	–	–	–	–	–	–	0.01	0.0–0.02	0.01	0.0–0.02	–	–	0.01	0.0–0.02
Unknown[c]	0.03	0.01–0.05	0.01	0.0–0.03	0.01	0.0–0.02	0.01	0.0–0.03	0.02	0.01–0.04	0.03	0.01–0.05	0.01	0.01–0.03	0.03	0.0–0.05

Abbreviations: CI, confidence interval, –, not obtained
[a] Seven cases of total sample were missing age
[b] Other are those cases with the serogroup noted as: A, E, Z, 29E and non-encapsulated
[c] Unknown are those cases missing serogroup information

As seen in **Table 3**, there was a statistically significant decrease in the overall age-standardized incidence rates from 2012 to 2016 (approximate decrease of 0.040 cases per year, 95% CI: 0.003–0.077). The opposite was true from 2016 to 2019, where the overall age-standardized incidence rate increased by 0.038 cases per year (95% CI: −0.005–0.076), although this increase was not statistically significant. Infants younger than one year of age had the highest average age-specific incidence rate of 3.6 cases per 100,000 population per year (95% CI: 2.8–4.3), while the incidence ranged from 0.13 to 0.93 per 100,000 population for the other age groups.

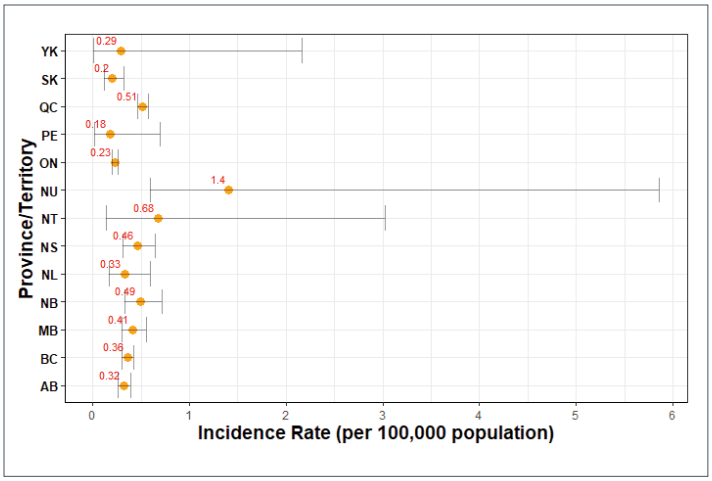
Spatial distribution of cases

Between 2012 and 2019, age-standardized incidence rates were highest in the territory of Nunavut (1.40 cases per 100,000 population per year, 95% CI: 0.59–5.86), which was significantly higher than British Columbia, Alberta, Saskatchewan, Manitoba, Québec and Ontario (**Figure 2**); however, only eight cases were reported in Nunavut between 2012 and 2019 resulting in wide 95% CIs. Ontario had the lowest age-standardized incidence rate at 0.23 cases per 100,000 population per year (95% CI: 0.20–0.26), which was significantly lower than Québec, Manitoba, Nova Scotia, New Brunswick, Nunavut and British Columbia. Overall, the provinces and territories had comparable age-standardized incidence rates.

Travel and seasonality

Between 2012 and 2019, 51 cases out of 376 cases with available data (14%) were associated with travel. Approximately half of the cases (n=27/51, 53%) travelled within Canada. The United States accounted for the largest proportion of cases associated with travel outside the country (n=5/51, 10%).

Figure 2: Age-standardized incidence rates (per 100,000 population-year, with 95% CIs) of invasive meningococcal disease in Canada by province or territory, 2012–2019 (N=976 cases)



Abbreviations: AB, Alberta; BC, British Columbia; CI, confidence intervals; MB, Manitoba; NB, New Brunswick; NL, Newfoundland and Labrador; NS, Nova Scotia; NT, Northwest Territories; NU, Nunavut; ON, Ontario; QC, Québec; PE, Prince Edward Island; SK, Saskatchewan; YK, Yukon

Data on month of onset were reported for 930 cases (95% of total sample). Overall, the fall and winter months accounted for the majority of cases (60%). Peaks of IMD onset were observed in the months of December/January (22%), March (12%) and October (10%). The summer months (July and August) were characterized by low IMD activity, with only 11% of all cases reported during the summer.

