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Summary of the National Advisory Committee on Immunization (NACI) Statement: Updated recommendations on herpes zoster vaccination for adults who are immunocompromised

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Abstract

Background: Herpes zoster (HZ), or shingles, results from the reactivation of latent varicella-zoster virus and poses a significant health burden and immunocompromised adults are at higher risk of HZ and its complications. In 2018, the recombinant zoster vaccine (RZV, Shingrix®) was strongly recommended by the National Advisory Committee on Immunization (NACI) for immunocompetent adults aged 50 years and older. Since then, evidence has accumulated on the use of RZV in immunocompromised adults and in 2021, Health Canada expanded the authorization of RZV to adults 18 years of age and older who are or will be immunocompromised.

Methods: NACI assessed the burden of HZ in immunocompromised populations, reviewed evidence on the efficacy, effectiveness, immunogenicity and safety of RZV, and published economic evaluations. Programmatic considerations were evaluated using NACI's ethics, equity, feasibility and acceptability framework. The evidence and programmatic considerations were organized using a process informed by the *Grading of Recommendations, Assessment, Development and Evaluation* framework, and this information was then used to facilitate NACI guidance development.

Results: The risk of HZ among younger adults who are immunocompromised is comparable to or higher than the general population of 50 years of age and older. High efficacy and robust immune responses after RZV administration was demonstrated in groups with various types of immunocompromising therapies and conditions, with an acceptable safety profile. Economic evaluations showed that RZV was cost-effective in some high-risk immunocompromised groups. Expanding access to RZV may reduce disease burden and address inequities in vaccine access.

Conclusion: NACI updated its guidance to strongly recommend that individuals 18 years of age and older who are or will be immunocompromised should receive two doses of RZV to prevent HZ and its associated complications.

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Introduction

Herpes zoster (HZ), commonly known as shingles, poses a substantial public health burden in Canada and globally. Herpes zoster is caused by a reactivation of varicella-zoster virus (VZV) and typically presents as a painful, unilateral vesicular rash usually localized to one dermatome, though it can result in a range of complications requiring medical intervention, such as postherpetic neuralgia (PHN), which can lead to chronic disabling pain. While anyone who has had varicella is at risk of developing HZ, it occurs more frequently among older adults and persons who are immunocompromised (1,2).

The National Advisory Committee on Immunization (NACI) last issued guidance on HZ vaccination in 2018, recommending that the recombinant zoster vaccine (RZV, Shingrix®) should be offered to immunocompetent adults 50 years of age and older (strong NACI recommendation) and may be considered for adults 50 years of age and older who are immunocompromised (discretionary NACI recommendation) (3). NACI was asked to review public health recommendations following Heath Canada's authorization on November 24, 2021 (4), of RZV for adults 18 years of age or older who are or will be at increased risk of HZ due to immunodeficiency or immunosuppression caused by known disease or therapy.

Methods

NACI reviewed evidence on the burden of disease for HZ and HZ-related complications in Canada, evidence on RZV efficacy, effectiveness, immunogenicity and safety in adults who are immunocompromised, and published economic evaluations comparing RZV to no vaccine in adults who are immunocompromised (5,6). NACI used a published, peer-reviewed framework and evidence-informed tools to ensure that issues related to ethics, equity, feasibility and acceptability were systematically assessed and integrated into the guidance. NACI also considered feedback from the Canadian Immunization Committee and leveraged a 2022 evidence synthesis from the United States (US) Centers for Disease Control and Prevention and Advisory Committee on Immunization Practices, which included a *Grading of Recommendations, Assessment, Development and Evaluation* (GRADE) assessment and an Evidence to Recommendations framework on RZV vaccine efficacy, effectiveness, immunogenicity and safety among individuals aged 19 years and older who are or will be at increased risk of HZ due to immunodeficiency or immunosuppression caused by known disease or therapy (7–9). Knowledge synthesis was performed by the NACI secretariat and reviewed by the Herpes Zoster Working Group. For complete details of the methods, refer to the NACI statement (10).

Results

Burden of disease in Canada

In Canada, the lifetime risk of developing HZ is estimated to be as high as 30% in the general population, with incidence and severity increasing markedly in older adults and in those with compromised immunity. A model has estimated that each year, approximately 130,000 new cases of HZ occur nationally, leading to about 17,000 cases of PHN, 252,000 physician consultations and 2,000 hospitalizations (11). A systematic review of Canadian data found that incidence rates of medically-attended HZ ranged between 316 and 450 per 100,000 person-years across several provinces (12).

Individuals who are immunocompromised face particularly elevated risk. An Ontario-based study reported that adults with immunocompromising conditions were 2.9 to 12.3 times more likely to experience hospital-attended HZ compared to immunocompetent individuals, after adjusting for age and sex (13). The incidence rates of HZ were higher for younger adults with immunosuppression and were similar to or greater than those of immunocompetent older adults. Similar findings from the US have shown HZ incidence rates of 17 to 43 per 1,000 person-years in specific immunocompromised groups (e.g., adults with solid organ transplant, adults with bone marrow or stem cell transplant and adults with HIV), compared to 4.8 per 1,000 person-years in the general adult population (14). Herpes zoster risk is lower for individuals who have only been exposed to VZV through vaccination with live-attenuated virus compared to those who have been exposed through infection (15–17).

The public health importance of the burden of disease due to HZ is underscored by the prevalence of individuals in Canada who are immunocompromised and therefore at high risk of HZ and its associated complications. Over 155,000 Canadians are estimated to be living with a hematologic malignancy, more than 62,000 are living with HIV and approximately 29,000 have primary immunodeficiencies (18–20). Between 2000 and 2019, more than 18,000 first hematopoietic stem cell transplants were performed in Canada (21).

Complications from acute HZ are more common in these populations, and potentially more severe. A systematic review reported that the risk of developing PHN ranged between 6% and 45% across immunocompromising conditions (22). This is particularly important given that PHN can impair quality of life to a degree comparable to serious chronic illnesses, including diabetes, myocardial infarction, congestive heart failure and depression (23).

Vaccine efficacy and effectiveness

Evidence from randomized-controlled trials (RCTs) demonstrated that a two-dose schedule of RZV is efficacious in preventing HZ in adults with a range of immunocompromising conditions. In RCTs, vaccine efficacy was 68% (95% CI: 56%–78%) in autologous hematopoietic stem cell transplant (HSCT) recipients and 87% (95% CI: 44%–99%) and 90.5% (95% CI: 74%–98%) in individuals with hematologic malignancies and immune-mediated diseases, respectively (7,9). Observational studies supported these findings, with vaccine effectiveness estimates of 64% (95% CI: 57%–70%) and 68% (95% CI: 62%–73%) for individuals with immunocompromising conditions and autoimmune conditions, respectively (7). Additionally, RZV was efficacious for the prevention of HZ-related hospitalization and PHN in HSCT recipients (7).

Vaccine immunogenicity

Recombinant zoster vaccine was demonstrated to be immunogenic in RCTs across a broad range of immunocompromising conditions, including autologous HSCT recipients, individuals with hematological malignancies, individuals with solid tumours, renal transplant recipients and people living with HIV (7). One study also showed that RZV immunogenicity was not impaired in individuals with autoimmune conditions treated with immune-targeted therapies when compared to individuals who were not treated with immunosuppressive therapies (24).

Immunogenicity was also assessed in RCTs where RZV was administered concurrently with or separately from one other vaccine—either quadrivalent inactivated influenza vaccine, 23-valent pneumococcal polysaccharide vaccine, COVID-19 mRNA-1273, reduced-antigen-content diphtheria-tetanus-acellular pertussis vaccine, 13-valent pneumococcal conjugate vaccine, or respiratory syncytial virus prefusion F3 subunit vaccine for older adults (25–30). Immune responses were comparable between concurrent and sequential administration. All immune responses met pre-specified non-inferiority criteria when comparing concurrent administration to sequential administration, except for one of the pertussis antigens in the tetanus, diphtheria and pertussis vaccine; study authors concluded that there is likely no clinically relevant interference between RZV and tetanus, diphtheria and pertussis vaccine.

Vaccine safety

Recombinant zoster vaccine has an acceptable safety profile that is comparable between immunocompromised and immunocompetent populations. In clinical trials conducted in immunocompromised populations, rates of serious events, risk of immune-mediated diseases, risk of graft-versus-host disease and risk of graft rejection were similar between vaccine and placebo recipients (7). The frequency of Grade 3 local and systemic reactogenicity was higher among vaccine recipients compared to placebo recipients (7), with pain at the injection site, fatigue and myalgia being the most commonly reported reactions. In studies assessing concurrent administration of RZV with one other vaccine (described above), no safety concerns were identified, with similar frequencies of local and systemic reactogenicity between sequential and concurrent administration groups.

Economic considerations

Two US-based economic evaluations were reviewed to assess the cost-effectiveness of RZV in immunocompromised adults aged under 50 years (5,6). Both studies found that RZV was cost-effective for certain high-risk groups such as HSCT recipients, individuals with multiple myeloma and renal transplant recipients. For other risk groups, incremental cost-effectiveness ratios ranged from $47,900 to $296,360 CAD per quality-adjusted life year gained, depending on the specific condition, model structure and perspective (healthcare sector vs. societal) (5,6). In these economic evaluations, the cost-effectiveness of RZV was strongly influenced by the incidence and healthcare costs of HZ, which vary considerably among immunocompromised adults, especially those with autoimmune and inflammatory conditions. Notably, the vaccine prices used in these economic evaluations ($271 CAD and $233 CAD per dose) (5,6) were higher than the current Canadian list price for RZV ($162.35 CAD per dose). While these analyses were conducted in the US context, this difference in vaccine prices indicates that, all else being equal, cost-effectiveness estimates would be more favourable if Canadian price assumptions were applied. Although these economic evaluations were conducted for the US population, the methods and key results were deemed generalizable to Canada.

Ethics, equity, feasibility and acceptability considerations

Expanding RZV use to adults who are immunocompromised could address disparities in disease risk and access to vaccination. There is variability in public funding for HZ vaccination across provinces and territories, with only a few jurisdictions publicly funding RZV for immunocompromised adults as of late 2024, when NACI deliberated on this topic. Expanding existing programs to include immunocompromised populations or creating new programs for immunocompromised populations could promote equitable protection for individuals at high risk of HZ and its complications who face financial barriers.

Feasibility was deemed higher in provinces and territories with existing RZV programs and in jurisdictions that have other vaccination programs that specifically include immunocompromised populations. Recombinant zoster vaccine is an inactivated, refrigerator-stable, two-dose vaccine that can be concurrently administered with other vaccines and is thus well-suited for routine immunization programs. While there was limited evidence on acceptability among healthcare providers and the public, some surveys have reported coverage estimates indicating that nearly half of immunocompromised adults aged 50 and older had received at least one dose of an HZ vaccine (31). Internationally, RZV is recommended for individuals who are immunocompromised in several jurisdictions, including Australia, US, the European Union, New Zealand and Japan.

Recommendations

The following recommendation is to inform RZV immunization programs for Canadian provinces and territories:

NACI recommends that individuals 18 years of age and older who are or will be immunocompromised should receive two doses of RZV to prevent HZ and its associated complications. ***(Strong NACI recommendation)***

The standard schedule is two doses administered two to six months apart; however, if needed, for individuals who will be at increased risk of HZ due to immunodeficiency or immunosuppression (for example, individuals who are about to start immunosuppressive therapy), the second dose can be administered at a minimum interval of at least four weeks after the first dose, as these individuals will benefit from completing the series before being immunosuppressed. To optimize immune response, the series should ideally be completed at least 14 days before the onset of immunosuppression.

The following list of immunocompromising conditions is intended to support the prioritization of individuals for vaccination but is not a comprehensive list of all immunosuppressive conditions or therapies. Since the degree of immunosuppression and associated risk of HZ can vary, clinical judgment and consultation with the patient's healthcare provider are recommended.

- Primary immunodeficiencies affecting innate, humoral and T cell-mediated immunity
- Hematopoietic stem cell transplants (HSCT)
- Solid organ transplants (SOT)
- Hematological malignancies
- Solid tumour malignancies on immunosuppressive treatment
- HIV infection
- Chronic or ongoing immunosuppressive therapy:
    - Immunosuppressive chemotherapy
    - Immunosuppressive radiation therapy
    - Calcineurin inhibitors
    - Cytotoxic medications
    - Anti-metabolites
    - Immune effector cell therapies (e.g., CAR T cell therapy)
    - Biological response modifiers, targeted therapies and antibodies that target lymphocytes and immune pathways (e.g., anti-CD20, anti-TNF-α, JAK inhibitors, etc.)
    - Long-term, high-dose systemic corticosteroids (prednisone equivalent of ≥2 mg/kg/day, or 20 mg/day if weight of >10 kg for ≥14 days)

Additional guidance

- There are no data on RZV use during pregnancy or breastfeeding, thus, precautions should be used in these situations. Ideally, vaccination should occur prior to pregnancy or deferred until after pregnancy. Recombinant zoster vaccine can be used in breastfeeding women and breastfeeding individuals if clinically indicated.
- Recombinant zoster vaccine can be concurrently administered with live and non-live vaccines.
- Individuals who have never been infected with VZV and have not received the varicella vaccine are not at risk of developing HZ; however, neither serologic testing nor confirmation of prior VZV exposure are required before administering RZV to eligible individuals.
- Individuals who have acquired immunity to VZV through vaccination rather than natural infection have a lower risk of HZ; however, RZV is still likely of benefit and should be offered if eligibility criteria are met.
- As RZV is not intended to prevent primary VZV infection, individuals known to be VZV-susceptible should be assessed according to current varicella vaccine guidelines in the Canadian Immunization Guide. It is important to consider that live vaccines, including varicella, may be contraindicated in some immunocompromised individuals.

Conclusion

This updated recommendation from NACI reflects a growing body of evidence supporting the safe and effective use of the RZV in adults who are immunocompromised. Immunocompromised individuals face a significantly higher risk of HZ and its complications compared to the general population. The demonstrated efficacy, effectiveness, immunogenicity and safety of RZV in this population, along with international alignment, underscore the importance of including this group in routine immunization strategies. Expanding access to RZV for adults aged 18 years and older who are or will be immunocompromised is expected to reduce the burden of HZ and promote equity by minimizing financial barriers to vaccination. As provinces and territories consider implementation, this guidance provides a foundation for the development or expansion of publicly funded RZV programs that prioritize individuals at greatest risk. NACI will continue to monitor the evidence of vaccine efficacy, effectiveness, immunogenicity and safety of RZV in immunocompromised populations and other research priorities as outlined in the statement.

Authors' statement

RK — Writing–original draft, writing–review & editing
OB — Writing–review & editing
AH — Writing–review & editing
AT — Writing–review & editing
MA — Writing–review & editing

The NACI statement on *Updated recommendations on herpes zoster vaccination for adults who are immunocompromised* was prepared by R Krishnan, O Baclic, A Haynes, L Coward, A Howarth, A Nunn, A Simmons, N Nguyen, RM Tazinya, A Tuite, and M Andrew on behalf of NACI Herpes Zoster Working Group, and was approved by NACI.

Competing interests

Dr. Melissa Andrew reported receiving grants from Merck & Co. and Icosavax outside the work described in this article.

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Isolation of toxigenic *Corynebacterium diphtheriae* from cutaneous lesions in a donkey in Ontario, Canada, 2024: Implications for zoonotic disease transmission and One Health approach

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Abstract

This rapid communication describes a case of cutaneous lesions in a donkey in Ontario, Canada, from which toxigenic *Corynebacterium diphtheriae* (*C. diphtheriae*) was isolated. Seven human close contacts were identified and assessed. This communication focuses on public health challenges, interagency response and implications for One Health initiatives to prevent zoonotic transmission. Furthermore, it underscores the importance, successes and challenges of interagency collaboration to coordinate timely laboratory investigation, reporting, contact tracing, potential post-exposure prophylaxis and public education in responding to zoonotic disease. This investigation demonstrates the need for enhanced surveillance, clear legislative authority to facilitate reporting, and more specific guidance for close contact management of *C. diphtheriae* and other zoonotic agents in animals, which can cause morbidity and mortality in humans.

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Keywords: diphtheria, *Corynebacterium diphtheriae*, Ontario, toxigenic, donkey, surveillance, One Health

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Introduction

Corynebacterium diphtheriae (*C. diphtheriae*), the primary agent of diphtheria, is an aerobic or facultatively anaerobic, Gram-positive, rod-shaped bacterium; some strains carry the diphtheria tox gene that produces a potent toxin that causes severe disease in humans (1). Other *Corynebacterium* species that can acquire the diphtheria toxin gene are *Corynebacterium ulcerans* and *Corynebacterium pseudotuberculosis* (2). *Corynebacterium* are very common in the environment, including soil, plants, animals and humans (1); however, toxigenic *C. diphtheriae* is rare and typically associated with human infection, although domestic animals such as cats, dogs, and horses have been identified as carriers of this organism (1). The incubation period for human *C. diphtheriae* infection ranges from 2–10 days; the mode of transmission to humans is direct contact for cutaneous lesions and via droplet for respiratory diphtheria (3,4). This case highlights a rare instance of toxigenic *C. diphtheriae* isolated from a domestic animal, underscoring the need for vigilance in zoonotic surveillance and cross-sectoral collaboration to mitigate public health risks.

Corynebacterium diphtheriae is of great public health significance due to its capacity to produce a potent toxin that can lead to severe complications such as myocarditis, kidney failure and death (5). Without prompt treatment, the case fatality rate for diphtheria ranges from 5% to 10%, with higher mortality rates (up to 30%) observed among unvaccinated individuals, particularly children under five years old and adults over 40 years of age (6,7). Before the introduction of the diphtheria toxoid vaccine in the 1920s, the disease caused approximately 100,000–200,000 cases and 13,000–15,000 deaths annually in the United States (8). In Canada, routine immunization has significantly reduced the incidence of diphtheria; however, 19 cases were reported between 1993 and 2012, with the most recent fatalities occurring in a Canadian resident in 2010 and a visitor to Canada in 2018 (9,10). Globally, diphtheria remains endemic in regions with low immunization coverage. In addition, displacement of populations due to political or economic instability, combined with disruptions in immunization infrastructure, has contributed to recent outbreaks in several countries, including among asylum seekers in Europe (5). Furthermore, a serosurvey of young healthy adult Canadians noted that approximately 20% of individuals do not have adequate levels of antibodies for diphtheria (11). The re-emergence of diphtheria underscores the critical importance of maintaining high vaccination coverage and robust public health systems to prevent the spread of this potentially fatal disease.

Based on available literature, this is the first documented case of toxigenic *C. diphtheriae* in a donkey. Previous reports have identified *C. diphtheriae* in various animals, including dogs, cats, horses, a cow and a fox, but only isolates from two dogs and two horses were confirmed to be toxigenic (12). To date, there are no confirmed cases of zoonotic transmission of toxigenic *C. diphtheriae* to humans. A 2022 case involving a toxigenic strain in a pet cat in Texas did not result in human infection; however, zoonotic transmission has been well documented with toxigenic *C. ulcerans*, a related species capable of producing diphtheria toxin, particularly from domestic dogs and cats to humans (13–16).

In September 2024, the Animal Health Laboratory (AHL) based in Guelph, Ontario reported to the Ontario Ministry of Health about the isolation of a potentially toxigenic *C. diphtheriae* isolate from a donkey with cutaneous lesions. Subsequently, the relevant local public health unit in Ontario was notified. In Ontario, toxin-producing *C. diphtheriae* in humans is a pathogen of public health significance that requires reporting to public health authorities, as there are interventions that can be implemented to prevent further transmission, such as the identification of asymptomatic carriage among close contacts and offering post-exposure chemoprophylaxis (antibiotics) and immunoprophylaxis (vaccine) (17). There is also a potential risk of transmission of toxigenic *C. diphtheriae* from animals or laboratory isolates to humans, necessitating human contact management that may include post-exposure antibiotic and vaccine advice, following a risk assessment (18,19). In animals, toxigenic *C. diphtheriae* bacteria are not designated as immediately notifiable in Ontario by laboratories or veterinarians to the Ontario Ministry of Agriculture, Food and Agribusiness (OMAFA) and/or to the Public Health Unit/Ministry of Health, which led to challenges for public health surveillance and timely response when a toxigenic case was identified, especially as this was the first known animal case of toxigenic *C. diphtheriae* in Ontario.

This report highlights the zoonotic risk of toxigenic *C. diphtheriae* isolated from animals and the challenges in public health surveillance and management due to the absence of legislative clarity for animal-to-human transmission. This case emphasizes the critical need for a One Health approach that integrates animal and human health systems to prevent zoonotic transmission and enhance response coordination. Hence, the objective of this report is to describe the epidemiological, diagnostic, and public health management of isolation of toxigenic *C. diphtheriae* from a donkey, highlighting the implications for zoonotic transmission and underscoring the need for policy enhancements to support timely outbreak response and public health safety.

Current situation

Case presentation

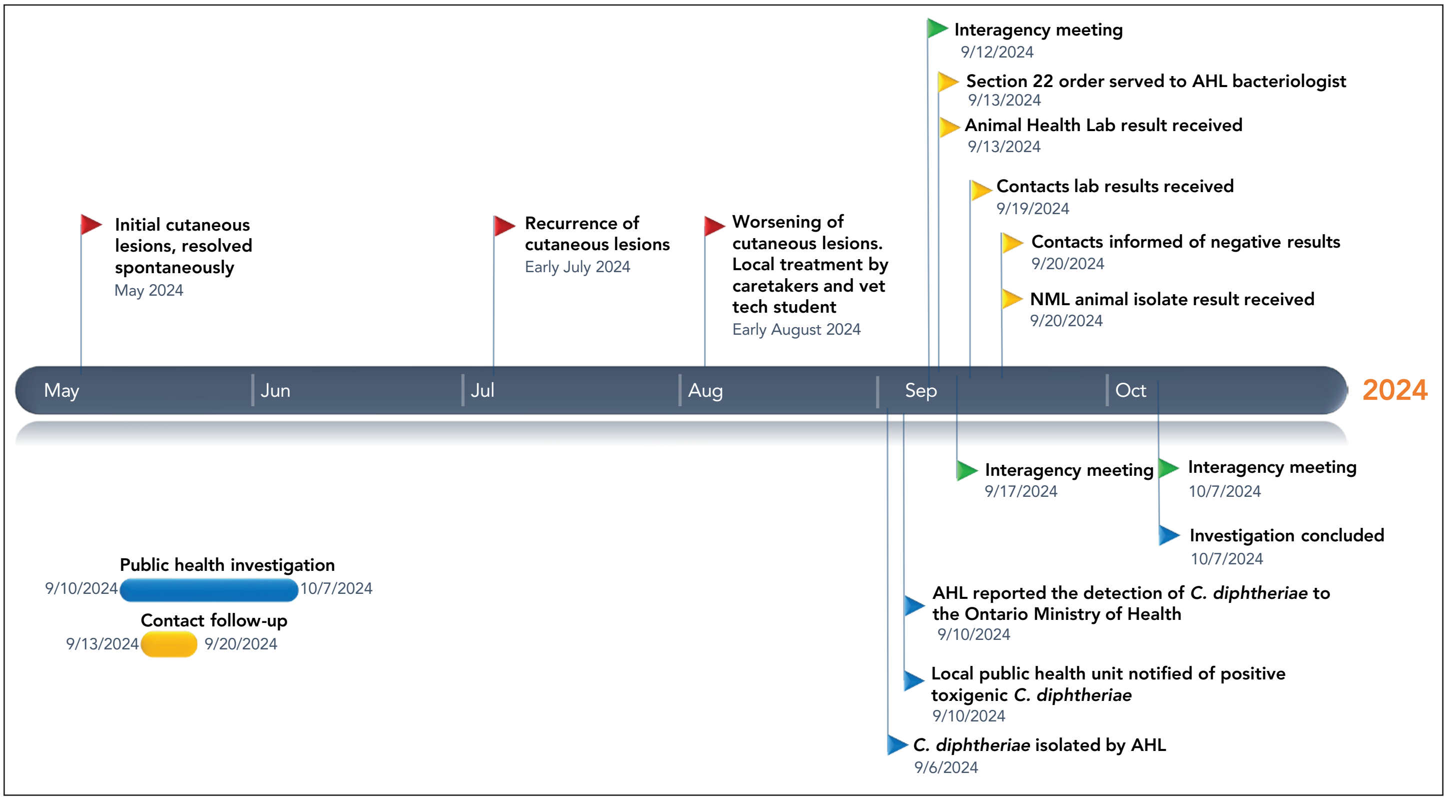
A 35-year-old donkey was evaluated by a veterinarian for non-healing cutaneous lesions on all four limbs (**Figure 1**). The lesions (wounds) first appeared in May 2024, resolved spontaneously and recurred in July 2024. The wounds worsened in August 2024 necessitating examination by the attending veterinarian in early September 2024. The veterinarian assessed and treated the donkey at the owner's property, collected samples from the wounds for bacterial culture and delivered treatment, including antibiotics and a topical cream application (corticosteroid with an antibiotic) on the wound surface.

Laboratory findings

The swabs of the lesions grew a mixed culture of *C. diphtheriae*, as well as *Pseudomonas aeruginosa* and *Streptococcus equi* subspecies *zooepidemicus*. The former was positive for the toxin gene at the AHL by a research use only (RUO) PCR assay (20). Molecular detection of the diphtheria toxin gene is not routinely done at AHL given the rarity of *C. diphtheriae* isolation from animal specimens; however, a noticeable rise in referrals of isolates to the National Microbiology Lab (NML) for diphtheria toxin testing and recent reports of diphtheria toxin gene carrying *C. ulcerans* isolates prompted the lab to keep the primers and a probe in stock (21). Despite the lack of real-time PCR (qPCR) verification at AHL, due to the high specificity of the published test, there was confidence in the high probability (approximately 92%) that this was a true positive.

The isolate was sent to NML for qPCR confirmation and for detection of toxin production by modified Elek test. At NML, the identification was confirmed to be *C. diphtheriae*, which was

Figure 1: Timeline of events in the investigation of a zoonotic cutaneous diphtheria case in a donkey, Ontario, Canada, 2024



Abbreviations: AHL, Animal Health Laboratory; *C.*, *Corynebacterium*; NML, National Microbiology Laboratory

positive by both the PCR for the diphtheria toxin gene and the modified Elek test for the phenotypic detection of the expressed diphtheria toxin.

Public health notifications and challenges

When the toxigenic *C. diphtheriae* isolate was identified at AHL, the potential risk to human health was recognized and this finding was reported to the Ontario Ministry of Health.

There is no supporting legislation or policy to support the release of personal information to any of the relevant provincial and local public health agencies, which is of critical importance for outbreak tracing and other public health measures. *Corynebacterium diphtheriae* in animals is not designated as a provincially notifiable hazard to OMAFA (22). Similarly, the *Health Protection and Promotion Act, R.S.O. 1990, c.H.7*, does not require confirmation of *C. diphtheriae* in animals to be reported to the Ontario Ministry of Health or the local public health agency. This led to a discussion among the AHL, OMAFA and the provincial and local public health authorities on how to proceed with the animal case and with human contact management while respecting both the legislation and the privacy of the donkey owner, including their location and caretaker identification. Eventually, it was agreed that, at that time, the best way forward was for the local medical officer of health to issue a section 22 order regarding a communicable disease under the *Health Protection and Promotion Act*. The order was issued to the AHL veterinary bacteriologist requiring the contact details and laboratory reports to be provided to the Medical Officer of Health to enable the local public health unit to conduct a public health investigation and potentially institute adequate control measures, such as further laboratory testing, and, where necessary, chemoprophylaxis and immunization of close human contacts.

The animal's history and clinical presentation were crucial in guiding the diagnostic approach and subsequent public health contact management. It is unclear how the donkey became infected with *C. diphtheriae*; however, the donkey's age (35 years), likely immunosenescence with a greater propensity to acquire and develop the disease from possible human and/or animal carriers (5), the potential for underlying skin disease from seasonal biting insects and chronic exposure to soil where *C. diphtheriae* may have been present (1) may have created the perfect situation for the development of cutaneous lesions. Of note, the donkey spent most of the summer outdoors. The initial lesions in May 2024 could plausibly be linked to environmental exposure, such as contact with contaminated soil, which is consistent with known reservoirs of *C. diphtheriae*. The recurrence and worsening of the lesions in July and August 2024 may have been exacerbated by seasonal factors like biting insects and increased outdoor exposure.

Diphtheria is a disease of public health significance; hence, there were concerns regarding human contact. Notably, the donkey did not display respiratory symptoms, so transmission by droplet was not deemed a concern.

Contact tracing and management

Close contacts were defined as persons who had close contact with the donkey and/or exposure to mucous membranes and/or provided direct care since the onset of symptoms in the animal. For the months during which the donkey had the cutaneous lesions, there were seven known human close contacts. The human contacts include two caretakers who provided regular care to the donkey, one veterinary technician student who provided direct wound care to the donkey when the caretakers travelled, a veterinarian who also provided direct care with gloves, took samples of lesions and submitted the wound culture, two individuals who reportedly had no direct contact with the wound but fed and held the chain of the donkey in close proximity at multiple times over the past two months, and one person who trimmed the donkey's hooves. Animal contacts on the same property included one horse that lived in the same barn with the donkey in the winter months, and a dog.

Post-exposure *C. diphtheriae* contact management includes chemoprophylaxis with either one dose of intramuscular benzathine penicillin G or 7–10 days with a macrolide antibiotic, and diphtheria vaccination if the contact's vaccine status is not up to date (17,21). Ontario's Infectious Disease Protocol and the United States Centers for Disease Control and Prevention (CDC) provide advice for contacts of toxigenic *C. diphtheria* species occurring in humans and recommend vaccinating close contacts if their last diphtheria-containing vaccination was more than five years ago (17,23). On the other hand, the United Kingdom (UK) and Australia have guidance on human contact management when toxigenic *Corynebacterium* spp. are identified in animals, with the UK's guidance document and Australian guidelines recommending a booster dose of diphtheria-containing vaccine if more than 12 months after the last dose (24,25). Following the precautionary principle, a dose of diphtheria-containing vaccine was offered to all close contacts if their last dose was more than 12 months ago.

Outcomes and follow-up

All contacts had received diphtheria vaccination within the past decade, most within the last five years, as shown in **Table 1**.

Table 1: Post-exposure prophylaxis (PEP) provided to close contacts

Human contacts	Year received last dose of diphtheria-containing vaccine	Interventions
1	2019	Tdap Provided; took antibiotic PEP 5/7 days
2	2022	Tdap Provided; took antibiotic PEP 5/7 days
3	2022	Declined Tdap; did not take antibiotic PEP
4	2018	Tdap Provided; took antibiotic PEP 5/7 days
5	Unsure	Tdap Provided; did not take antibiotic PEP
6	2021	Tdap Provided; did not take antibiotic PEP
7	2019	Declined Tdap; did not take antibiotic PEP

Abbreviations: PEP, post-exposure prophylaxis; Tdap, tetanus, diphtheria, pertussis

Given the high probability that a PCR tox positive isolate would express the toxin (26), we elected to offer post-exposure prophylaxis, as per the UK and Australian guidelines on human exposure to animal *Corynebacterium* spp. (24,25), while we waited for confirmation of toxigenicity by the NML (turnaround time for testing was about one week). Post-exposure prophylaxis consisted of seven days of azithromycin 500 mg oral daily and a diphtheria-containing vaccine if the last dose was more than 12 months prior. In addition, health education on asymptomatic carriage, signs and symptoms to monitor, as well as proper hygiene practices, was provided. All contacts remained asymptomatic from the period of contact to the period of assessment, except for one contact who developed a sore throat two weeks after contact with the donkey. Nasopharyngeal swabs for *C. diphtheriae* culture were taken from all contacts to assess potential human transmission, and at the same time, antibiotic prophylaxis was offered, with three individuals accepting the antibiotics. No swabs yielded growth of *C. diphtheriae* on culture, and the contacts were informed of the negative laboratory results. Consequently, the three contacts who started the medication stopped on day 5/7, while the others who were awaiting the lab results before the start of the antibiotics did not start the medication. Follow-up with the donkey owner revealed that the donkey was doing better with only one wound that required dressing, and there was no further requirement for pain medications. Although the human contacts tested negative for *C. diphtheriae* carriage, given the positive modified Elek testing of the animal isolate, there was a potential ongoing risk of transmission from animal to human. Hence, the owner was advised to take precautions, particularly the use of personal protective equipment, when dealing with the donkey's secretions. The contact investigation was a critical component of the public health response, requiring rapid identification and risk assessment of potentially exposed individuals.

Recommendations

Legislative changes to strengthen reporting protocols for human contact management are needed to improve the surveillance and prevention of transmission of *C. diphtheriae* and other zoonotic infections. It is essential to establish and strengthen routine communication and collaboration between veterinary diagnostic laboratories and public health laboratories that process human specimens. This collaboration would allow for the timely submission of suspicious isolates from veterinary sources to public health laboratories for confirmation. Currently, this practice is not routinely implemented, and public health laboratories do not typically accept isolates from animal sources. As the global health landscape evolves, preparedness for re-emerging zoonotic diseases like diphtheria will remain a critical challenge for public health authorities; hence, the need to streamline reporting of diphtheria and other relevant diseases of public health significance in humans, through a lens of the One Health approach.

Conclusion

Current findings establish that isolation of toxigenic *C. diphtheriae* from cutaneous lesions in animals, although rare, can carry zoonotic transmission risks, particularly through direct contact with open lesions. The investigation confirmed the presence of toxigenic *C. diphtheriae* in the affected donkey and highlighted the necessity for considering vigilant health measures, including close contact management and post-exposure prophylaxis for at-risk individuals. Precautionary post-exposure antibiotic treatment and vaccination were provided at the same time *C. diphtheriae* cultures were taken from the close contacts. The cultures did not grow *C. diphtheriae*. Nonetheless, this incident highlights the importance of maintaining up-to-date diphtheria booster vaccinations within the population. Despite the excellent interagency collaboration in this case, critical uncertainties remain, notably regarding the specific transmission dynamics of toxigenic *C. diphtheriae* from animals to humans and the potential for other domestic or wild animals to act as carriers. Additionally, the absence of standardized surveillance and mandatory reporting for toxigenic *C. diphtheriae* and other diphtheria toxin gene carrying *Corynebacterium* spp. cases in animals pose a significant gap, complicating timely public health responses.

Authors' statement

CO — Conceptualization, investigation, writing–original draft, writing–review & editing
SR — Investigation, writing–review & editing
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Competing interests

None.

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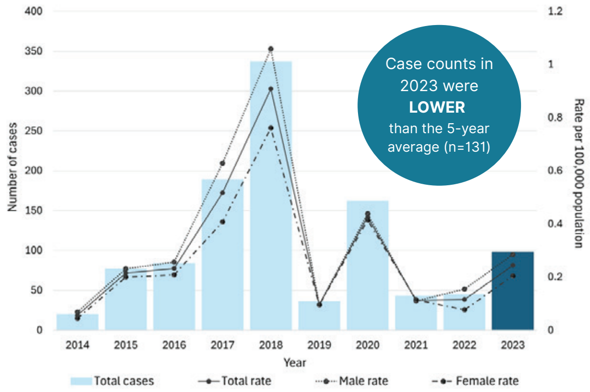
Vector-borne Disease Surveillance in Canada 2023

WEST NILE VIRUS

In 2023, 98 cases of West Nile virus (WNV) were reported at a rate of 0.24 per 100,000 population. Forty-six cases developed severe neurological disease and of these, two died.

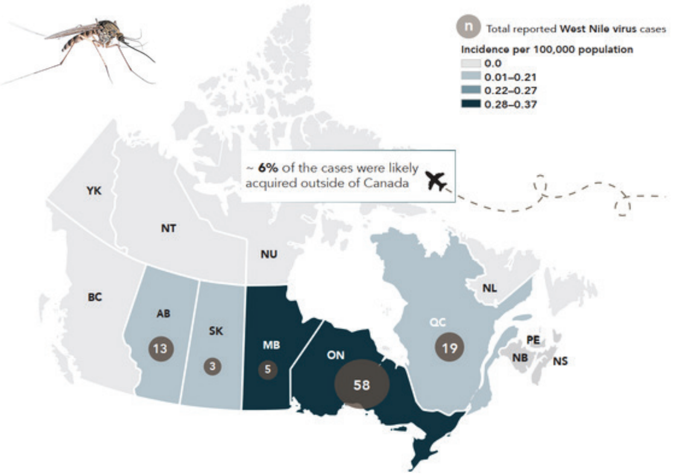
Disease rates were highest among males. People 60 years and older had a higher risk of severe disease and death.

Reported WNV cases and rates, 2014 to 2023



Case counts in 2023 were **LOWER** than the 5-year average (n=131)

GEOGRAPHIC DISTRIBUTION

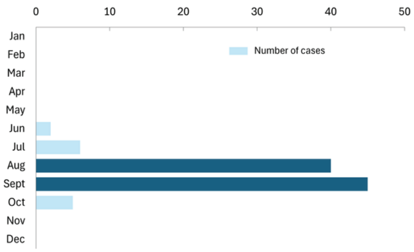


~ **6%** of the cases were likely acquired outside of Canada

SEASONALITY

June 20 Earliest reported illness onset date

83% Illness onset in **August** and **September**

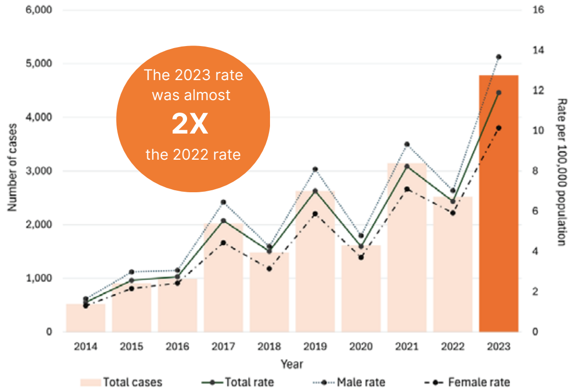


LYME DISEASE

In 2023, 4,785 cases of Lyme disease were reported at a rate of 11.9 per 100,000 population.

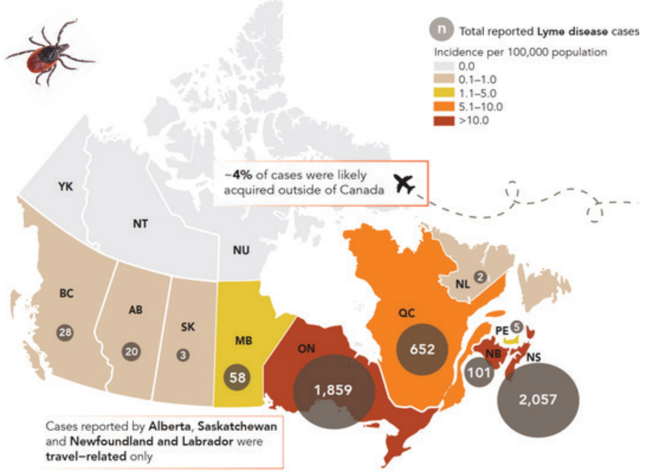
Disease rates were higher among males, people aged 60—79 and, among children, those aged 5—14, compared to similar age groups.