Table 3: Incidence rates (per 100,000 population) of invasive meningococcal disease in Canada by age group and year, 2012–2019 (N=976 cases[a])

Age group (years)	Incidence rates (per 100,000 population) by year									
	2012	2013	2014	2015	2016	2017	2018	2019	2012–2019	
									Mean	95% CI
<1	3.42	3.65	4.96	2.86	1.56	3.38	4.20	4.46	3.56	2.83–4.29
1–4	1.18	1.17	0.97	0.91	0.84	0.51	0.83	1.02	0.93	0.78–1.08
5–9	0.44	0.27	0.10	0.05	0.20	0.20	0.05	0.15	0.18	0.09–0.27
10–14	0.68	0.16	0.11	0.21	0.10	0.16	0.05	0.10	0.20	0.06–0.34
15–19	1.17	0.73	0.84	0.66	0.52	0.71	0.47	0.47	0.70	0.54–0.86
20–24	0.51	0.25	0.17	0.33	0.25	0.79	0.37	0.53	0.40	0.26–0.54
25–29	0.25	0.25	0.12	0.12	0.16	0.08	0.12	0.39	0.19	0.12–0.26
30–39	0.13	0.13	0.06	0.15	0.10	0.10	0.16	0.20	0.13	0.10–0.16
40–59	0.31	0.16	0.18	0.20	0.13	0.15	0.31	0.20	0.20	0.15–0.25
60+	0.28	0.42	0.22	0.33	0.41	0.42	0.52	0.42	0.38	0.31–0.44
Overall: crude	0.45	0.35	0.29	0.30	0.27	0.33	0.37	0.37	0.34	0.34
Overall: age-standardized	0.45 (0.38–0.52)	0.35 (0.29–0.41)	0.29 (0.24–0.35)	0.31 (0.25–0.37)	0.27 (0.22–0.33)	0.33 (0.27–0.39)	0.37 (0.31–0.44)	0.37 (0.31–0.44)	0.34 (0.32–0.36)	0.34 (0.32–0.36)

Abbreviation: CI, confidence interval
[a] N=7 cases of total sample missing age

Clinical presentation and severity

Clinical presentation data were available for 532 samples (51% of total sample), of which 278 cases (52%) presented with meningitis, 182 (34%) with septicemia/bacteremia, 12 (2%) with septicemia/arthritis and 60 (11%) with other manifestations (**Table 4**). Among the 17 cases with "other manifestations" reported, the most frequently reported clinical presentations were fever (35%), pneumonia (24%) and purpura rash (18%). Meningitis was the most common clinical presentation among all serogroups, except for serogroup W-135 where septicemia/bacteremia was most common.

Table 4: Number and proportion of invasive meningococcal disease cases in Canada with a clinical presentation by serogroup, (N=503)

Serogroup	Number and proportion of invasive meningococcal disease cases[a]								
	Meningitis		Septicemia/ bacteremia		Septicemia/ arthritis		Other		Total
	n	%	n	%	n	%	n	%	
B	135	64	53	25	2	1	20	10	210
C	24	52	17	37	3	7	2	2	46
W-135	38	36	43	41	3	3	21	20	105
Y	66	47	57	41	4	3	13	9	140
Other[b]	4	50	4	50	0	0	0	0	8
Non-groupable	0	0	1	100	0	0	0	0	1
Unknown[c]	11	50	7	32	0	0	4	18	22
Total	278	52	182	34	12	2	60	11	532

[a] 23 cases presented with two diagnoses and three cases presented with three diagnoses
[b] Other are those cases with the serogroup noted as: A, E, Z, 29E, and non-encapsulated
[c] Unknown are those cases missing serogroup information