Reported Lyme disease cases and rates, 2014 to 2023



The 2023 rate was almost **2X** the 2022 rate

GEOGRAPHIC DISTRIBUTION



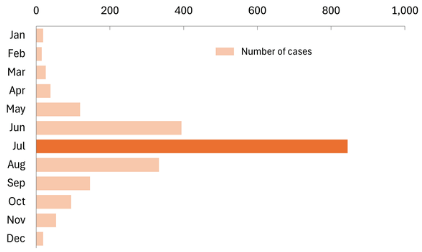
~**4%** of cases were likely acquired outside of Canada

Cases reported by **Alberta**, **Saskatchewan** and **Newfoundland and Labrador** were **travel-related** only

SEASONALITY

40% Illness onset in **July**

94% Illness onset between **May** and **November**



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Canada

Surveillance for *Ixodes scapularis* and *Ixodes pacificus* ticks and their associated pathogens in Canada, 2021

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Abstract

Background: *Ixodes scapularis* and *Ixodes pacificus* ticks pose risk of infection with tick-borne diseases in Eastern and Pacific Western Canada, respectively.

Objective: In 2021, passive and active tick surveillance programs collected ticks and associated data elements, including location, infection and other characteristics, to monitor their populations and inform public health prevention and mitigation activities.

Methods: Surveillance data for ticks were compiled from the National Microbiology Laboratory (Public Health Agency of Canada), provincial public health, Canadian Lyme Disease Research Network and eTick (an image-based online platform). A descriptive analysis of tick records and infection prevalence of tick-borne pathogens is presented. Seasonal trends are described.

Results: During 2021, 6,892 *I. scapularis* ticks were identified across all ten provinces via passive surveillance with 777 *I. pacificus* ticks collected from British Columbia. Most were adult female ticks, collected from human hosts in the spring (March–May) or fall (October–November) seasons. The most common pathogen, *Borrelia burgdorferi*, was detected in 18.6% (95% CI: 17.2%–20.1%) of samples. Active surveillance resulted in 1,929 *I. scapularis* and 18 *I. pacificus* ticks collected in six provinces. Among *I. scapularis*, 22.3% were infected with *B. burgdorferi*, 11.8% with *Babesia odocoilei* and 4.3% with *Anaplasma phagocytophilum*. Fewer than 1% were infected with each of *Borrelia miyamotoi* (0.7%), *Babesia microti* (0.1%) and Powassan virus (0.1%).

Conclusion: As the risk of infection with tick-borne diseases continues to grow in many parts of Canada, monitoring trends in infection prevalence and the geographical range expansion of ticks provides essential data to inform public health actions and messaging.

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Introduction

Ixodes scapularis and *Ixodes pacificus* ticks are known to transmit several bacterial, viral and protozoan pathogens to humans in Eastern/Central and Western Canada, respectively. They are doing so in increasing population numbers and across a broader geographical range due to climate and environmental changes (1–5). The resulting increase in potential for tick-borne diseases in the country, especially in Southern Central and Eastern Canada, has been emphasized in previous reports and in research literature and requires ongoing surveillance so prevention efforts can be successful (1,6–8). Case numbers of Lyme disease reported in Canada in 2022 have increased more than sevenfold since 2012 (9). Additional tick-borne diseases transmitted by *I. scapularis* or *I. pacificus*, namely, anaplasmosis, babesiosis and Powassan virus disease, are nationally notifiable diseases in Canada as of early 2024 (10–13).

Although tick surveillance has been conducted in Canada since the 1990s, data started to be summarized annually at the national-level by the Centre for Food-borne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada (PHAC) in 2019, and provide a baseline for tick-borne disease risk that, over time, will help to identify trends (14).

The objective of this annual surveillance report is to update the summary of characteristics of the main Lyme disease vectors in Canada, *I. scapularis* and *I. pacificus*, collected through passive and active surveillance during 2021. This article also summarizes the prevalence and spatial distribution of their associated pathogens.

Methods

Data sources

This report uses two types of surveillance data from more than 20 different providers. Passive surveillance datasets were provided by the National Microbiology Laboratory (NML) branch of PHAC, British Columbia Centre for Disease Control, Saskatchewan Ministry of Health and eTick. Active surveillance datasets were provided by the Canadian Lyme Disease Research Network, 12 Ontario health units, *Laboratoire de santé publique du Québec*, University of Manitoba, Manitoba Health, Seniors and Long-Term Care Department, New Brunswick Department of Health, University of New Brunswick and University of Ottawa.

Passive tick surveillance: As in 2020, this analysis was limited to *I. scapularis* and *I. pacificus* collected in Canada in the pertinent year (6). Provinces with five or fewer ticks of a given species submitted for species identification and laboratory testing were excluded to avoid misinterpretation of results. Ticks with a location of acquisition outside of the province of submission were not geocoded.

Additional regional passive tick surveillance programs have been discontinued since the publication of the previous report due to laboratory capacity constraints and as *I. scapularis* populations have become established. As before, ticks (or their images) acquired in these jurisdictions could be submitted by the public directly to NML or eTick.

eTick is a web-based, community-science project inviting the public to help with population tick monitoring and is used as a passive surveillance system for ticks in Canada (15). Individuals submit images of ticks they encounter online or via the mobile application, which are then examined by trained personnel to identify the species. Only one tick can be submitted in a single image-based submission.

Ticks collected and submitted from Alberta, Manitoba, Ontario, Québec, New Brunswick and Nova Scotia and tested for *Anaplasma phagocytophilum*, *Borrelia burgdorferi*, *Borrelia miyamotoi* and *Babesia microti* at the NML using methods previously described were included in this report (16,17). Among ticks tested by the British Columbia Centre for Disease Control, only results for *B. burgdorferi* were included in this report. Additional details regarding methodology are available in the previously published annual report (6).

Active tick surveillance: In active surveillance, ticks are collected from the environment using drag sampling or capturing host mammals that are then examined for ticks. This analysis used data from efforts to collect ticks from 10 sites in British Columbia, six in Alberta, at least eight in Saskatchewan, nine sites in Manitoba, more than 60 in Ontario, 36 in Québec, 14 sites in New Brunswick and 10 in Nova Scotia. Drag sampling took place in late spring/summer (May–July) and fall (September–November). Ticks were tested for some or all of the following pathogens: *A. phagocytophilum*; *B. microti*; *B. odocoilei*; *B. burgdorferi*; *B. miyamotoi* and Powassan virus.

Analysis

Tick characteristics: For passive surveillance, descriptive statistics were calculated for submission type (sample-based or image-based), tick species, province of acquisition, stage (larva, nymph, adult female or adult male), level of engorgement (unfed or engorged), host (human, dog, cat or other) and month of collection. For active surveillance, descriptive statistics were calculated for province of collection and stage (larva, nymph, adult female or adult male). All data were cleaned and analysed in R (version 4.0.2).

Ticks submitted through passive surveillance that were acquired in Canada and not associated with a travel history to other provinces or countries were mapped using QGIS software (version 3.34.7) based on their location of acquisition. Ticks submitted with a record of history of travel in the previous 14 days within the same province as the locality of acquisition were geocoded to the submitter-provided location of exposure during travel. In active surveillance, the site location of tick dragging was geocoded from data obtained from the NML and mapped for all data.

Infection prevalence: To account for pooled testing of ticks collected by passive surveillance from some jurisdictions, maximum likelihood estimates of prevalence were calculated with 95% confidence intervals (CI) using the PooledInfRate R package (version 1.6) (18,19). This estimates the probability of infection for an individual tick in the population using the results of testing of the pooled samples (i.e., a group of one or more ticks submitted and tested together). The package was developed by the United States' Centers for Disease Control and Prevention (19). Co-infection prevalence was calculated among single submissions only to ascertain true co-infections, that is, two or more pathogens in a single tick. Where ticks were not tested in pools, prevalence was the number of positive ticks divided by the number of ticks tested.

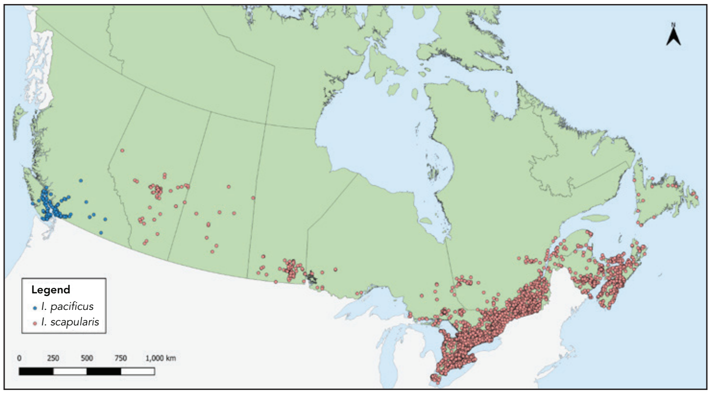
Results

Passive surveillance tick characteristics

In 2021, 7,669 *I. scapularis* (n=6,892) and *I. pacificus* (n=777) ticks were submitted by provinces across Canada, with at least 14 submissions per province (**Table 1**, **Figure 1**). Image-based submissions comprised 54.9% of ticks submitted (n=4,210) and the remainder were sample-based submissions (n=3,459). Ticks from Ontario, Québec and Nova Scotia comprised 83.5% of all ticks submitted. The majority (98.3%) of ticks were from single submissions.

Tick stage, level of engorgement and host were available for 98.2%, 89.3% and 100% of *I. pacificus* records and for 80.3%, 40.0% and 99.9% of *I. scapularis* records, respectively (data not shown in table). Ticks submitted only via eTick did not include information about engorgement. The majority of ticks submitted in sample-based submissions were adult female ticks (*I. pacificus*: 96.2%; *I. scapularis*: 86.8%) (**Table 2**).

Figure 1: *Ixodes pacificus* and *Ixodes scapularis* ticks submitted through passive tick surveillance, Canada, 2021[a]



[a] Each dot represents a probable location of acquisition for a single or multiple submission of *I. scapularis* (n=6,832 submissions) or *I. pacificus* (n=755 submissions) made via passive surveillance programs

A larger proportion of *I. scapularis* were engorged upon submission than *I. pacificus* (41.8% vs 11.1%, respectively) (Table 2). Most *I. pacificus* submissions were obtained from human hosts (91.4%) while a majority of *I. scapularis* were obtained from human and dog hosts (69.8% and 24.2%, respectively).

Records including both month of acquisition and tick stage made up 98.2% of *I. pacificus* and 80.2% of *I. scapularis* submissions (**Figure 2**). All submissions missing tick stage information were image-based submissions, comprising 32.6% of those submissions (n=1,374/4,210).

Table 1: Number of *Ixodes pacificus* and *Ixodes scapularis* ticks and submissions collected through passive surveillance by province, Canada, 2021[a]

Province	Tick species (number of ticks)			Type of surveillance (number of ticks)		Type of submission[b] (number of submissions)	
	Ixodes pacificus	*Ixodes scapularis*	Total	Sample-based	Image-based[c]	Single submissions	Multiple submissions
British Columbia[d]	777	2	779	696	83	743	12
Alberta	0	78	78	16	62	63	1
Saskatchewan	0	15	15	9	6	13	1
Manitoba[d]	0	90	90	5	85	90	0
Ontario[e]	0	4,415	4,415	1,973	2,442	4,365	23
Québec[e]	0	1,377	1,377	659	718	1,356	9
Newfoundland and Labrador	0	18	18	0	18	18	0
New Brunswick	0	214	214	69	145	214	0
Nova Scotia[e]	0	610	610	32	578	602	4
Prince Edward Island	0	73	73	0	73	73	0
Total	777	6,892	7,669	3,459	4,210	7,537	50

[a] No ticks were reported in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus*
[b] Single submissions consist of one tick; multiple submissions consist of two or more ticks submitted together by the same individual
[c] Where ticks were submitted as both samples and images, image submission records were removed
[d] Sample-based submissions from Manitoba and *I. scapularis* submissions from British Columbia were excluded from subsequent analyses below since ≤5 ticks were submitted of each
[e] Passive tick surveillance has been discontinued in some regions of Ontario and Québec and all of Nova Scotia; however, individuals could submit ticks directly to the National Microbiology Laboratory or through eTick

Table 2: Stage, level of engorgement and host of *Ixodes pacificus* and *Ixodes scapularis* ticks submitted through passive surveillance, Canada, 2021[a,b]

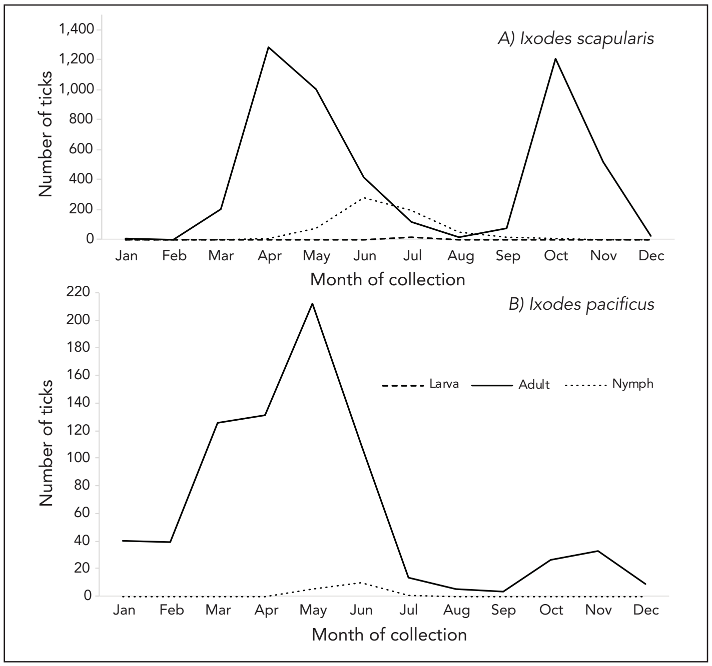
Characteristics	Tick species			
	Ixodes pacificus		*Ixodes scapularis*	
	n	%	n	%
Stage				
Larva	0	0	24	0.46
Nymph	16	2.09	284	5.48
Adult female	735	96.20	4,501	86.84
Adult male	13	1.70	374	7.22
Total	764	100	5,183	100
Level of engorgement				
Engorged	77	11.10	1,144	41.80
Unfed	617	88.90	1,593	58.20
Total	694	100	2,737	100
Host				
Human	711	91.50	4,809	69.81
Dog	49	6.31	1,670	24.24
Cat	1	0.13	271	3.93
Other[c]	16	2.06	139	2.02
Total	777	100	6,889	100

[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 ticks were reported from the Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus*. 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 or through eTick from these jurisdictions

[c] Includes environment, horse, pony, chicken and deer

Figure 2: Number of *Ixodes pacificus* and *Ixodes scapularis* ticks submitted through passive surveillance, by month and tick stage, Canada, 2021[a,b]



[a] Data are presented for *I. pacificus* (n=764) and *I. scapularis* (n=5,529) ticks submitted through passive surveillance

[b] No ticks were reported from the Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus*. 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 or through eTick from these jurisdictions

Adult *I. scapularis* submissions, comprising 80.2% of total *I. scapularis* submitted through passive surveillance, peaked in April and again in October and nymph submissions, comprising 11.4%, peaked in June. For adult *I. pacificus*, submissions peaked in May with a subsequent marginal peak in November.

Infection prevalence in passive surveillance

Data on laboratory testing was available for 98.6% of *I. pacificus* and 99.4%–99.8% of *I. scapularis* from sample-based submissions, depending on pathogen. Nearly one in five *I. scapularis* ticks in Canada is estimated to be infected with at least one tick-borne pathogen (*A. phagocytophilum*, *B. burgdorferi*, *B. miyamotoi* or *B. microti*) (95% CI: 18.3%–21.3%). The most prevalent pathogen was *B. burgdorferi*, detected in 18.6% of *I. scapularis* (95% CI: 17.2%–20.1%). *Anaplasma phagocytophilum* was detected in 1.1% of *I. scapularis* (95% CI: 0.8%–1.6%). Other tick-borne pathogens were estimated to have a prevalence of fewer than 1% each (0.04% positive for *B. microti* (95% CI: 0.00%–0.18%) and 0.4% positive for *B. miyamotoi* (95% CI: 0.2%–0.7%) (**Table 3**).

Table 3: Prevalence of *Anaplasma phagocytophilum*, *Babesia microti*, *Borrelia burgdorferi* and *Borrelia miyamotoi* infection in *Ixodes scapularis* ticks submitted through passive surveillance, Canada, 2021[a]

Pathogen	Infection prevalence	
Single agent	**Maximum likelihood estimate**	
	%	**95% CI**
A. phagocytophilum	1.13	0.78–1.57
B. microti	0.04	0.00–0.18
B. burgdorferi	18.60	17.18–20.09
B. miyamotoi	0.36	0.19–0.65
Total single agent	19.79	18.33–21.31
Co-infection	**Co-infection rate**	
	%	**Number co-infected ticks[b]/ number ticks tested**
A. phagocytophilum + *B. microti*	0	0/2,655
A. phagocytophilum + *B. burgdorferi*	0.30	8/2,664
A. phagocytophilum + *B. miyamotoi*	0.04	1/2,655
B. microti + *B. burgdorferi*	0	0/2,655
B. microti + *B. miyamotoi*	0	0/2,655
B. burgdorferi + *B. miyamotoi*	0.08	3/2,655
Total co-infected[c]	0.38	10/2,664

Abbreviation: CI, confidence interval

[a] Number of *I. scapularis* ticks tested for infection prevalence: *A. phagocytophilum* (n=2,752), *B. microti* (n=2,743), *B. burgdorferi* (n=2,752), *B. miyamotoi* (n=2,743). Only ticks submitted in single submissions could be tested for co-infection (n=2,664). Of the ticks that are excluded, 99.7% (4,210/4,221) were image-based submissions to eTick and 0.4% (n=16) were sample-based submissions missing test results

[b] Numbers are not mutually exclusive due to the presence of a triple co-infection

[c] This figure includes nine double co-infections [*A. phagocytophilum* + *B. burgdorferi* (n=7), *B. burgdorferi* + *B. miyamotoi* (n=2)] and one triple co-infection

Among 684 *I. pacificus* ticks, 0.9% indicated presence of *B. burgdorferi* (95% CI: 0.4%–1.8%) (**Table 4**). Co-infections in *I. scapularis* ticks were also estimated to have a prevalence of fewer than 1.0% each (Table 3).

Ticks infected with tick-borne pathogens were primarily found in Southern and Eastern Ontario, Southern Québec, New Brunswick and in Nova Scotia (**Figure 3**, **Figure 4**). Of the seven provinces where sample-based submissions were included in our analysis, *B. burgdorferi*-infected tick specimens were found in five: British Columbia, Ontario, Québec, New Brunswick and Nova Scotia (Table 4).

Table 4: Prevalence of *Anaplasma phagocytophilum*, *Babesia microti*, *Borrelia burgdorferi* and *Borrelia miyamotoi* infection in *Ixodes scapularis* and *Ixodes pacificus* ticks submitted through passive surveillance, by province, Canada, 2021[a,b]

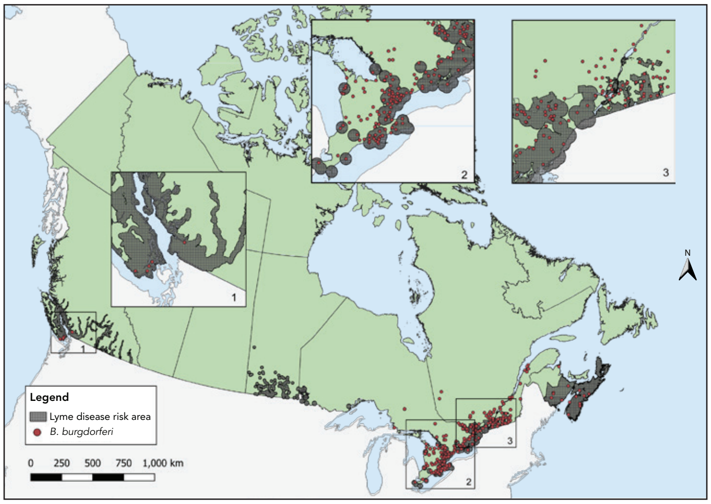
Province	Infection prevalence Maximum likelihood estimate							
	A. phagocytophilum		*B. microti*		*B. burgdorferi*		*B. miyamotoi*	
	%	95% CI	%	95% CI	%	95% CI	%	95% CI
Ixodes pacificus								
British Columbia	N/A	N/A	N/A	N/A	0.73	0.31–1.70	N/A	N/A
Ixodes scapularis								
Alberta	0	0–19.36	0	0–19.36	0	0–19.36	0	0–19.36
Saskatchewan	22.22	6.32–54.74	N/A	N/A	0.00	0.00–29.91	N/A	N/A
Ontario	0.86	0.52–1.35	0	0–0.19	19.20	17.50–20.99	0.30	0.12–0.63
Québec	1.67	0.88–2.88	0.15	0.01–0.73	17.72	14.94–20.80	0.30	0.05–0.99
New Brunswick	1.45	0.26–7.76	0	0–5.27	11.59	5.99–21.25	1.45	0.26–7.76
Nova Scotia	6.23	1.14–18.77	0	0–10.72	28.55	15.14–45.71	3.16	0.18–14.45
Total	1.13	0.78–1.57	0.04	0–0.18	18.60	17.18–20.09	0.36	0.19–0.65

Abbreviations: CI, confidence interval; N/A, not available

[a] No ticks were reported in Yukon, Northwest Territories or Nunavut for *I. scapularis* or *I. pacificus*. 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 or through eTick from these jurisdictions

[b] Number of ticks tested: British Columbia (n=684), Alberta (n=16), Saskatchewan (n=9), Ontario (n=1,972), Québec (n=664), New Brunswick (n=69), Nova Scotia (n=32). Sample-based submissions from Manitoba and *I. scapularis* tick submissions from British Columbia were excluded due to small sample size (n=fewer than five for each). Only image-based submissions were received from Newfoundland and Labrador and Prince Edward Island

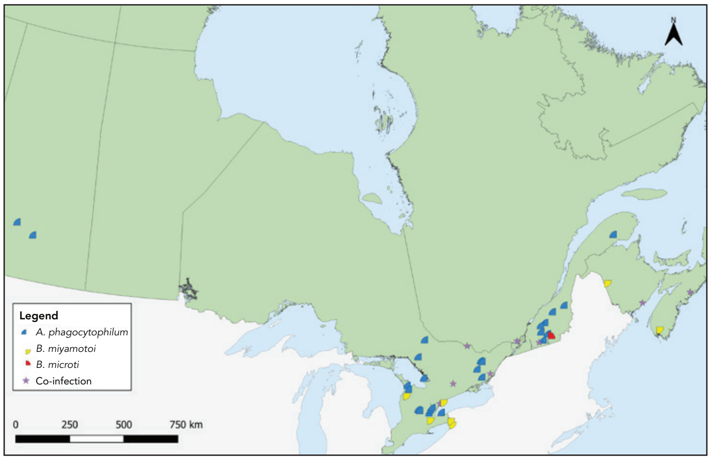
Figure 3: *Ixodes scapularis* and *Ixodes pacificus* ticks submitted through passive surveillance infected with *Borrelia burgdorferi*, Canada, 2021[a,b]



[a] Each dot represents the probable location of acquisition of at least one *I. scapularis* (n=510) or *I. pacificus* (n=5) submitted through passive surveillance that was infected with *B. burgdorferi*. The inlays zoom in on regions in British Columbia (Inlay 1) and parts of Ontario (Inlay 2) and Ontario and Québec (Inlay 3) where these ticks were found

[b] Lyme disease risk areas are identified by the provinces as of 2021 using the methods described in the 2016 national Lyme disease case definition (20). On the map, risk areas are identified as hatched grey areas

Figure 4: *Ixodes scapularis* ticks with associated pathogens (*Anaplasma phagocytophilum*, *Borrelia miyamotoi*, *Babesia microti*) and co-infections collected through passive surveillance, Canada, 2021[a]



[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=33), *B. microti* (n=1), *B. miyamotoi* (n=11) or a coinfection. Coinfections were limited to only single submissions of ticks and include *A. phagocytophilum* + *B. burgdorferi* (n=7), *B. burgdorferi* + *B. miyamotoi* (n=2) and one triple coinfection including all three pathogens, all in *I. scapularis*

Anaplasma phagocytophilum was found in *I. scapularis* in all provinces where ticks were tested except Alberta; *B. burgdorferi* in all except Alberta and Saskatchewan (infection prevalence of 1.1% and 18.6%, respectively) (Figure 3, Figure 4, Table 4). *Borrelia miyamotoi* was found in Ontario, Québec, New Brunswick and Nova Scotia, while a single *Babesia microti*-infected tick was found in Québec.

Active surveillance tick characteristics

In 2021, *I. scapularis* (n=1,935) were collected and tested from five provinces: New Brunswick (n=475), Ontario (n=850), Québec (n=393), Manitoba (n=119) and Nova Scotia (n=98). Of these, the majority of specimens were adults and nymphs followed by larvae (14; 0.7%). In addition, 18 *I. pacificus* were collected in British Columbia.

Infection prevalence in active surveillance

Laboratory testing results for at least one pathogen were available for 99.5% of *I. scapularis*. The most prevalent pathogen was *B. burgdorferi*, present in all five provinces where *I. scapularis* were collected through active surveillance: Manitoba, Ontario, Québec, New Brunswick and Nova Scotia (**Table 5**). *Borrelia burgdorferi* was detected in 22.3% of ticks tested, compared to 29.3% in 2020 (6).

Babesia odocoilei- and *A. phagocytophilum*-infected *I. scapularis* ticks were found in the same five provinces, with overall prevalences of 11.8% and 4.3%, respectively (Table 5, **Figure 5**, **Figure 6**). The overall infection prevalence of the remaining pathogens was less than 1.0% in *I. scapularis*: Twelve *B. miyamotoi*-positive ticks were collected from Manitoba (n=1), Ontario (n=4), Québec (n=2) and New Brunswick (n=5) (Table 5, Figure 6). *Babesia microti*-positive ticks (n=2) and Powassan virus positive ticks (n=2) were found in Manitoba and New Brunswick (Table 5, Figure 6). Among 18 *I. pacificus* ticks collected from six sites in British Columbia, no pathogens were detected.

Discussion

This report provides an update on the national epidemiology of *I. scapularis* and *I. pacificus* ticks, previously published in 2019 and in 2020 (6,16). In 2021, there were 6,892 *I. scapularis* and 777 *I. pacificus* submitted in passive surveillance from ten provinces.

In active surveillance, 1,929 *I. scapularis* and 18 *I. pacificus* were collected in six provinces: British Columbia; Manitoba; Ontario; Québec; New Brunswick; and Nova Scotia. Testing identified the presence of *A. phagocytophilum*, *B. burgdorferi*, *B. miyamotoi*, *B. microti*, *B. odocoilei* and Powassan virus in *I. scapularis*.

Through passive surveillance, 3,459 ticks were sample-based submissions, 41% fewer than the 5,899 ticks submitted as samples in 2020 (6). This is likely a result of the discontinuation of passive surveillance programs. As noted in the 2020 tick surveillance report, this could also be due to the continuing effects of COVID-19 pandemic restrictions on traditional passive surveillance, as health units, medical and veterinary clinics could accept fewer physical tick specimens. During 2021, 54% of all passive surveillance data were from eTick, compared to 29% in the previous year (6). Active surveillance was also affected by pandemic restrictions, as in-person activities such

Table 5: Prevalence of *Anaplasma phagocytophilum*, *Babesia microti*, *Babesia odocoilei*, *Borrelia burgdorferi*, *Borrelia miyamotoi* and Powassan virus infection in *Ixodes scapularis* ticks submitted through active surveillance, by province, Canada, 2021[a,b]

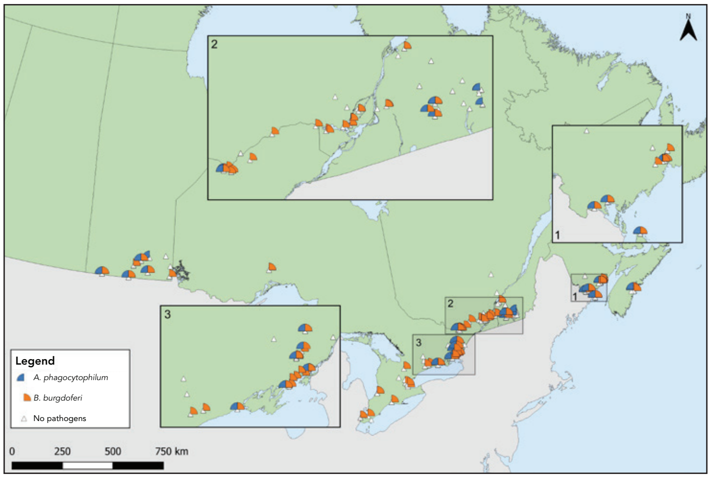
Province	Infection prevalence											
	A. phagocytophilum		*B. microti*		*B. odocoilei*		*B. burgdorferi*		*B. miyamotoi*		Powassan virus	
	Proportion of positive ticks[c]	%	Proportion of positive ticks[c]	%	Proportion of positive ticks[c]	%	Proportion of positive ticks[c]	%	Proportion of positive ticks[c]	%	Proportion of positive ticks[c]	%
Manitoba	6/119	5.04	1/119	0.84	6/119	5.04	36/119	30.25	1/119	0	1/119	0.84
Ontario	36/834	4.32	0/641	0.00	60/641	9.36	247/843	29.30	4/648	0.62	0/641	0.00
Québec	7/391	1.79	0/391	0.00	57/391	14.58	62/391	15.86	2/391	0.51	0/391	0.00
New Brunswick	29/475	6.11	1/475	0.21	64/475	13.47	68/475	14.32	5/475	1.05	1/475	0.21
Nova Scotia	5/98	5.10	0/98	0.00	16/98	16.33	17/98	17.35	0/98	0	0/98	0.00
Total	83/1917	4.33	2/1724	0.12	203/1724	11.7	430/1926	22.33	12/1733	0.69	2/1724	0.12

[a] Only results from tests on *I. scapularis* are included. No *I. scapularis* ticks were collected or tested from sites in Alberta, Saskatchewan, Newfoundland and Labrador, Prince Edward Island, Yukon, Northwest Territories or Nunavut

[b] Infection prevalence is influenced by varying numbers of sites for 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 2021 in Canada were included in this table

[c] The proportion of positive ticks represents the number of ticks tested positive for the specified pathogen over the total number of ticks tested

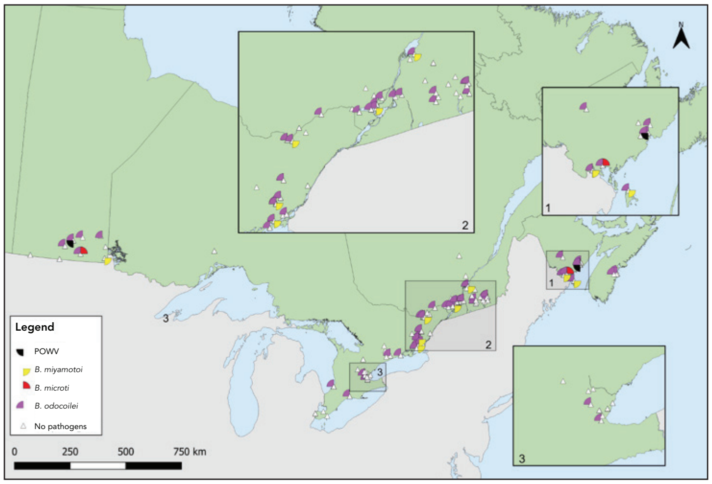
Figure 5: *Ixodes scapularis* ticks with associated pathogens (*Anaplasma phagocytophilum* and *Borrelia burgdorferi*) collected through active surveillance, Canada, 2021[a,b]



[a] Each symbol represents an active surveillance site where *A. phagocytophilum* (n=83) or *B. burgdorferi* (n=430) were found in *I. scapularis* ticks. Sites were mapped based on best available information and do not represent precise locations of tick acquisition. The inlays zoom in on regions in New Brunswick (Inlay 1), Québec and Ontario (Inlay 2) and Ontario (Inlay 3) where these ticks were found close together

[b] No pathogens were found among 18 *I. pacificus* ticks tested from six sites in British Columbia. Map has been zoomed-in for better visibility of tick-borne pathogen distribution

Figure 6: *Ixodes scapularis* ticks with associated pathogens (Powassan virus, *Borrelia miyamotoi*, *Babesia microti* and *Babesia odocoilei*) collected through active surveillance, Canada, 2021[a,b]



Abbreviation: POWV, Powassan virus

[a] Each symbol represents an active surveillance site where POWV (n=2), *B. miyamotoi* (n=12), *B. microti* (n=2) or *B. odocoilei* (n=203) were found in *I. scapularis* ticks. Sites were mapped based on best available information and do not represent precise locations of tick acquisition. The inlays zoom in on regions in New Brunswick (Inlay 1), Québec and Ontario (Inlay 2) and Ontario (Inlay 3) where these ticks were found close together

[b] No pathogen was found among 18 *I. pacificus* ticks tested from six sites in British Columbia. Map has been zoomed-in for better visibility of tick-borne pathogen distribution

as field surveillance were limited in Prince Edward Island and Newfoundland and Labrador.

Ticks submitted through passive surveillance followed distinct species-specific temporal patterns (6). The bimodal peaks for *I. scapularis* adults observed between May and November were consistent with those seen historically in Central and Eastern Canada (21–23) and for *I. pacificus* as observed in the past in British Columbia (16) and the Western United States (24).

However, tick stage development appears to be occurring earlier in the tick season than observed in previous years. There also seems to be a prolongation of the tick season, with individuals reporting tick exposure throughout the year in passive surveillance data. Thus, the overall risk of tick-borne diseases is increasing due to the temporal and spatial expansion of tick activity, though this will also depend on tick infection prevalence in a given area and individual use of preventative measures. These trends should be monitored in the coming years to determine if the shift in tick submissions is due to weather or other factors, or if it reflects selection bias from current surveillance methods.

The proportion of ticks submitted from dogs or cats continued to increase, almost doubling from 15.1% in 2020 to 26.0% in 2021 (6). Like 2020, this is in part due to the inclusion of data from eTick, which does not have any host-based restrictions. The inclusion of eTick data may also have contributed to a shift in the distribution of the life stage of ticks collected; for example, nearly three times the number of nymphs were collected in passive surveillance during 2021 compared with 2020 (6).

The national estimates for prevalence for each pathogen through passive surveillance, except *B. miyamotoi* in *I. scapularis*, were slightly higher than the results for 2020 (6). *Borrelia burgdorferi* was detected in 18.6% of *I. scapularis* compared to 17.2% in 2020, *A. phagocytophilum* in 1.1% compared to 0.9%, *B. microti* in 0.04% compared to 0.02% and *B. miyamotoi* in 0.4% compared to 0.5% in 2020 (6). Among *I. pacificus* ticks, 0.9% were positive for *B. burgdorferi* compared to none in 2020.

For active surveillance, infection prevalence results were similar to those obtained in 2020 for all pathogens except *B. burgdorferi*, which was less prevalent in 2021 in Ontario, Québec and New Brunswick (6). This may be partially explained by the larger total tick numbers collected during 2021; 3.5 times for Québec and 6.5 times for Ontario in 2021 versus 2020 (6). Other factors that influence infection prevalence estimates from year-to-year or between provinces include variation in sites selected and their ecological and host-related characteristics (25).

Our results also include the infection prevalence of *B. odocoilei*, indicating a prevalence close to 15% in samples tested from each of Québec, New Brunswick and Nova Scotia. It was also present in other provinces where it was tested for, namely, Manitoba and Ontario.

Strengths and limitations

While several traditional passive surveillance programs have been phased out, incorporating data from eTick allows us to continue monitoring the geographic presence of these vectors across the country. Combining passive and active surveillance information allows the strengths and weaknesses of the systems to complement each other. While active surveillance is limited in geographic and temporal scope, passive surveillance programs are not limited to specific site locations so data can be gathered from large areas throughout the year.

As noted in 2020, COVID-19 pandemic restrictions affected public health surveillance efforts in 2021. Second, tick specimens collected from eTick, though useful for consistent geographic surveillance, are not routinely requested for tick-borne pathogen testing (15). Recall bias in reporting travel history and other variables in passive surveillance might create uncertainty. For active surveillance, it is likely that other programs were conducted in 2021 that did not submit ticks for pathogen testing at NML and were not included in this summary.

Conclusion

Despite data limitations and resource constraints, efforts in tick surveillance over time have permitted the identification of increasing prevalence and emergence of tick-borne disease pathogens in Canada. Healthcare professionals and the public should be reminded that there is a risk of exposure to infected ticks outside of Lyme disease at-risk areas, even if the risk is low in those areas. Tick surveillance data are an important source of information for public health authorities as they endeavour to identify risk areas, target prevention and education efforts.

Authors' statement

SA — Formal analysis, visualization, writing–original draft, writing–review & editing
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Competing interests

None.

ORCID numbers

None.

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Surveillance for *Ixodes scapularis* and *Ixodes pacificus* ticks and their associated pathogens in Canada, 2022

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Abstract

Background: This article continues the annual series on tick surveillance in Canada, tracking two of the primary tick vectors of concern in the country, *Ixodes scapularis* and *Ixodes pacificus*, which can transmit the agent of Lyme disease alongside several other tick-borne pathogens.

Objective: This study analyzed passive and active tick surveillance data, including geographic distribution, pathogen prevalence and other characteristics to inform public health prevention.

Methods: Passive and active surveillance data were compiled from eTick (an online, image-based platform), the National Microbiology Laboratory (Public Health Agency of Canada), provincial and local public health authorities and the Canadian Lyme Disease Research Network. Descriptive statistics of ticks and their associated pathogens are presented, including infection prevalence estimates.

Results: In 2022, a total of 7,030 *I. scapularis* were submitted through passive surveillance from all provinces, while 911 *I. pacificus* were submitted from British Columbia (n=909) and Yukon (n=2). *Ixodes scapularis* submissions peaked in May and again in October. For *I. pacificus*, submissions peaked in May with a second, smaller peak in November. Six tick-borne pathogens (*Anaplasma phagocytophilum*, *Borrelia burgdorferi*, *Borrelia miyamotoi*, *Babesia microti*, *Babesia odocoilei*, Powassan virus) were identified from the *I. scapularis* collected by dragging in Manitoba, Ontario, Québec, New Brunswick or Nova Scotia.