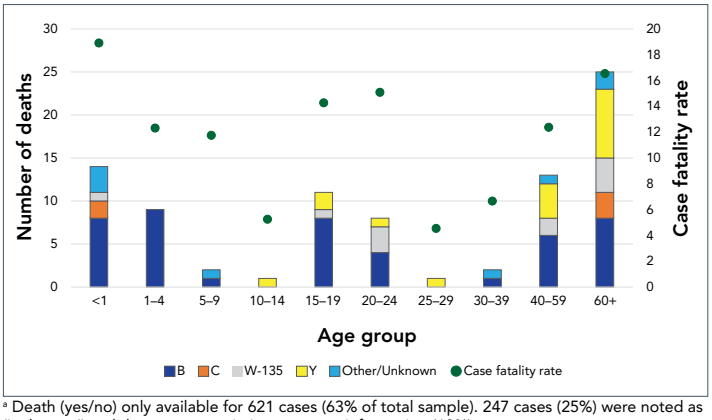
Between 2012 and 2019, of the 621 cases with outcome data available (yes/no for death), 86 deaths associated with IMD were reported. This represents an overall case fatality rate of 13.8%. As seen in **Figure 3**, serogroup B accounted for the majority (52%) of deaths reported. The case fatality rate was highest in those younger than one year of age (19%), followed closely by those 60 years and over (17%) and those aged 20–24 years of age (15%). The proportion of cases who died from IMD was highest in cases for which the positive specimen was blood (n=68/432, 16%) compared with cerebrospinal fluid specimens (n=15/182, 8%) (difference of 8%, 95% CI 1.8–13.1%). Of the 15 cases whose positive specimen was joint fluid, there were no deaths reported.

Strain characteristics

Serogroup distribution of culture-confirmed invasive meningococcal disease

The NML received a total of 772 (79%) case isolates of *N. meningitidis* between 2012 and 2019. Serogroup B was the most common (accounted for 48.9% of all isolates),

Figure 3: Number of invasive meningococcal disease deaths and case fatality ratio by age group and serogroup, Canada, 2012–2019 (N=621[a])



[a] Death (yes/no) only available for 621 cases (63% of total sample). 247 cases (25%) were noted as "unknown" and the rest were missing outcome information (12%)

followed by serogroup Y (23.8%), serogroup W (20.0%) and serogroup C (6.0%), with the remaining 1.3% or 10 isolates identified as serogroup E (three isolates), serogroup Z (two isolates) or non-encapsulated (five isolates). A steady increase in serogroup W was observed over time with 2.7% of the IMD case isolates received at the NML in 2012, to 3.9% in 2013, 4.8% in 2014, 10.1% in 2015, 18.8% in 2016, 27.1% in 2017, 44.7% in 2018 and 39.7% in 2019. By 2018, and into 2019 and 2020 (*unpublished data, data for 2020, NML*) serogroup W was the most encountered serogroup among all IMD isolates received at the NML.

Serogroup B

No particular clone appeared to predominant in Canada. The most encountered serogroup B clonal complexes (CC) (in order of frequency of occurrence) were sequence type (ST)-269 CC, ST-41/44 CC, ST-213 CC, ST-32 CC, ST-35 CC and ST-1157 CC (each with at least five isolates), which together made up 90% of all the serogroup B IMD isolates from 2012 to 2019. From 2015 to 2019, there were only 189 serogroup B IMD case isolates received at the NML and the most encountered CCs were ST-41/44 CC, ST-269 CC, ST-213 CC, ST-32 CC and ST-1157 CC (each with at least five isolates). Together, they accounted for 84% of all the serogroup B isolates.

Serogroup W

Prior to 2015, most invasive serogroup W isolates were identified as ST-22 CC and the increase in serogroup W in Canada in recent years was associated with the replacement of the endemic ST-22 CC with the hyper-virulent ST-11 CC (6). They were characterized by the antigenic formula of W:2a:P1.5,2 with most typed as ST-11 and of the sub-lineage 11.1 (7).