Conclusion: This report provides a summary of tick surveillance data collected in 2022. Tick characteristics and tick-borne pathogen infection prevalence were similar to previous years. Tick surveillance continues to play an important role in monitoring infection prevalence among ticks and their geographic distribution, which will help inform public health prevention and intervention efforts.

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Keywords: *Ixodes scapularis*, *Ixodes pacificus*, surveillance, ticks, Borrelia, Anaplasma, Babesia, Powassan virus

Introduction

Tick-borne diseases (TBDs) continue to be a public health concern in Canada (1). *Ixodes scapularis* (blacklegged tick) and *Ixodes pacificus* (western blacklegged tick) are the primary tick vectors of importance in Canada, and are capable of transmitting several bacterial, viral and protozoan pathogens (2,3). These pathogens include *Borrelia burgdorferi* (senso stricto) (causing

Lyme disease, LD), *Borrelia miyamotoi* (tick-borne relapsing fever), *Anaplasma phagocytophilum* (anaplasmosis), *Babesia* spp. (babesiosis) and Powassan virus–Lineage II (2,3). *Ixodes scapularis* are usually identified in Central and Eastern Canada and *I. pacificus* in British Columbia (4–7). In addition to LD becoming nationally notifiable in 2009, anaplasmosis, babesiosis and Powassan virus disease are nationally notifiable in humans as of 2024 (8).

Tick surveillance in Canada continues to play an important role in understanding the increasing risk of TBDs (4). By 2022, the national LD incidence had increased 6.5-fold relative to 2012 (from 338 to 2,525 cases) (9). Together, the increasing incidence of LD and the updated nationally notifiable status of other TBDs emphasize the importance of tick surveillance. Furthermore, *I. scapularis* ticks have been testing positive for *B. burgdorferi* since the 1990s (4,5). Continued surveillance efforts help identify the expanding geographic distribution of *I. scapularis* and their infection with relevant tick-borne pathogens (10,11). In addition, tick surveillance data can help inform prevention efforts such as where and when to target awareness campaigns.

Since 2019, *I. scapularis* and *I. pacificus* surveillance data collected in Canada has been summarized at the national level (7). These annual surveillance reports help monitor the current situation in Canada by summarizing the geographic distributions and seasonal activity of the selected *Ixodes* species (6,7). The objective of this surveillance report is to summarize characteristics of *I. scapularis* and *I. pacificus*, collected through passive and active surveillance in 2022. This article will also summarize the prevalence and spatial distribution of several tick-borne pathogens.

Methods

Data sources

This report uses passive and active tick surveillance data from seven organizations including public health authorities and academics. Passive surveillance data were provided by eTick (Bishop's University), British Columbia Centre for Disease Control (BCCDC), Public Health Ontario (PHO), Saskatchewan Ministry of Health, Institut national de santé publique du Québec (INSPQ) and the National Microbiology Laboratory (NML) of the Public Health Agency of Canada. Active surveillance data were provided by the Canadian Lyme Disease Research Network (CLyDRN). The CLyDRN conducts active surveillance across all 10 provinces. In addition, active surveillance data was provided by BCCDC, PHO and INSPQ.

Passive tick surveillance

This report follows similar methodology as previous annual reports (6,7,12). This analysis was limited to *I. scapularis* and *I. pacificus* collected in Canada in 2022. Submission records of ticks acquired outside of the submission province, as well as ticks acquired outside of Canada, were excluded, as were all records associated with a prior two-week history of travel outside of Canada. Ticks were either submitted individually (single submission) or in groups of two or more (multiple submission).

Since 2009, regional passive tick surveillance and testing programs have been gradually discontinued in several jurisdictions. This could be due, in part, to limited laboratory capacity as *I. scapularis* populations become established in various parts of the country and are more often encountered. eTick remains open to the public to submit images and spatiotemporal data of ticks encountered throughout Canada. eTick is a web-based, community-science project inviting the public to help with tick monitoring and used as a passive surveillance system for ticks in Canada (13). The images and associated data of ticks encountered by members of the public are submitted to the eTick website or through the eTick application, for identification by trained personnel. While images of *Dermacentor* ticks are only identified to genus, those of *Ixodes* and other genera are identified to species, unless the picture quality is inadequate in which case the specimen is requested to be submitted for further examination.

Ticks submitted from Saskatchewan and INSPQ were tested for *A. phagocytophilum*, *B. burgdorferi*, *B. miyamotoi* and *B. microti* using methods previously described (7,14). *Ixodes pacificus* submitted by the BCCDC were tested for *B. burgdorferi* (15). Ticks submitted from PHO were not tested for pathogens. Ticks submitted through eTick were not routinely requested for testing for tick-borne pathogens, but they could be forwarded onto a laboratory for this purpose at the request of local public health authorities.

Active tick surveillance

Ticks were collected from the environment using drag sampling. This report analyzed *I. scapularis* collected via drag sampling from 19 sites in Alberta, 10 sites in Saskatchewan, 12 sites in Manitoba, 95 sites in Ontario, 124 sites in Québec, 10 sites in New Brunswick, 24 sites in Nova Scotia, five sites in Prince Edward Island and 10 sites in Newfoundland and Labrador. Also included in this report are *I. pacificus* data collected from 22 sites throughout British Columbia. Drag sampling took place in late spring/summer (May–July) across all regions. Some sentinel sites included a second sampling period in the fall (September–November).

Ticks submitted through CLyDRN and INSPQ were tested for *A. phagocytophilum*, *B. burgdorferi*, *B. miyamotoi*, *B. microti*, *B. odocoilei* and Powassan virus. *Ixodes pacificus* submitted by the BCCDC were tested for *B. burgdorferi*. Ticks that tested positive for *A. phagocytophilum* underwent further testing to identify the strain as pathogenic (*A. phagocytophilum*–human active, Ap-ha) or non-pathogenic (*A. phagocytophilum*–Ap-V1). The protocols for testing the ticks have been previously described (7,14,16).

Analysis

Descriptive and spatiotemporal characteristics: For passive surveillance, descriptive statistics were calculated for several characteristics including submission type, the tick species covered in this report, province of acquisition, life stage (larva, nymph, adult female or adult male), level of engorgement (unfed or engorged), host (human, dog, cat or other) and month of collection. For active surveillance, descriptive statistics were calculated for province of collection and life stage (larva, nymph or adult). All data were cleaned and analysed in R (version 4.3.2) (17).

Ticks submitted through passive surveillance were mapped using QGIS (version 3.34.7) based on their location of acquisition. Records with a history of travel in Canada in the previous 14 days were geocoded to the probable location of exposure during travel. Data records were excluded from geocoding but kept in the overall analysis if the submitter had a history of multiple travel locations within Canada, travel to another province or were missing a location of tick acquisition. In active surveillance, the location of tick dragging was geocoded before being mapped except where site coordinates were already provided.

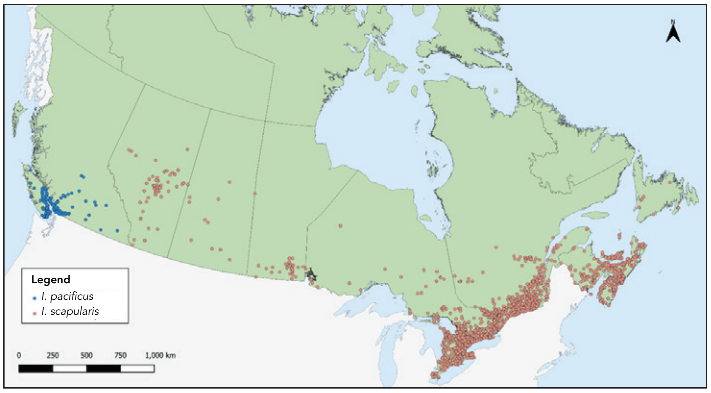
Infection prevalence: Prevalence was calculated as the number of positive ticks divided by the total number of ticks tested. Using the binom package in R, 95% confidence intervals were calculated.

Results

Overview of passive surveillance data

In 2022, there were 911 *I. pacificus* and 7,030 *I. scapularis* submitted from 10 provinces and one territory (**Table 1**, **Figure 1**). No ticks were submitted from Northwest Territories or Nunavut. A higher proportion (54%) of the records were obtained from image-based submissions (n=4,324) while the rest were sample-based submissions (n=3,617). Submissions from Ontario, Québec and Nova Scotia comprised 83.4% of all ticks submitted. The majority (99.2%) of ticks were from single submissions, but there were 61 multiple submissions (range: 2–4 ticks per submission).

Figure 1: *Ixodes pacificus* and *Ixodes scapularis* submitted through passive tick surveillance, Canada, 2022[a]



[a] Each dot represents the probable location of acquisition for an *I. pacificus* (n=891) or *I. scapularis* (n=5,307) tick specimen submitted through passive surveillance. There were 20 *I. pacificus* and 1,723 *I. scapularis* that had locations that could not be geocoded or did not have any location information (missing data not shown in figure)

Table 1: Number of *Ixodes pacificus* and *Ixodes scapularis* submissions collected through passive surveillance by province, Canada, 2022

Province	Tick species (number of ticks)			Type of surveillance (number of ticks)[a]		Type of submission (number of submission)[b]	
	Ixodes pacificus	*Ixodes scapularis*	Total	Sample-based	Image-based	Single submissions	Multiple submissions
British Columbia	909	3	912	628	284	871	19
Alberta	0	126	126	0	126	126	0
Saskatchewan	0	17	17	0	17[c]	17	0
Manitoba	0	51	51	N/A	51	51	0
Ontario	0	4,338	4,338	2,211	2,127	4,249	42
Québec	0	1,629	1,629	778	851	1,629	0
Newfoundland and Labrador	0	12	12	0	12	12	0
New Brunswick	0	146	146	0	146	146	0
Nova Scotia	0	657	657	0	657	657	0
Prince Edward Island	0	51	51	0	51	51	0
Yukon	2	0	2	0	2	2	0
Total	911	7,030	7,941	3,617	4,324	7,811	61

[a] Sample-based submissions are physical tick specimens; image-based submissions are images submitted to eTick
[b] Single submissions consist of one tick; multiple submissions consist of two or more ticks submitted together by the same submitter
[c] There were seven *I. scapularis* that were submitted through eTick and also tested for pathogens in Saskatchewan

Most ticks submitted were adult female (*I. pacificus*: 89.7%; *I. scapularis*: 89.9%) (**Table 2**). Adult males, nymphs and larvae were submitted less frequently (*I. pacificus*: 2.3%, 6.9% and 1.1%; *I. scapularis*: 5.6%, 4.4% and 0.1%, respectively). Overall, 11.3% of *I. pacificus* and 62.7% of *I. scapularis* adult females were engorged. Humans were the most common host among *I. pacificus* and *I. scapularis* (75.2% and 59.1%, respectively) followed by dogs (16.2% and 34.0%, respectively).

Table 2: Life stage, level of engorgement and host of *Ixodes pacificus* and *Ixodes scapularis* submitted through passive surveillance, Canada, 2022[a,b]

Characteristics	Tick species			
	Ixodes pacificus		*Ixodes scapularis*	
	n	%	n	%
Life stage				
Larva	10	1.1	4	0.1
Nymph	62	6.9	282	4.4
Adult female	810	89.7	5,701	89.9
Adult male	21	2.3	353	5.6
Total	903	100	6,340	100
Level of engorgement[c]				
Adult female				
Engorged	70	11.3	1,663	62.7
Unfed	548	88.7	991	37.3
Total	618	100	2,654	100
Nymph				
Engorged	N/A	N/A	74	63.8
Unfed	N/A	N/A	42	36.2
Total	N/A	N/A	116	100
Host				
Human	685	75.2	2,849	59.1
Dog	148	16.2	1,640	34.0
Cat	5	0.6	219	4.5
Other[d]	73	8.0	111	2.3
Total	911	100	4,819	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

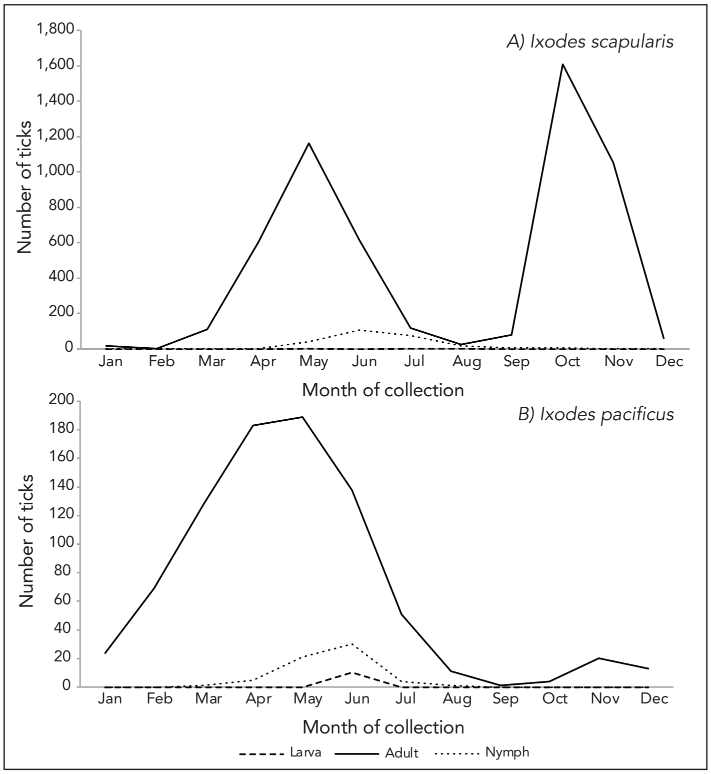
[b] Life stage, level of engorgement and host were available for 99.1%, 68.6% and 100% of *I. pacificus*, respectively. Life stage, level of engorgement and host were available for 90.2%, 39.8% and 68.5% of *I. scapularis*, respectively. Ticks submitted only via eTick did not include information about level of engorgement (missing data not shown in table)

[c] Level of engorgement was calculated for the adult female and nymph life stage. No engorgement data was available for *I. pacificus* nymphs

[d] Includes environment, horse, goat, deer and bobcat

Two submission peaks for adult *I. scapularis* were observed, one in May and a second slightly larger peak in October (**Figure 2**). The number of adult *I. pacificus* submissions peaked in May with a second, considerably smaller peak in November.

Figure 2: Number of *Ixodes scapularis* and *Ixodes pacificus* submitted through passive surveillance, by month and life stage, Canada, 2022[a,b]



[a] Available data are presented for A) *I. scapularis* (n=5,690) and B) *I. pacificus* (n=903) ticks submitted through passive surveillance

[b] Month of acquisition and tick life stage data were available for 99.1% of *I. pacificus* and 80.9% of *I. scapularis* records (missing data not shown in figure)

Passive surveillance infection prevalence

The majority of *I. pacificus* submitted by BCCDC were tested for *B. burgdorferi* (n=624/625; 99.8%). In comparison, 64.6% (n=509/788) to 65.0% (n=512/788) of sample-based *I. scapularis* submissions were tested, depending on the pathogen of interest. Of 788 *I. scapularis*, three were submitted from BCCDC, seven from Saskatchewan and 778 from INSPQ. Although most of the prevalence data for *I. scapularis* came from Québec, one tick was found positive for *B. burgdorferi* in British Columbia, and another tick was found positive for *B. miyamotoi* in Saskatchewan (**Table 3**).

While ticks from human (95.7%) and non-human hosts (4.3%) were both tested, pathogens were found only in *I. scapularis* and *I. pacificus* submitted from human hosts. Pathogen testing information from Québec identified five ticks co-infected with *A. phagocytophilum* and *B. burgdorferi*, and one tick coinfected with *B. burgdorferi* and *B. miyamotoi* (**Table 4**).

Table 3: Prevalence of *Borrelia burgdorferi* and *Borrelia miyamotoi* infection in physical specimens of *Ixodes pacificus* and *Ixodes scapularis* obtained through passive surveillance, by province and life stage, Canada, 2022

Province	Infection prevalence (% positive, 95% CI)					
	Borrelia burgdorferi			*Borrelia miyamotoi*		
	Adult	Nymph	Total	Adult	Nymph	Total
Ixodes pacificus						
British Columbia	7/624 (1.1, 0.5–2.3)	0	7/624 (1.1, 0.5–2.3)	NT	NT	NT
Ixodes scapularis						
British Columbia	1/3 (33.3, 0.8–90.6)	0	1/3 (33.3, 0.8–90.6)	NT	NT	NT
Saskatchewan	0/7 (0.0, 0.0–41.0)	0	0/7 (0.0, 0.0–41.0)	1/7 (14.3, 0.4–57.9)	0	1/7 (14.3, 0.4–57.9)
Québec	113/477 (23.7, 19.9–27.8)	2/25 (8.0, 1.0–26.0)	115/502 (22.9, 19.3–26.8)	5/477 (1.0, 0.3–2.4)	0/25 (0.0, 0.0–13.7)	5/502 (1.0, 0.3–2.3)
Total	114/487 (23.4, 19.7–27.4)	2/25 (8.0, 1.0–26.0)	116/512 (22.7, 19.1–26.5)	6/484 (1.2, 0.5–2.7)	0/25 (0.0, 0.0–13.7)	6/509 (1.2, 0.4–2.6)

Abbreviations: CI, confidence interval; NT, not tested

Table 4: Prevalence of *Anaplasma phagocytophilum* and *Babesia microti* in physical specimens of *Ixodes pacificus* and *Ixodes scapularis* obtained through passive surveillance, by province and life stage, Canada, 2022

Province	Infection prevalence[a] (% positive, 95% CI)					
	Anaplasma phagocytophilum			*Babesia microti*		
	Adult	Nymph	Total	Adult	Nymph	Total
Ixodes pacificus						
British Columbia	NT	NT	NT	NT	NT	NT
Ixodes scapularis						
British Columbia	NT	NT	NT	NT	NT	NT
Saskatchewan	0/7 (0.0, 0.0–41.0)	0	0/7 (0.0, 0.0–41.0)	0/7 (0.0, 0.0–41.0)	0	0/7 (0.0, 0.0–40.96)
Québec	13/477 (2.7, 1.5–4.6)	2/25 (8.0, 1.0–26.0)	15/502 (3.0, 1.7–4.9)	0/477 (0.0, 0.0–0.8)	0/25 (0.0, 0.0–13.7)	0/502 (0.0, 0.0–0.7)
Total	13/484 (2.7, 1.4–4.6)	2/25 (8.0, 1.0–26.0)	15/509 (3.0, 1.7–4.8)	0/484 (0.0, 0.0–0.8)	0/25 (0.0, 0.0–13.7)	0/509 (0.0, 0.0–0.7)

Abbreviations: CI, confidence interval; NT, not tested

[a] Infection prevalence is presented as number positive/number tested (percentage positive, 95% confidence interval)

Overview of active surveillance data

In 2022, *I. scapularis* (n=2,292) were collected in six provinces via active surveillance: Alberta (n=1), Manitoba (n=12), Ontario (n=904), Québec (n=1,077), New Brunswick (n=56) and Nova Scotia (n=242). Nymphs (n=1,116/2,292; 48.7%) were collected most often, followed by adults (n=894/2,292; 39.0%) and larvae (n=282/2,292; 12.3%). One *I. scapularis* was found in Alberta and it was not tested for pathogens. No *I. scapularis* were found by dragging in Saskatchewan, Prince Edward Island and Newfoundland and Labrador. *Ixodes pacificus* were collected in British Columbia (n=109). *Ixodes pacificus* nymphs (n=58/109; 53.2%) were collected most often, followed by larvae (n=26/109; 23.9%) and adults (n=25/109; 22.9%).