Serogroup Y

The ST-23 CC continued to be the most encountered serogroup Y CC, followed by ST-167 CC and ST-174 CC.

Serogroup C

Of the 49 serogroup C IMD case isolates received at the NML, 36 were typed as ST-11 CC and 13 were typed as non-ST-11 CC. Of the 36 ST-11 CC isolates; 15 were further subtyped as the ET-15 type (sub-lineage 11.2), 20 were non-ET-15 type or sub-lineage 11.1 and one was without further subtyping information.

Non-ST-11 CC serogroup C isolates included three typed as ST-1195 (ST-269 CC) and all three were found in Alberta (in 2017, 2018 and 2019) and had the antigenic formula C:NT:P1.9. There were also two serogroup C isolates typed as ST-4821 (ST-4821 CC) and both were found in British Columbia (in 2013 and 2014) and had the antigenic formula C:NT:P1.1. Additionally, there were three serogroup C isolates typed as ST-35 CC, three typed as ST-103 CC, one typed as ST-41/44 CC and one with a sequence type not assigned to any known CC.

Discussion

Since the implementation of publicly funded meningococcal C and meningococcal quadrivalent vaccination programs in Canada, the overall incidence of IMD has decreased significantly. Over the surveillance period, vaccination coverage for the meningococcal conjugate C vaccine has remained stable in children under two years of age, ranging from 87.6% to 88.7% between 2013 and 2017 (8).

The downward trend in incidence was noted across all Canadian regions as early as the year following implementation of publicly funded programs. Between 2012 and 2019, the Prairies and Central regions reached an all-time low incidence rate. Consistent with the previous surveillance report, Nunavut continued to report the highest incidence rate (9). The overall mean incidence in the previously published surveillance report was 0.58 cases per 100,000 population for 2006–2011 compared with 0.34 cases per 100,000 population for 2012–2019 (6). Serogroup B accounted for the largest proportion of cases, and disproportionately affected infants under the age of one year. Similar to previously published reports, cases of IMD predominated in the winter months with the highest levels in January and March (4,10).

Beginning in 2016, the number of IMD cases associated with serogroup W increased by at least 50% every year in Canada. Between 2012 and 2019, the largest proportion of serogroup W cases associated with clonal complex 11 were reported in adults aged 60 years and older. The emergence of serogroup W cases associated with clonal complex 11 has been reported in previous studies (10,11) and our results are consistent with these findings. The NML also reported on the growing number of serogroup W strains in Canada over time (4,12). Genomic isolates of the Canadian serogroup W isolates showed the majority of the recent isolates belonged to the South American strain type or sub-lineage, although a small number isolated up to 2016 belonged to the Hajj-type strain (13).

During the time period 2012–2019, there were three documented Canadian outbreaks (14). One outbreak spanned from 2006 to 2013 in the region of Saguenay-Lac-Saint-Jean, Québec, and was due to serogroup B. A vaccination campaign was launched the following year in the region using the 4CMENB vaccine (15). The incidence of IMD due to serogroup B fell dramatically in the targeted population of the vaccination campaign (up to 20 years of age) and in 2015, an outbreak was reported in a university in Nova Scotia (14). The first documented outbreak due to serogroup CC-11 was reported in British Columbia in 2017 and resulted in five cases in adolescents aged 15–19 years (14).

Antibiotic resistant *N. meningitidis* was recently observed in some serogroup Y isolates that belonged to ST-3587 (ST-23 CC) clone and was characterized by the production of β-lactamase due to presence of the bla_{ROB-1} gene likely to be acquired from *Haemophilus influenzae* (16). This strain has also been identified in France (17) and in the United States, which led to the release of a health alert in June 2020 (16). In the United States, this strain has also acquired resistance to ciprofloxacin, an antibiotic commonly used for chemoprophylaxis of close contacts of IMD cases (18). Up to now, the expansion and spread of this clone has not been observed in Canada (u*npublished data, NML*).

Laboratory surveillance is important for the identification of novel strains that may contribute to the evolving nature of IMD. For example, the novel South American-United Kingdom strain of ST-11 serogroup W has been responsible for the increase in meningococcal W disease globally and has led to reports of unusual clinical presentations (7,19,20). The recent increase in meningococcal C disease in the African meningitis belt was due to a new strain that arose when a ST-10217 non-encapsulated strain from a healthy carrier in Burkina Faso acquired a serogroup C capsule (21). The recent emergence in the United States of β-lactamase positive serogroup Y *N. meningitidis* with additional resistance to fluoroquinolones has important implications for treatment and chemoprophylaxis of IMD (22).

Imported cases via travel accounted for a small proportion of cases, and the majority of cases due to travel were within Canada or the United States. Laboratory characterization of strains identified two potential imported cases with unusual characteristics of C:NT:P1.14, ST-4821 and resistance to ciprofloxacin. These strain characteristics have not been found in any Canadian isolates previously but were commonly associated with a unique serogroup C clone in China (4), which suggested that these two isolates were from imported cases.

Serogroup B accounted for the largest proportions of clinical presentations. Between 2012 and 2019, the mortality rate associated with IMD continued to decline over time and serogroup B accounted for the majority of deaths. The trends

observed in this report are consistent with evidence from other publications (6). Mortality rates in Canada were comparable to those of Australia and England (7,13). Positive specimens from blood resulted in nearly double the mortality ratio when compared with positive specimens from cerebrospinal fluid. This finding was statistically significant.

In recent years, evidence of atypical clinical presentation of IMD serogroup W characterized by gastrointestinal symptoms has been reported across the world (23–26). Among the cases reported with other clinical manifestations in Canada between 2012 and 2019, the majority were associated with serogroup W-135. Heightened surveillance of atypical presentations in Canada is recommended to better understand the evolving epidemiology of IMD.

The World Health Organization established a plan to defeat meningitis by 2030 (27). The plan includes three main goals pertaining to epidemics, disease transmission and disabilities and long-term effects of infection: 1) the elimination of IMD epidemics; 2) the reduction of cases and deaths from vaccine preventable bacterial meningitis; and 3) the reduction of disability associated with infections. Although IMD remains endemic in Canada, evidence from this article shows noteworthy reductions in incidence rates in some geographic areas in Canada. The introduction of publicly funded vaccination programs in Canada has sharply decreased the incidence of IMD associated with strains covered by the vaccines. New strains of IMD will continue to pose challenges for disease target reductions such as the ones outlined by the World Health Organization. Canada has a strong public health infrastructure that allows for early detection of cases and the implementation of prompt public health actions; however, the current routine surveillance at the national level does not collect data on cases post-infection, such as long-term disabilities.

Limitations

Several limitations should be noted. First, data reported to the eIMDSS surveillance system are not epidemiologically linked with laboratory data. To connect the two data sources, deterministic matching was done. Some cases may have been missed due to insufficient data to match the two data sources. Second, many cases might not be recognized, as antibiotics are frequently given prior to taking cultures and the organism would not be identified. Third, certain data variables, such as immunization history, were often missing or incomplete. Finally, limited outbreak information represents a gap in national IMD surveillance.

Conclusion

Invasive meningococcal disease is a rare but severe infection that continues to affect the very young population in Canada. While serogroup B continues to account for the greatest proportion of disease, serogroup W associated with CC-11 is becoming a growing contributor of disease in older adults. The evolving nature of *N. meningitidis* requires a comprehensive approach to its surveillance, which should include a laboratory component that documents strain characteristics.

Authors' statement

MS — Conceptualization, methodology, software, formal analysis, investigation, data curation, writing–original draft, writing–review and editing, visualization
RSWT — Methodology, formal analysis, investigation, data curation, writing–original draft, writing–review and editing, visualization
RM — Methodology, formal analysis, writing–original draft, writing–review and editing
AA — Methodology, formal analysis, writing–original draft, writing–review and editing
YAL — Conceptualization, methodology, review and editing
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Competing interests

None.