Active surveillance infection prevalence

The most prevalent pathogen detected in *I. scapularis* was *B. burgdorferi* (24.4%, 95% CI: 22.5–26.4) (**Table 5**). *Anaplasma phagocytophilum* (2.9%, 95% CI: 2.2–3.7) was found in *I. scapularis* in all provinces where *I. scapularis* were recovered by active surveillance except Manitoba and Alberta (**Table 6**). Of the 57 ticks testing positive for *A. phagocytophilum*, 29 were tested to determine the strain variant, with 15 (51.7%) carrying the strain that is pathogenic to humans (Ap-ha). *Babesia odocoilei* was found in *I. scapularis* (10.6%, 95% CI: 9.3–12.1) in all provinces where active surveillance was conducted except Alberta (Table 6). The remaining pathogens (*B. miyamotoi*, *B. microti* and Powassan virus) were each found in less than

Table 5: Prevalence of *Borrelia burgdorferi*, *Borrelia miyamotoi*, and Powassan virus in *Ixodes pacificus* and *Ixodes scapularis* obtained through active surveillance, by province and life stage, Canada, 2022

Province	Infection prevalence[a] (% positive, 95% CI)								
	Borrelia burgdorferi			*Borrelia miyamotoi*			Powassan virus		
	Adult	Nymph	Total	Adult	Nymph	Total	Adult	Nymph	Total
Ixodes pacificus									
British Columbia	0/25 (0.0, 0.0–13.7)	1/58 (1.7, 0.0–9.2)	1/83 (1.2, 0.0–6.5)	0/9 (0.0, 0.0–33.6)	0/58 (0.0, 0.0–6.2)	0/67 (0.0, 0.0–5.4)	0/9 (0.0, 0.0–33.63)	0/58 (0.0, 0.0–6.2)	0/67 (0.0, 0.0–5.4)
Ixodes scapularis									
Manitoba	2/10 (20.0, 2.5–55.6)	0/2 (0.0, 0.0–84.2)	2/12 (16.7, 2.1–48.4)	0/10 (0.0, 0.0–30.9)	0/2 (0.0, 0.0–84.2)	0/12 (0.0, 0.0–26.5)	0/10 (0.0, 0.0–30.9)	0/2 (0.0, 0.0–84.2)	0/12 (0.0, 0.0–26.5)
Ontario	176/674 (26.1, 22.8–29.6)	70/223 (31.4, 25.4–37.9)	246/897 (27.4, 24.5–30.5)	3/676 (0.4, 0.1–1.3)	0/223 (0.0, 0.0–1.6)	3/899 (0.3, 0.1–1.0)	0/672 (0.0, 0.0–0.5)	0/223 (0.0, 0.0–1.6)	0/895 (0.0, 0.0–0.4)
Québec	43/113 (38.1, 29.1–47.7)	101/668 (15.1, 12.5–18.1)	144/781 (18.4, 15.8–21.3)	0/113 (0.0, 0.0–3.2)	2/668 (0.3, 0.0–1.1)	2/781 (0.3, 0.0–0.9)	1/113 (0.9, 0.0–4.8)	1/668 (0.1, 0.0–0.8)	2/781 (0.3, 0.0–0.9)
New Brunswick	7/16 (43.8, 19.8–70.1)	17/40 (42.5, 27.0–59.1)	24/56 (42.9, 29.7–56.8)	0/16 (0.0, 0.0–20.6)	0/40 (0.0, 0.0–8.8)	0/56 (0.0, 0.0–6.4)	0/16 (0.0, 0.0–20.6)	0/40 (0.0, 0.0–8.8)	0/56 (0.0, 0.0–6.4)
Nova Scotia	30/73 (41.1, 29.7–53.2)	38/163 (23.3, 17.1–30.6)	68/236 (28.8, 23.1–35.0)	0/73 (0.0, 0.0–4.9)	0/163 (0.0, 0.0–2.2)	0/236 (0.0, 0.0–1.6)	0/73 (0.0, 0.0–4.9)	0/163 (0.0, 0.0–2.2)	0/236 (0.0, 0.0–1.6)
Total	258/886 (29.1, 26.1–32.2)	226/1,096 (20.6, 18.3–23.1)	484/1,982 (24.4, 22.5–26.4)	3/888 (0.3, 0.1–1.0)	2/1,096 (0.2, 0.0–0.7)	5/1,984 (0.3, 0.1–0.6)	1/884 (0.1, 0.0–0.6)	1/1,096 (0.1, 0.0–0.5)	2/1,980 (0.1, 0.0–0.4)

Abbreviation: CI, confidence interval

[a] Infection prevalence is presented as number positive/number tested (percentage positive, 95% confidence interval)

Table 6: Prevalence of *Anaplasma phagocytophilum*, *Babesia microti*, and *Babesia odocoilei* in *Ixodes pacificus* and *Ixodes scapularis* obtained through active surveillance, by province and life stage, Canada, 2022

Province	Infection prevalence[a] (% positive, 95% CI)								
	Anaplasma phagocytophilum			*Babesia microti*			*Babesia odocoilei*		
	Adult	Nymph	Total	Adult	Nymph	Total	Adult	Nymph	Total
Ixodes pacificus									
British Columbia	1/9 (11.1, 0.3–48.2)	1/58 (1.7, 0.0–9.2)	2/67 (3.0, 0.4–10.4)	0/9 (0.0, 0.0–33.6)	0/58 (0.0, 0.0–6.2)	0/67 (0.0, 0.0–5.4)	0/9 (0.0, 0.0–33.6)	3/58 (5.2, 1.1–14.4)	3/67 (4.5, 0.9–12.5)
Ixodes scapularis									
Manitoba	0/10 (0.0, 0.0–30.8)	0/2 (0.0, 0.0–84.2)	0/12 (0.0, 0.0–26.5)	0/10 (0.0, 0.0–30.8)	0/2 (0.0, 0.0–84.2)	0/12 (0.0, 0.0–26.5)	2/10 (20.0, 2.5–55.6)	0/2 (0.0, 0.0–84.2)	2/12 (16.7, 2.1–48.4)
Ontario	27/676 (4.0, 2.6–5.8)	7/223 (3.1, 1.3–6.4)	34/899 (3.8, 2.6–5.2)	0/676 (0.0, 0.0–0.5)	0/223 (0.0, 0.0–1.6)	0/899 (0.0, 0.0–0.4)	32/676 (4.7, 3.3–6.6)	18/223 (8.1, 4.9–12.5)	50/899 (5.6, 4.2–7.3)
Québec	2/113 (1.8, 0.2–6.2)	13/668 (1.9, 1.0–3.3)	15/781 (1.9, 1.1–3.1)	0/113 (0.0, 0.0–3.2)	4/668 (0.6, 0.2–1.5)	4/781 (0.5, 0.1–1.3)	18/113 (15.9, 9.7–24.0)	104/668 (15.6, 12.9–18.5)	122/781 (15.6, 13.1–18.4)
New Brunswick	2/16 (12.5, 1.6–38.3)	3/40 (7.5, 1.6–10.4)	5/56 (8.9, 3.0–19.6)	0/16 (0.0, 0.0–20.6)	0/40 (0.0, 0.0–8.8)	0/56 (0.0, 0.0–6.4)	4/16 (25.0, 7.3–52.4)	9/40 (22.5, 10.8–38.5)	13/56 (23.2, 13.0–36.4)
Nova Scotia	0/73 (0.0, 0.0–4.9)	3/163 (1.8, 0.4–5.3)	3/236 (1.3, 0.3–3.7)	0/73 (0.0, 0.0–4.9)	1/163 (0.6, 0.0–3.4)	1/236 (0.4, 0.0–2.3)	11/73 (15.1, 7.8–25.4)	13/163 (8.0, 4.3–13.3)	24/236 (10.2, 6.6–14.8)
Total	31/888 (3.5, 2.4–4.9)	26/1,096 (2.4, 1.6–3.5)	57/1,984 (2.9, 2.2–3.7)	0/888 (0.0, 0.0–0.4)	5/1,096 (0.5, 0.1–1.1)	5/1,984 (0.3, 0.1–0.6)	67/888 (7.5, 5.9–9.5)	144/1,096 (13.1, 11.2–15.3)	211/1,984 (10.6, 9.3–12.1)

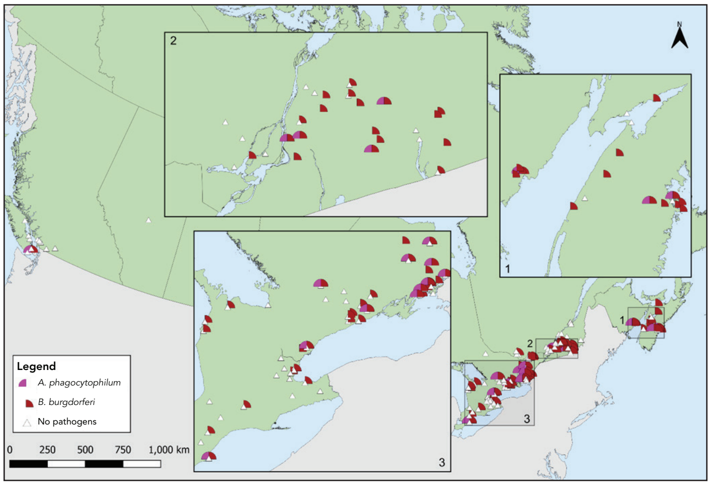
Abbreviation: CI, confidence interval

[a] Infection prevalence is presented as number positive/number tested (percentage positive, 95% confidence interval)

0.3% of tested ticks. Four *B. microti*-positive ticks were found in Québec and one in Nova Scotia (Table 6). Three *B. miyamotoi*-positive ticks were collected in Ontario and two in Québec (Table 5). Two ticks from Québec tested positive for Powassan virus Lineage II (Table 5). A higher infection prevalence was found in adult ticks versus nymphs for *B. burgdorferi*, *B. miyamotoi* and *A. phagocytophilum* (Table 5 and Table 6). In contrast, a higher infection prevalence was found in nymphs versus adult ticks for *B. microti* and *B. odocoilei* (Table 6).

Among *I. pacificus*, *B. burgdorferi* (1.2%, 95% CI: 0.0–6.5), *A. phagocytophilum* (3.0%, 95% CI: 0.4–10.4) and *B. odocoilei* (4.5%, 95% CI: 0.9–12.5) were found (Table 6). The site locations where *I. scapularis* and *I. pacificus* were collected in active surveillance and the pathogens detected therein are shown in **Figure 3** and **Figure 4**.

Figure 3: *Ixodes pacificus* or *Ixodes scapularis* with *Anaplasma phagocytophilum* or *Borrelia burgdorferi* collected through active surveillance, Canada, 2022[a]



Abbreviations: *A. phagocytophilum*; *Anaplasma phagocytophilum*; *B. burgdorferi*, *Borrelia burgdorferi*

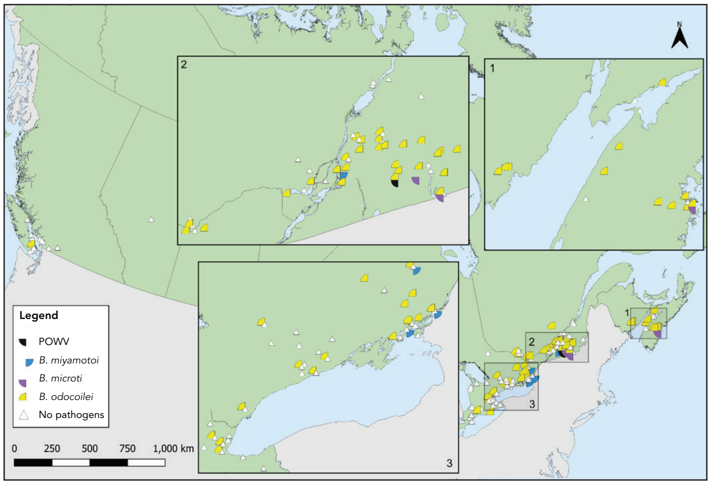
[a] Each symbol represents an active surveillance site where *A. phagocytophilum* (n=59) or *B. burgdorferi* (n=485) were found in *I. pacificus* or *I. scapularis*. There were 56 sites where no pathogens were detected. The inlays zoom in on regions in New Brunswick and Nova Scotia (Inlay 1), Québec and Ontario (Inlay 2) and Ontario (Inlay 3) where these ticks were found close together

Discussion

This annual summary provides an update on the characteristics, geographic distribution, and pathogen prevalence of *I. scapularis* and *I. pacificus* in Canada, previously analyzed in 2021 (unpublished data). In 2022, a total of 7,941 *I. pacificus* and *I. scapularis* were submitted through passive surveillance from 10 provinces and one territory.

Compared to 2021, infection prevalence estimates from passive surveillance for all pathogens tested are slightly higher across both tick species (12). Seven *I. pacificus* tested positive for *B. burgdorferi* from British Columbia (1.1% which is similar to the prevalence reported in 2021) (0.9%, 95% CI: 0.4–1.8).

Figure 4: *Ixodes pacificus* or *Ixodes scapularis* with Powassan virus, *Borrelia miyamotoi*, *Babesia microti* or *Babesia odocoilei* collected through active surveillance, Canada, 2022[a]



Abbreviations: *B. microti*; *Babesia microti*; *B. miyamotoi*, *Borrelia miyamotoi*; *B. odocoilei*, *Babesia odocoilei*; *I. pacificus*, *Ixodes pacificus*; *I. scapularis*, *Ixodes scapularis*; POW, Powassan virus

[a] Each symbol represents an active surveillance site where POW (Powassan virus) (n=2), *B. miyamotoi* (n=5), *B. microti* (n=5) or *B. odocoilei* (n=211) were found in *I. pacificus* or *I. scapularis*. There were 56 sites where no pathogens were detected. The inlays zoom in on regions in New Brunswick and Nova Scotia (Inlay 1), Québec and Ontario (Inlay 2) and Ontario (Inlay 3) where these ticks were found close together

For *I. scapularis*, the prevalence of pathogens ranged from 0% to 22.7%, with *B. burgdorferi* being the most prevalent. A somewhat higher prevalence of *I. scapularis* infected with *B. burgdorferi* (22.7%, 95% CI: 19.1–26.5) was recorded in 2022 compared to 2021 (18.6%, 95% CI: 17.2–20.1).

Pathogen testing for passive surveillance specimens identified two distinct types of co-infections in Québec (*A. phagocytophilum* and *B. burgdorferi*; *B. burgdorferi* and *B. miyamotoi*), both of which have been reported in previous years (6,7). Adult ticks had a higher prevalence of infection across all pathogens except *A. phagocytophilum*; however, it is important to note that there was a considerably larger number of adult ticks collected and tested compared to nymphs in passive surveillance.

Passive surveillance data showed that tick life stage and month of collection continued to follow similar patterns as previous years (6,7); for example, a higher proportion of submitted ticks were adult females and found on human hosts. Furthermore, *I. scapularis* adult submissions showed a bimodal distribution in the month of collection with peaks occurring in May and October. This distribution has been consistently demonstrated to occur in Central and Eastern Canada through previous reports (6,7,18–20). *Ixodes pacificus* tick submissions were also consistent with previous reports, showing a large peak across April and May and a considerably smaller peak in November (6,7,15). These bimodal peaks reflect when ticks are most active due to suitable weather conditions. It is well recognized that Lyme disease symptom onset occurs around seasons where ticks are most active (9,21,22). In addition, tick engorgement, which reflects the ticks' feeding activity, is slightly different compared to previous years, with adult female and nymphal *I. scapularis* showing a higher proportion of engorgement compared to previous years. This may also be due to the higher proportion of image-based submissions where engorgement data are missing.

Active surveillance data in 2022 identified six tick-borne pathogens (*A. phagocytophilum*, *B. burgdorferi*, *B. miyamotoi*, *B. microti*, *B. odocoilei*, Powassan virus) among the *I. scapularis* collected in Manitoba, Ontario, Québec, New Brunswick and Nova Scotia. The most prevalent pathogen was *B. burgdorferi* (24.4%, 95% CI: 22.5–26.4). The least prevalent pathogen was Powassan virus and was only identified in Québec. In contrast, three tick-borne pathogens (*A. phagocytophilum*, *B. burgdorferi* and *B. odocoilei*) were identified among *I. pacificus* collected in British Columbia.

Infection prevalence determined through active surveillance was comparable to previous years with slight differences depending on the pathogen (6,7,12). For example, the total prevalence for *B. burgdorferi* in *I. scapularis* increased from 22.3% in 2021 to 24.4% in 2022. To highlight, ticks in Ontario had a lower *B. burgdorferi* infection prevalence in 2022 (27.4%) compared to 2021 (29.3%), while ticks in Québec had a higher prevalence (18.4% in 2022 and 15.9% in 2021). *A. phagocytophilum* had a lower total infection prevalence in 2022 (2.9%) compared to 2021 (4.3%). *Babesia microti* had a higher total infection prevalence in 2022 compared to previous years. Finally, *B. odocoilei* had the highest infection prevalence in New Brunswick (23.2%) followed by Manitoba (16.7%) and Québec (15.6%). Infection prevalence should be interpreted with caution due to the varying number of ticks tested between provinces and years. Other factors that influence infection prevalence estimates from year-to-year or between provinces include variation in sites selected and their ecological and host-related characteristics (23).

Strengths and limitations

In 2022, there were fewer pathogen testing data available for ticks collected through passive surveillance compared to previous years. This was in part due to the gradual discontinuation of passive surveillance programs over time; however, active surveillance data continued to provide standardized information on infection prevalence across Canada, with a larger number of sites and enhanced efforts to span more areas. Available passive surveillance data continued to provide comprehensive geographic and temporal information on *I. scapularis* and *I. pacificus*.

Other limitations included missing data across several tick characteristics such as life stage, which made interannual comparisons challenging. Furthermore, possible recall bias may have introduced uncertainty to existing passive surveillance data including tick location and date of collection. The annual variation in pathogen testing, including differing sample size and inconsistent surveillance site selection, reduced comparability of infection prevalence estimates. As additional annual data become available, interannual comparisons will be completed using appropriate statistical methods; therefore, comparisons to previous years were purely descriptive and did not assess statistical significance. Finally, this report provides an overview of tick surveillance across Canada but may not include all tick surveillance activities conducted in the country.

Conclusion

Tick surveillance data in 2022 continued to highlight the characteristics of two important TBD vectors in Canada; *I. scapularis* and *I. pacificus*. *Borrelia burgdorferi* continued to be the most prevalent pathogen particularly in *I. scapularis*. The collection and spatiotemporal data, as well as infection prevalence data, were similar to previous years with slight increases or decreases depending on the pathogen and province.

These findings support public health initiatives such as public education on tick bite prevention and TBD risk area identification. Surveillance activity helps identify stable or shifting trends in pathogen prevalence or geographic distribution, especially as factors such as climate change and resulting expanding tick habitats are expected to continue to affect future tick and pathogen dynamics. Thus, continued investment in tick surveillance and prevention strategies will remain essential to reduce the burden of tick-borne disease on public health and the healthcare system.

Authors' statement

GW — Formal analysis, writing–original draft, writing–review & editing
SA — Visualization, writing–review & editing
CW — Writing–review & editing
HC — Writing–review & editing
JS — Writing–review & editing
MN — Writing–review & editing
KCronin — Writing–review & editing
PZ — Writing–review & editing
KT — Writing–review & editing
KCrandall — Writing–review & editing
PG — Writing–review & editing
LS — Writing–review & editing
EJ — Writing–review & editing
MM — Writing–review & editing
CH — Writing–review & editing
MKL — Writing–review & editing
PB — Writing–review & editing
ACB — Writing–review & editing
SG — Conceptualization, supervision, writing–review & editing

Competing interests

None.

ORCID numbers

None.

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Appendix

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Invasive pneumococcal disease surveillance in Canada, 2023

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Abstract

Background: Invasive pneumococcal disease (IPD), which is caused by *Streptococcus pneumoniae*, has been a nationally notifiable disease in Canada since 2000. This report summarizes the demographics, serotypes and antimicrobial resistance of IPD isolates collected in Canada in 2023.

Methods: The Public Health Agency of Canada's National Microbiology Laboratory (Winnipeg, Manitoba) collaborates with provincial and territorial public health laboratories to conduct national surveillance of IPD. Serotypes and minimum inhibitory concentrations were obtained from whole genome sequencing data.

Results: The incidence of IPD in Canada was 10.2 cases per 100,000 population in 2022, increasing from the low rate of 5.6 cases per 100,000 population in 2021. A total of 4,760 IPD isolates were collected during 2023. The most common serotypes overall were 3 (12.3%, n=587), 4 (12.2%, n=580), 22F (8.2%, n=391) and 9V (7.1%, n=340). Serotypes 4 (7.1%–12.2%, $p<0.0001$) and 9V (1.3%–7.1%, $p<0.0001$) also increased significantly in prevalence since 2019, resulting in an overall increase in the proportion of PCV15 and PCV20/non-V116 serotypes causing disease. The highest rates of antimicrobial resistance in 2023 were seen with clarithromycin (25.8%), doxycycline (17.5%) and trimethoprim/sulfamethoxazole (15.9%). Multidrug-resistance continued to increase from 2019 to 2023 (8.4%–13.2%, $p<0.0001$) and rates were highest in serotypes 9V, 15A, 19A, 23A and 35B.

Conclusion: The high number of IPD cases collected in 2023 represents a return to pre-SARS-CoV-2 pandemic disease activity. Several serotypes included in previous conjugate vaccine formulations are highly common or are increased in prevalence, including 3, 4 and 9V. Continued surveillance of pneumococcal serotypes is imperative to evaluate vaccine effectiveness, particularly as new vaccine formulations are approved and integrated into immunization schedules in Canada.

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Keywords: IPD, Canada, *Streptococcus pneumoniae*, PCV15, PCV20, V116, pneumococcus, serotype, surveillance, antimicrobial resistance

Introduction

Streptococcus pneumoniae is a common gram-positive microorganism that can cause severe invasive pneumococcal diseases (IPDs), such as bacteremia and meningitis. Children, the elderly and immunocompromised individuals are at greatest risk (1). Pneumococcal conjugate vaccines (PCVs) have been used with great success, decreasing the burden of IPD worldwide.

Recently, PCVs with expanded coverage were approved for use in Canada, including 15-valent (PCV15: 1, 3, 4, 5, 6A, 6B, 7F, 9V, 14, 18C, 19A, 19F, 22F, 23F, and 33F), 20-valent (PCV20: PCV15 serotypes plus 8, 10A, 11A, 12F and 15BC) and 21-valent (V116: 3, 6A, 7F, 8, 9N, 10A, 11A, 12F, 15A, 15BC, 16F, 17F, 19A, 20A, 22F, 23A, 23B, 24F, 31, 33F and 35B) formulations. While PCV15 and PCV20 have followed the pattern of adding additional serotypes to a previous formulation, V116 is the first PCV specifically designed for use in adults over 18 years of age, containing a series of unique serotypes commonly responsible for adult pneumococcal disease (2). As of the time of writing, PCV15 and PCV20 are the pneumococcal vaccines recommended by Canada's National Advisory Committee on Immunization for routine paediatric immunization, while PCV20 and V116 are recommended for adults over 65 years of age (3–5). The objective of this annual surveillance report is to provide a summary of the serotypes and antimicrobial resistance associated with IPD in Canada in 2023.

Methods

Surveillance program

As previously described, surveillance of IPD in Canada consists of a passive, laboratory-based system where invasive isolates from the provincial and territorial public health laboratories are sent to the National Microbiology Laboratory (NML, Winnipeg), Alberta Provincial Laboratory for Public Health or *Laboratoire de santé publique du Québec* for serotyping (6). In 2023, a total of 4,760 IPD isolates were reported, including 2,932 submitted directly to NML by provincial and territorial public health laboratories and data for a further 824 and 1,004 isolates collected and tested by Alberta Provincial Laboratory for Public Health and *Laboratoire de santé publique du Québec*, respectively (**Table 1**). Sterile clinical isolation sites include blood, cerebrospinal fluid, peritoneal, pericardial or joint fluid, internal body sites and deep tissue including surgical or biopsy samples. For this report, isolates from pleural fluid (empyema) are included, despite not meeting the current national case definition for invasive disease, as they are considered invasive in some jurisdictions (7,8). Note that this analysis does not include typing data for PCR-positive samples with no culture data.

Population-based incidence of IPD up to 2022 were obtained through the Canadian Notifiable Disease Surveillance System (CNDSS). Incidence rates for 2023 were not available at the time of writing. Population data for incidence rates were obtained from Statistics Canada's July 1st annual population estimates.

Isolate testing

All IPD isolates submitted to NML in 2023 were tested by whole-genome sequencing (WGS) using the Illumina platform. Isolates were confirmed as *S. pneumoniae* using *rpoB* sequence analysis (9). Serotypes were identified directly using the WADE pipeline (https://github.com/phac-nml/wade). Isolates that were nontypeable by WGS were confirmed by Quellung reaction, using commercial antisera (SSI Diagnostica; Statens Serum Institut, Copenhagen, Denmark) (10). Serotyping of IPD at Alberta Provincial Laboratory for Public Health and *Laboratoire de santé publique du Québec* was performed by the Quellung reaction. For this study, serotypes 15B and 15C were grouped together as 15BC because of reported reversible switching between them *in vivo* during infection, making it difficult to differentiate between the two types (11,12).

For all isolates submitted to NML, minimum inhibitory concentrations were predicted using WADE and previously described algorithms for penicillin, ceftriaxone, chloramphenicol, clarithromycin, clindamycin, doxycycline, levofloxacin and trimethoprim/sulfamethoxazole (13). Minimum inhibitory concentrations were interpreted using Clinical and Laboratory Standards Institute breakpoints (14); penicillin was interpreted using the oral penicillin V breakpoints, and ceftriaxone using the meningitis breakpoints. Multidrug-resistance (MDR) was defined as resistance to three or more different classes of antimicrobials. Genomes were scanned for *van* family genes to identify any emergence of vancomycin-nonsusceptibility (15).

Table 1: Number of invasive *Streptococcus pneumoniae* submitted by province, 2023

Province	Age group (years)						Not given	Total
	Younger than 2	2–4	5–14	15–49	50–64	65 and older		
British Columbia[a]	3	9	6	195	196	199	3	611
Alberta	16	15	18	317	230	207	21	824
Saskatchewan	5	3	5	146	73	85	0	317
Manitoba	7	4	13	136	86	81	1	328
Ontario	47	61	48	312	428	587	2	1,485
Québec	53	40	29	175	245	450	12	1,004
Atlantic[b]	4	6	5	23	54	77	4	173
Northern[c]	0	1	0	5	4	8	0	18
Total	135	139	124	1,309	1,316	1,694	43	4,760

[a] Includes isolates from Yukon
[b] Includes isolates from New Brunswick, Prince Edward Island, Nova Scotia and Newfoundland and Labrador
[c] Includes isolates from Northwest Territories and Nunavut

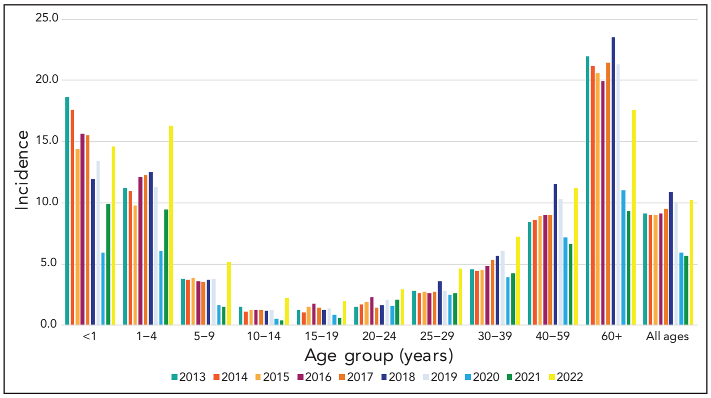
Data analysis

Demographic data submitted with bacterial isolates included patient age, sex, clinical source, province and date of collection. Duplicate isolates collected from the same patient within 21 days were counted once if they were the same serotype, with the most invasive isolation site assigned. Meningitis related isolates were regarded as most invasive, followed by blood and then other sterile sites. Data was aggregated by age into younger than two, 2–4, 5–14, 15–49, 50–64 and 65 years and older age groups and regionally into Western (British Columbia, Alberta, Saskatchewan, Manitoba), Central (Ontario and Québec), Eastern (New Brunswick, Nova Scotia, Prince Edward Island, Newfoundland and Labrador) and Northern (Yukon Territories, Northwest Territories and Nunavut) regions of Canada. Statistical significance of trends was assessed using the Cochran-Armitage test of trend, with a *p*-value of <0.05 considered significant.

Results

The overall incidence of IPD in Canada increased to 10.2 cases per 100,000 population in 2022. This represents a sharp increase from the 2021 incidence of 5.6 cases per 100,000 population, and a return to pre-COVID-19 pandemic incidence that peaked in 2018 at 10.9 cases per 100,000 population (**Figure 1**). There was a large increase in the number of IPD isolates submitted in 2023 (n=4,760) in comparison to 2022 (n=3,867), representing the highest annual IPD isolate total collected by NML to-date.

Figure 1: Annual incidence of invasive pneumococcal disease cases per 100,000 population in Canada by age group, 2013–2022[a]

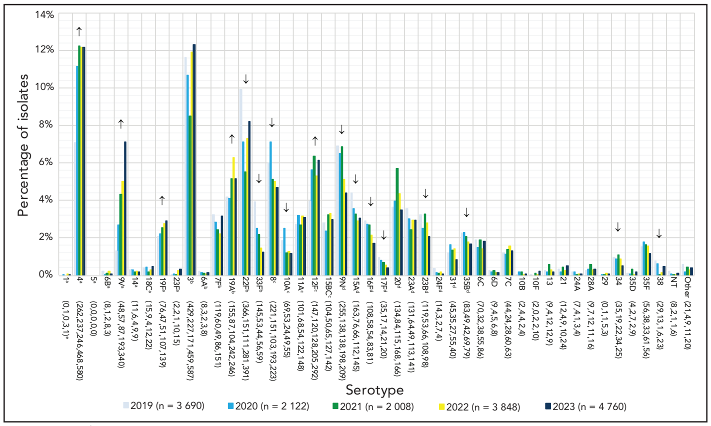


[a] Data from Canadian Notifiable Disease Surveillance System

Of the 4,760 IPD isolates tested in 2023, 4,717 (99.1%) had patient ages. Infants younger than two years of age accounted for 2.9% (n=135), toddlers aged 2–4 years for 2.9% (n=139), children aged 5–14 years for 2.6% (n=124), patients aged 15–49 years for 27.8% (n=1,309), older adults aged 50–64 years for 27.9% (n=1,316) and seniors aged 65 years and older for 35.9% (n=1,694). Forty-three isolates had no ages provided. Of the isolates for which sex information was available, isolates from male patients represented 57.0% (n=2,653) of isolates. Blood was the main clinical isolation site, accounting for 92.8% (n=4,418) of isolates collected.

The most commonly collected serotypes overall in 2023 were 3 (12.3%, n=587), 4 (12.2%, n=580), 22F (8.2%, n=391) and 9V (7.1%, n=340). Other common types included 12F, 19A, 8 and 9N. Serotypes that demonstrated significant increasing trends in prevalence from 2019 to 2023 include PCV15 and PCV20/non-V116 serotypes 4 (7.1%−12.2%, *p*<0.0001), 9V (1.3%−7.1%, *p*<0.0001) and 19F (2.1%−2.9%, *p*=0.0051); PCV15/PCV20/V116 serotype 19A (4.2%–5.2%, *p*=0.0011); and PCV20/V116 serotype 12F (4.0%–6.1%, *p*=0.0002) (**Figure 2**). Vaccine serotypes that significantly decreased in prevalence from 2019 to 2023 included PCV15/PCV20/V116 serotypes 22F and 33F (*p*≤0.018), PCV20/V116 serotypes 8 and 10A (*p*≤0.0002) and V116-unique serotypes 9N, 15A, 16F, 17F, 23B, 35B (*p*≤0.0196) (Figure 2).

Figure 2: Invasive *Streptococcus pneumoniae* serotype prevalence trends, all age groups combined, 2019–2023[a,b,c,d,e]



[a] PCV15 and PCV20/non-V116 serotype

[b] PCV15, PCV20 and V116 serotype

[c] PCV20 and V116 serotype

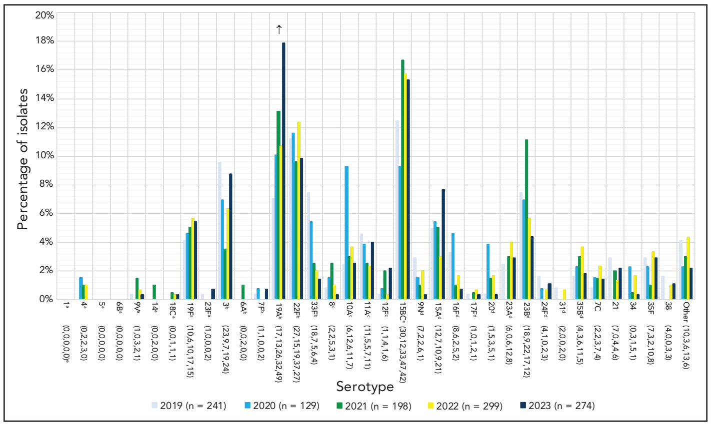
[d] V116/non-PCV15/20 serotype

[e] Number of isolates for 2019, 2020, 2021, 2022 and 2023, respectively. For serotypes with an overall (2019–2023) N≥50: up or down arrows indicate statistically significant trends toward increasing or decreasing prevalence for the 2019–2023 timespan, using the chi-squared test for trend. Serotypes with no arrow either did not demonstrate a statistically significant trend, or did not have an overall N≥50. Serotypes 15B and 15C were grouped together as 15B/C because of reported reversible switching between them *in vivo* during infection, making it difficult to precisely differentiate between the two types (11,12)

The most common serotypes in children younger than two years during 2023 were 15BC (17.8%, n=24) and 19A (16.3%, n=22). For children aged 2–4 years and 5–14 years, serotypes 19A (19.4%, n=27; 16.1%, n=20, respectively) and 3 (15.1%, n=21; 18.5%, n=23) were most common. For patients aged 15–49 years, serotype 4 was the most prevalent (22.6%, n=296), followed by serotypes 9V (10.8%, n=141), 12F (10.0%, n=131) and 3 (9.8%, n=128). Serotypes 4 (13.3%, n=175), 3 (12.8%, n=169) and 9V (8.8%, n=116) were the most common in adults 50–64 years, while serotypes 3 (14.1%, n=239) and 22F (11.7%, n=198) were dominant in adults over 65 years of age.

A significant increase of serotype 19A (7.1%–17.9%, *p*=0.0007) was observed in children younger than five years of age from 2019 to 2023 (**Figure 3**), however no significant changes were noted for children five to 14 years. Patients aged 15–49 years and 50–64 years experienced large, significant increases of serotypes 4 (14.5%–22.6%, *p*<0.0001; 8.4%–13.3%, *p*<0.0001, respectively) and 9V (2.2%–10.8%, *p*<0.0001; 1.6%–8.8%, *p*<0.0001). Adults 65 years and older also experienced increases of serotypes 4 and 9V, but to a lesser extent (3.6%–5.8%, *p*=0.0064; 0.8%–4.6%, *p*=0.0093, respectively) (**Figure 4**). Patients 15–49 years of age also saw a small but significant increase in serotype 11A (1.3%–2.8%, *p*=0.0098), while adults 50–64 years saw an increase in serotype 19F (1.0%–2.7%, *p*=0.0033). Adults 50–64 years and 65 years of age and older both saw an increase of serotype 12F (4.6%–7.1%, *p*=0.0298; 1.8%–3.5%, *p*=0.0121, respectively).

Figure 3: Invasive *Streptococcus pneumoniae* serotype prevalence trends, younger than five years of age, 2019–2023[a,b,c,d,e]

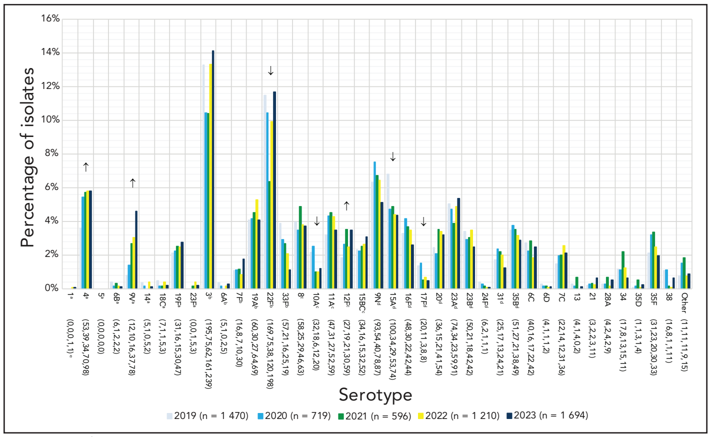


[a] PCV15 and PCV20/non-V116 serotype
[b] PCV15, PCV20 and V116 serotype
[c] PCV20 and V116 serotype
[d] V116/non-PCV15/20 serotype
[e] Number of isolates for 2019, 2020, 2021, 2022 and 2023, respectively. For serotypes with an overall (2019–2023) N≥50: up or down arrows indicate statistically significant trends toward increasing or decreasing prevalence for the 2019–2023 timespan, using the chi-squared test for trend. Serotypes with no arrow either did not demonstrate a statistically significant trend, or did not have an overall N≥50. Serotypes 15B and 15C were grouped together as 15B/C because of reported reversible switching between them *in vivo* during infection, making it difficult to precisely differentiate between the two types (11,12)

The most common serotypes isolated in Western Canada in 2023 were 4 (17.4%, n=362), 3 (11.3%, n=235) and 9V (10.5%, n=217). In Central Canada, serotype 3 remained most prevalent (13.1%, n=325), followed by 22F (9.4%, n=234) and 19A (8.2%, n=205). In Eastern Canada, serotypes 3 (14.5%, n=25), 22F (11.6%, n=20) and 4 (11.0%, n=19) were the most common in 2023. Serotypes 20 (22.7%, n=5) and 9V (18.2%, n=4) were most common in Northern Canada, though submissions from this region remained low (**Appendix**, **Figure S1**).