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References

1. David L. Heymann. Control of Communicable Diseases Manual. 20th ed. Washington DC, USA: American Public Health Association; 2014. ISBN-10: 087550184.

2. Public Health Agency of Canada. Invasive Meningococcal Disease. Ottawa (ON): PHAC: 2014 (accessed 2020-10-26). https://www.canada.ca/en/public-health/services/immunization/vaccine-preventable-diseases/invasive-meningococcal-disease/risks.html

3. National Advisory Committee on Immunization. The Recommended Use of the Multicomponent Meningococcal B (4CMenB) Vaccine in Canada. NACI; (updated 2014; accessed 2022-01-16). https://www.canada.ca/en/public-health/services/immunization/national-advisory-committee-on-immunization-naci/recommended-use-multicomponent-meningococcal-b-4cmenb-vaccine-canada.html#toc_4a

4. Tsang RS, Deeks SL, Wong K, Marchand-Austin A, Jamieson FB. Invasive serogroup W Neisseria meningitidis (MenW) in Ontario, Canada shows potential clonal replacement during the period January 1, 2009 to June 30, 2016. Can Commun Dis Rep 2016;42(12):263–6. DOI PubMed

5. Statistics Canada. Population and demography statistics. Ottawa (ON): StatCan; 2022 (accessed 2022-01-20). https://www.statcan.gc.ca/en/subjects-start/population_and_demography

6. European Centre for Disease Control. Invasive meningococcal disease. Annual epidemiological report for 2017. Solna (SE): ECDC; 2019. https://www.ecdc.europa.eu/en/publications-data/invasive-meningococcal-disease-annual-epidemiological-report-2017

7. Government of Australia Department of Health. Invasive Meningococcal Disease National Surveillance Report. Canberra (AU): Government of Australia; 2018 (accessed 2020-10-26). https://www1.health.gov.au/internet/main/publishing.nsf/Content/5FEABC4B495BDEC1CA25807D001327FA/$File/1Oct-31Dec19-qrt3-IMD.pdf

8. Public Health Agency of Canada. Highlights from the 2019 Childhood National Immunization Coverage Survey (cNICS). Ottawa (ON): PHAC; (updated 2022-02-07). https://www.canada.ca/en/public-health/services/publications/vaccines-immunization/2019-highlights-childhood-national-immunization-coverage-survey.html

9. Li YA, Tsang R, Desai S, Deehan H. Enhanced surveillance of invasive meningococcal disease in Canada, 2006-2011. Can Commun Dis Rep 2014;40(9):160–9. DOI PubMed

10. Li YA, Martin I, Tsang R, Squires SG, Demczuk W, Desai S. Invasive Bacterial Diseases in Northern Canada, 2006-2013. Can Commun Dis Rep 2016;42(4):74–80. DOI PubMed

11. Booy R, Gentile A, Nissen M, Whelan J, Abitbol V. Recent changes in the epidemiology of Neisseria meningitidis serogroup W across the world, current vaccination policy choices and possible future strategies. Hum Vaccin Immunother 2019;15(2):470–80. DOI PubMed

12. Tsang R, Hoang L, Tyrrell GJ, Horsman G, Van Caeseele P, Jamieson F, Lefebvre B, Haldane D, Gad RR, German GJ, Zahariadis G. Increase in Neisseria meningitidis serogroup W invasive disease in Canada: 2009-2016. Can Commun Dis Rep 2017;43(7-8):144–9. DOI PubMed

13. Public Health England. Invasive meningococcal disease in England: annual laboratory confirmed reports for epidemiological year 2018 to 2019. London (UK): PHE; 2019 (accessed 2020-10-26). https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/842368/hpr3819_IMD-ann.pdf

14. Soumahoro L, Abitbol V, Vicic N, Bekkat-Berkani R, Safadi MA. Meningococcal Disease Outbreaks: A Moving Target and a Case for Routine Preventative Vaccination. Infect Dis Ther 2021;10(4):1949–88. DOI PubMed

15. De Wals P. Epidemiology and Control of Meningococcal Disease in Canada: A Long, Complex, and Unfinished Story. Can J Infect Dis Med Microbiol 2019;2019:8901847. DOI PubMed

16. Lucidarme J, Scott KJ, Ure R, Smith A, Lindsay D, Stenmark B, Jacobsson S, Fredlund H, Cameron JC, Smith-Palmer A, McMenamin J, Gray SJ, Campbell H, Ladhani S, Findlow J, Mölling P, Borrow R. An international invasive meningococcal disease outbreak due to a novel and rapidly expanding serogroup W strain, Scotland and Sweden, July to August 2015. Euro Surveill 2016;21(45):30395. DOI PubMed

17. Tsang RSW, Ahmad T, Tyler S, Lefebvre B, Deeks SL, Gilca R, Hoang L, Tyrrell G, Van Caeseele P, Van Domselaar G, Jamieson FB. Whole genome typing of the recently emerged Canadian serogroup W Neisseria meningitidis sequence type 11 clonal complex isolates associated with invasive meningococcal disease. Int J Infect Dis 2018;69:55–62. DOI PubMed

18. Tsang RSW, Ahmad T, Jamieson FB, Tyrrell GJ. WGS analysis of a penicillin-resistant Neisseria meningitidis strain containing a chromosomal ROB-1 β-lactamase gene. J Antimicrob Chemother 2019;74(1):22–8. DOI PubMed

19. United States Centres for Disease Control and Prevention. Detection of Ciprofloxacin-resistant, β-lactamase-producing Neisseria meningitidis Serogroup Y Isolates, United States, 2019–2020 (accessed 2021-04-09). https://emergency.cdc.gov/han/2020/han00433.asp

20. McNamara LA, Potts C, Blain AE, Retchless AC, Reese N, Swint S, Lonsway D, Karlsson M, Lunquest K, Sweitzer JJ, Wang X, Hariri S, Fox LM; Antimicrobial-Resistant Neisseria meningitidis Team. Detection of Ciprofloxacin-Resistant, β-Lactamase-Producing Neisseria meningitidis Serogroup Y Isolates - United States, 2019-2020. MMWR Morb Mortal Wkly Rep 2020;69(24):735–9. DOI PubMed

21. Campbell H, Parikh SR, Borrow R, Kaczmarski E, Ramsay ME, Ladhani SN. Presentation with gastrointestinal symptoms and high case fatality associated with group W meningococcal disease (MenW) in teenagers, England, July 2015 to January 2016. Euro Surveill 2016;21(12):30175. DOI PubMed

22. Beltrami D, Guilcher P, Longchamp D, Crisinel PA. Meningococcal serogroup W135 epiglottitis in an adolescent patient. BMJ Case Rep 2018;2018:bcr2017223038. DOI PubMed

23. Campbell H, Andrews N, Parikh S, Ribeiro S, Gray S, Lucidarme J, Ramsay ME, Borrow R, Ladhani SN. Variable clinical presentation by the main capsular groups causing invasive meningococcal disease in England. J Infect 2020;80(2):182–9. DOI PubMed

24. Russcher A, Fanoy E, van Olden GD, Graafland AD, van der Ende A, Knol MJ. Necrotising fasciitis as atypical presentation of infection with emerging Neisseria meningitidis serogroup W (MenW) clonal complex 11, the Netherlands, March 2017. Euro Surveill 2017;22(23):30549. DOI PubMed

25. Sudbury EL, O'Sullivan S, Lister D, Varghese D, Satharasinghe K. Case Manifestations and Public Health Response for Outbreak of Meningococcal W Disease, Central Australia, 2017. Emerg Infect Dis 2020;26(7):1355–63. DOI PubMed

26. Loenenbach AD, van der Ende A, de Melker HE, Sanders EA, Knol MJ. The Clinical Picture and Severity of Invasive Meningococcal Disease Serogroup W Compared With Other Serogroups in the Netherlands, 2015-2018. Clin Infect Dis 2020;70(10):2036–44. DOI PubMed

27. World Health Organization. Defeating meningitis by 2030. Geneva (CH): WHO; 2021 (accessed 2021-04-25). https://www.who.int/initiatives/defeating-meningitis-by-2030

Annex: National case definition of invasive meningococcal disease as of November 2009

Confirmed case

Clinical evidence of invasive disease with laboratory confirmation of infection:

- Isolation of *Neisseria meningitidis* (*N. meningitidis*) from a normally sterile site (blood, cerebrospinal fluid (CSF], joint, pleural or pericardial fluid)

OR

- Demonstration of *N. meningitidis* DNA by an appropriately validated nucleic acid test (NAT) from a normally sterile site

Probable case

Clinical evidence of invasive disease with purpura fulminans or petechiae, with no other apparent cause and with non-confirmatory laboratory evidence:

- Detection of *N. meningitidis* antigen in the CSF

Note: Positive antigen test results from urine and serum samples are unreliable for diagnosing meningococcal disease.

Clinical evidence

Clinical illness associated with invasive meningococcal disease usually manifests itself as meningitis and/or septicaemia, although other manifestations may be observed (e.g. orbital cellulitis, septic arthritis). Invasive disease may progress rapidly to petechiae or purpura fulminans, shock and death.

Both confirmed and probable cases of disease should be notified as of January 1, 2006.

Lyme disease surveillance report, 2019

Source: Public Health Agency of Canada. Lyme disease surveillance in Canada: Preliminary annual report 2019. https://www.canada.ca/en/public-health/services/publications/diseases-conditions/lyme-disease-surveillance-report-2019.html

Lyme disease is the most commonly reported vector-borne disease in Canada. Over the past decade, there has been a rise in the number of locally-acquired Lyme disease cases in central and eastern Canada. The risk of human infection is expected to continue to increase in Canada in part because of the warming climate that drives the northward range-expansion of the main vector of Lyme disease, blacklegged ticks, in eastern Canada and additional factors including the uptake of outdoor activity, landscape changes, and the abundance, activity and range of ticks and hosts. Surveillance for ticks and human Lyme disease cases is conducted using a One Health approach to minimize the burden of Lyme disease and other emerging tick-borne diseases and protect the health of Canadians. The annual Lyme disease surveillance report focuses on the human component of Lyme disease surveillance, by providing an overview of surveillance data for cases reported in 2019.

For more information:

Please click here to access the Lyme disease surveillance in Canada: Preliminary Annual Report 2019

Please click here to access the Lyme disease surveillance in Canada: Preliminary Annual Infographic 2019

Mosquito-borne diseases surveillance report, 2019

Source: Public Health Agency of Canada. Mosquito-borne diseases surveillance report: Annual edition (2019 - Preliminary). https://www.canada.ca/en/public-health/services/publications/diseases-conditions/mosquito-borne-diseases-surveillance-annual-report-2019.html

West Nile virus (WNV), California serogroup viruses (CSGV), specifically Jamestown Canyon and snowshoe hare virus, as well as eastern equine encephalitis virus (EEEV) are known to cause human infections, and all four mosquito-borne viruses are endemic in parts of Canada. Mosquito-borne diseases have complex transmission cycles with viruses generally circulating between specific wild animals and competent mosquito vectors. Sometimes, however, a broad range of other animals, including humans and horses, can be infected. Recognizing that the health of humans is interconnected with that of animals and the environment, mosquito-borne disease surveillance applies a One Health approach. The 2019 mosquito-borne disease surveillance report and infographic integrates findings from human and animal health surveillance, conducted in collaboration with multi-disciplinary health partners.

For more information:

Please click here to access the Mosquito-borne diseases surveillance report (2019)

Please click here to access the Mosquito-borne diseases surveillance infographic (2019)

Please click here to access 2021 weekly Mosquito-borne Diseases National Surveillance Reports

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