Serotypes belonging to the currently recommended PCV15 and PCV20 vaccines, but not V116 (1, 4, 5, 6B, 9V, 14, 18C, 19F and 23F) have significantly increased in prevalence overall from 2019 to 2023 (11.4%–23.3%, *p*<0.0001); this increase was noted in all adult age groups. The proportion of serotypes included in all three formulations (3, 6A, 7F, 19A, 22F and 33F) increased in children 5–14 years of age (35.7%–50.8%, *p*=0.186), but decreased in patients 15–49 years (32.2%–24.1%, *p*=0.0007). The category of serotypes shared by PCV20 and V116 (8, 10A, 11A, 12F and 15BC) remained stable over time. The proportion of V116-unique serotypes (9N, 15A, 16F, 17F, 20, 23A, 23B, 24F, 31 and 35B) decreased significantly overall (29.5%–20.7%, *p*<0.0001); this decrease was seen in all age groups except children younger than five years, where no significant changes were identified for any vaccine category. Overall, the proportion of non-vaccine serotypes has not significantly changed (**Figure 5**; Appendix, Table S1).

Figure 4: Invasive *Streptococcus pneumoniae* serotype prevalence trends, 65 years of age and older, 2019–2023[a,b,c,d,e]

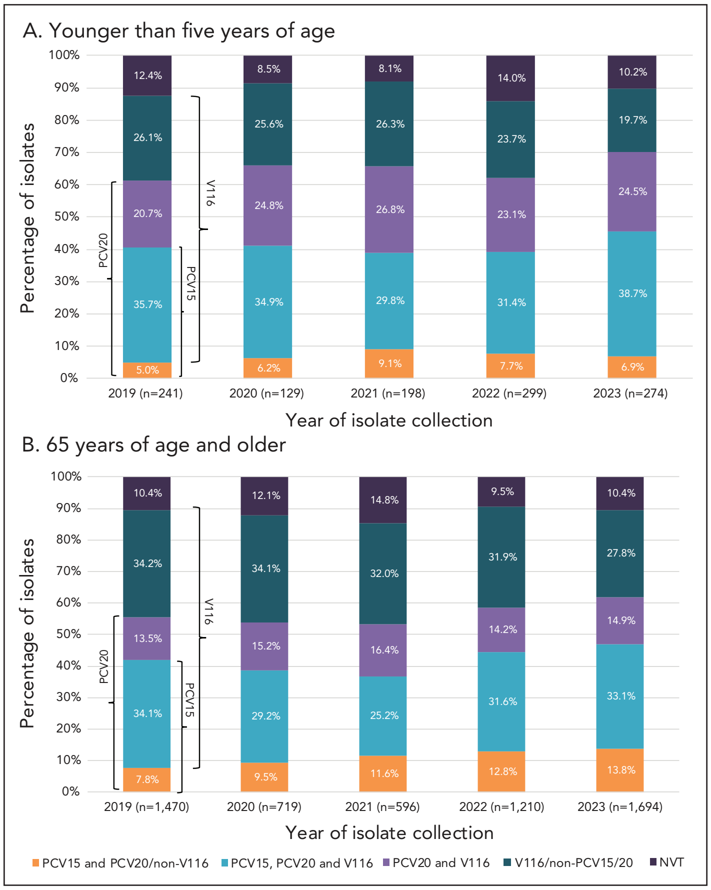


[a] PCV15 and PCV20/non-V116 serotype
[b] PCV15, PCV20 and V116 serotype
[c] PCV20 and V116 serotype
[d] V116/non-PCV15/20 serotype
[e] Number of isolates for 2019, 2020, 2021, 2022 and 2023, respectively. For serotypes with an overall (2019–2023) N≥50: up or down arrows indicate statistically significant trends toward increasing or decreasing prevalence for the 2019–2023 timespan, using the chi-squared test for trend. Serotypes with no arrow either did not demonstrate a statistically significant trend, or did not have an overall N≥50. Serotypes 15B and 15C were grouped together as 15B/C because of reported reversible switching between them *in vivo* during infection, making it difficult to precisely differentiate between the two types (11,12)

Whole-genome sequencing-based prediction of antimicrobial susceptibilities was performed on 3,058 *S. pneumoniae* isolates collected in 2023 (**Table 2**). The highest rate of resistance during 2023 was observed for clarithromycin at 25.8% (n=790) but has remained stable from 2019 to 2023. Penicillin resistance increased over the 2019 to 2023 period, from 2.9% (n=60) to 8.0% (n=246; *p*<0.0001). Other antimicrobial resistance rates for 2023 included doxycycline at 17.5% (n=535), trimethoprim-sulfamethoxazole at 15.9% (n=486), clindamycin at 7.9% (n=242) and chloramphenicol at 2.7% (n=83). There was limited resistance to ceftriaxone (0.2%, n=5), and all isolates were susceptible to levofloxacin. No vancomycin resistance determinants were identified. Resistance rates for specific serotypes in 2023 are listed in **Table 3**.

Multidrug-resistant IPD increased from 8.4% (n=175) of the isolates tested in 2019 to 13.2% (n=404) in 2023 (*p*<0.0001) (**Figure 6**). Of the serotypes where 10 or more isolates were collected in 2023, the highest rates of MDR were

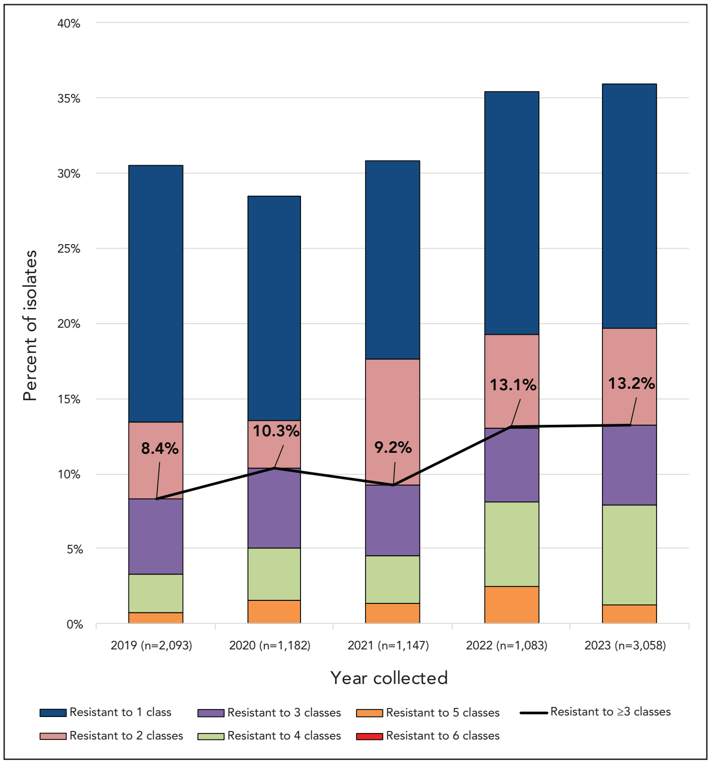
Figure 5: Invasive *Streptococcus pneumoniae* serotype trends by vaccine and age[a], 2019–2023



Abbreviations: NVT, non-vaccine serotype; PCV, pneumococcal conjugate vaccine

[a] Antimicrobial classes include: β-lactams (penicillin using the Clinical & Laboratory Standards Institute (CLSI) oral penicillin V interpretive criteria, ceftriaxone using the CLSI parenteral meningitis interpretive criteria); macrolides (clarithromycin); fluoroquinolones (levofloxacin); tetracyclines (doxycycline); folate pathway inhibitors (trimethoprim-sulfamethoxazole); phenicols (chloramphenicol); lincosamides (clindamycin)

Figure 6: Annual trend of multidrug resistance of invasive *Streptococcus pneumoniae*, 2019–2023[a]



[a] Antimicrobial classes include: β-lactams (penicillin using the Clinical & Laboratory Standards Institute (CLSI) oral penicillin V interpretive criteria, ceftriaxone using the CLSI parenteral meningitis interpretive criteria); macrolides (clarithromycin); fluoroquinolones (levofloxacin); tetracyclines (doxycycline); folate pathway inhibitors (trimethoprim-sulfamethoxazole); phenicols (chloramphenicol); lincosamides (clindamycin)

identified in 9V (67.2%, n=137), 15A (43.9%, n=36), 19A (30.4%, n=35), 23A (26.4%, n=23) and 35B (21.1%, n=12) (Table 3; Appendix, **Figure S2**). Together these serotypes accounted for 59.9% (n=242/404) of MDR isolates collected in 2023. The most common MDR pattern in 2023 was β-lactam-macrolide-tetracycline-trimethoprim/sulfamethoxazole, with serotype 9V accounting for the majority (n=130). Serotypes 15A and 23A both had macrolide-clindamycin-tetracycline as their most common MDR pattern (n=23 and n=22, respectively). Multidrug-resistant serotype 19A isolates were most commonly resistant to five antimicrobial classes (β-lactam, macrolide, clindamycin, tetracycline and trimethoprim/sulfamethoxazole; n=23), while the most common MDR pattern for serotype 35B was β-lactam-macrolide-trimethoprim/sulfamethoxazole (n=10) (Appendix, **Table S2**).

Table 2: Proportion of antimicrobial resistant invasive *Streptococcus pneumoniae* isolates by year, 2019–2023

Antimicrobial	Year, n (%)				
	2019	2020	2021	2022	2023
PEN	60 (2.9)	46 (3.9)	58 (5.1)	90 (8.3)	246 (8.0)
CRO	6 (0.3)	6 (0.5)	6 (0.5)	2 (0.2)	5 (0.2)
CHL	60 (2.9)	46 (3.9)	40 (3.5)	37 (3.4)	83 (2.7)
CLR	517 (24.7)	271 (22.9)	245 (21.4)	273 (25.2)	790 (25.8)
CLI	166 (7.9)	90 (7.6)	101 (8.8)	100 (9.2)	242 (7.9)
DOX	237 (11.3)	143 (12.1)	163 (14.2)	186 (17.2)	535 (17.5)
LEV	9 (0.4)	1 (0.1)	0 (0.0)	2 (0.2)	0 (0.0)
SXT	127 (6.1)	99 (8.4)	122 (10.6)	164 (15.1)	486 (15.9)
Total tested	2,093	1,182	1,147	1,083	3,058

Abbreviations: CHL, chloramphenicol; CLI, clindamycin; CLR, clarithromycin; CRO, ceftriaxone using the Clinical & Laboratory Standards Institute parenteral meningitis interpretive criteria; DOX, doxycycline; LEV, levofloxacin; PEN, penicillin using the Clinical & Laboratory Standards Institute oral penicillin V interpretive criteria; SXT, trimethoprim/sulfamethoxazole

Table 3: Percentage of antimicrobial resistance among invasive *Streptococcus pneumoniae* serotypes collected in 2023

Serotype[a]	Percentage of isolates with antimicrobial resistance[b]								
	PEN	CRO	CHL	CLR	CLI	DOX	LEV	SXT	MDR
1[c] (n=1)	-	-	-	-	-	-	-	100	-
4[c] (n=354)	-	-	2.0	5.1	4.2	8.2	-	19.8	4.2
9V[c] (n=204)	64.7	1.0	0.5	67.2	-	66.7	-	69.1	67.2
14[c] (n=9)	88.9	-	-	88.9	77.8	66.7	-	88.9	77.8
18C[c] (n=8)	-	-	-	37.5	-	37.5	-	37.5	37.5
19F[c] (n=98)	5.1	-	-	6.1	6.1	5.1	-	1.0	5.1
23F[c] (n=15)	-	-	-	26.7	20.0	20.0	-	20.0	13.3
3[d] (n=351)	0.3	-	9.4	10.8	8.5	12.0	-	0.9	8.3
6A[d] (n=8)	12.5	-	-	75.0	-	-	-	-	-
7F[d] (n=116)	-	-	-	15.5	15.5	15.5	-	0.9	15.5
19A[d] (n=112)	24.1	1.8	3.6	51.8	41.1	27.7	-	25.0	30.4
22F[d] (n=234)	-	-	2.1	51.3	2.1	2.6	-	1.3	2.1
33F[d] (n=42)	4.8	-	-	90.5	-	-	-	19.0	-
8[e] (n=143)	-	-	0.7	1.4	-	2.1	-	-	-
10A[e] (n=29)	-	-	-	6.9	-	-	-	-	-
11A[e] (n=97)	-	-	-	25.8	4.1	4.1	-	14.4	3.1
12F[e] (n=235)	-	-	3.4	39.6	0.9	41.7	-	41.3	3.8
15BC[e,f] (n=113)	4.4	0.9	-	26.5	5.3	8.8	-	5.3	6.2
9N[g] (n=130)	2.3	-	-	12.3	3.1	10.8	-	4.6	7.7
15A[g] (n=82)	13.4	-	1.2	51.2	42.7	43.9	-	2.4	43.9
16F[g] (n=51)	-	-	3.9	9.8	7.8	7.8	-	2.0	7.8
17F[g] (n=17)	-	-	-	11.8	5.9	5.9	-	-	5.9
20[g] (n=123)	-	-	-	4.1	4.1	4.1	-	0.8	4.1
23A[g] (n=87)	1.1	-	-	26.4	26.4	26.4	-	2.3	26.4
23B[g] (n=65)	1.5	-	1.5	7.7	4.6	3.1	-	10.8	1.5
24F[g] (n=3)	-	-	-	100	100	100	-	-	100
31[g] (n=26)	-	-	-	3.8	-	-	-	-	-
35B[g] (n=57)	66.7	-	1.8	59.6	3.5	3.5	-	21.1	21.1
6C (n=44)	6.8	-	6.8	29.5	4.5	13.6	-	27.3	15.9
6D (n=8)	-	-	87.5	12.5	12.5	75.0	-	87.5	75.0
7A (n=1)	-	-	-	100	100	100	-	-	100
7C (n=39)	-	-	2.6	7.7	7.7	7.7	-	64.1	7.7
9A (n=1)	100	-	-	100	-	100	-	100	100
10B (n=3)	-	-	33.3	33.3	33.3	100	-	33.3	33.3
12A (n=2)	-	-	-	-	-	-	-	50.0	-
13 (n=7)	-	-	-	85.7	85.7	85.7	-	42.9	85.7
17A (n=1)	-	-	-	100	100	100	-	-	100
21 (n=22)	-	-	-	-	-	-	-	13.6	-
24A (n=4)	-	-	-	25.0	-	-	-	75.0	-
28A (n=12)	-	-	58.3	-	-	58.3	-	-	-
34 (n=23)	-	-	-	13.0	13.0	26.1	-	30.4	13.0
35A (n=2)	-	-	-	100	-	100	-	100	100
35D (n=9)	55.6	-	-	55.6	-	11.1	-	11.1	22.2
35F (n=39)	-	-	-	10.3	2.6	-	-	-	-
38 (n=16)	-	-	-	12.5	-	25.0	-	6.3	-
NT (n=4)	50.0	-	-	100	25.0	100	-	25.0	50.0

Abbreviations: CHL, chloramphenicol; CLI, clindamycin; CLR, clarithromycin; CRO, ceftriaxone using the Clinical & Laboratory Standards Institute parenteral meningitis interpretive criteria; DOX, doxycycline; LEV Levofloxacin; PEN, penicillin using the Clinical & Laboratory Standards Institute oral penicillin V interpretive criteria; SXT, trimethoprim/sulfamethoxazole

[a] The following serotypes were fully antimicrobial susceptible in 2023: 10F (n=3), 11B (n=1), 18A (n=1), 22A (n=1), 24B (n=1), 28F (n=1), 37 (n=3)

[b] "-" denotes no resistance (0%) to the antimicrobial

[c] PCV15 and PCV20/non-V116 serotype

[d] PCV15, PCV20 and V116 serotype

[e] PCV20 and V116 serotype

[f] Serotypes 15B and 15C were grouped together as 15B/C because of reported reversible switching between them *in vivo* during infection, making it difficult to precisely differentiate between the two types (11,12)

[g] V116/non-PCV15/20 serotype

Discussion

The COVID-19 pandemic and subsequent containment measures had a significant impact on the spread of respiratory pathogens such as *S. pneumoniae* (16). In 2020 and 2021, IPD incidence in Canada was the lowest seen since 2001, at 5.89 and 5.63 cases per 100,000, respectively. In 2022, 3,984 cases of IPD were reported to CNDSS, with a national incidence rate of 10.2 cases per 100,000 population. This represents a return to pre-pandemic incidence, where rates had gradually increased to a high of 10.86 cases per 100,000 population in 2018. Though 2023 incidence was not available at the time of publication, the sharp increase in the number of isolates submitted for testing in 2023 (n=4,760) in comparison to the previous highest annual count reported to CNDSS in 2018 (n=4,026) suggests that 2023 incidence was higher than 2022. This situation is not unique to Canada; reports from other countries have also indicated a return to pre-pandemic disease activity in 2023 (17–19), including some where rates have now surpassed pre-pandemic years (20,21).

Serotype 3, a PCV13 vaccine serotype, was the most common type collected in Canada in 2023, edging out serotype 4 by a very small margin. With the exception of 2021, prevalence of serotype 3 has been stable across Canada during the study period, and particularly high among adult age groups. Annual reports from Hong Kong, Spain and Denmark list serotype 3 as the most common serotype in 2023 (17,19,20), with Ireland, Belgium and New Zealand placing it in their top three most common types (18,21,22). Other vaccine serotypes were also common in Canada during 2023, particularly serotypes 4 and 9V, which have been included in conjugate vaccines since the original PCV-7 formulation. Serotype 4 has been increasing in Canada for a number of years (6,23). In 2023 it was particularly common in Western Canada, and the most common type collected from adults aged 15–49 years and 50–64 years. The most recent annual report from Belgium described a similar distribution, with serotype 4 as the third most common type overall, but the most common type in adults 16–49 years of age (18). A recent study in the United States has identified that risk of invasive disease is highest at the time of first acquisition, noting that serotype 4 has a particularly low duration of carriage which allows it to transition quickly to disease in susceptible populations (24). Thus, Beall *et al.* have postulated that serotype 4 is rapidly transmitted directly between adults, causing IPD shortly after initial acquisition (25). This supports the results of previous studies in Western North America that have associated serotype 4 infections with susceptible adult populations with risk factors such as homelessness and substance use (26,27).

Serotype 9V has not been described as readily in the literature as other vaccine types and was not mentioned in the 2023 annual reports of other countries published at the time of writing this manuscript (18,19,21,22). In our study, serotype 9V was the second most common invasive serotype in adults 15–49 years, the third most common type in adults 50–64 years and the third most common type collected from Western Canada. Prevalence of serotype 9V has consistently increased in Canada over the course of the pandemic; in contrast, minimal numbers of 9V isolates were collected by the 30 participating countries comprising the Invasive Respiratory Infections Surveillance Consortium, with an overall decrease in prevalence going into the pandemic years (16). Based on the comparable age distributions, it is possible that serotype 9V is similar to serotype 4 in that it is associated with certain risk factors that are less common in children and older adults (e.g., substance use). Epidemiological data is required to confirm this theory. Serotypes 4 and 9V are also similar in that neither is included in the novel, adult-specific V116 vaccine. While advisory boards such as the United States Advisory Committee on Immunization Practices have recommended this vaccine for use in adults for whom PCV use is indicated, the Advisory Committee on Immunization Practices has also noted that this vaccine may not be an appropriate choice in jurisdictions where serotype 4 is highly prevalent in adults (28). In Canada, this logic may be applied similarly for both serotype 4 and 9V.

Serotype 9V was one of the most highly antimicrobial-resistant serotypes in 2023, with high rates of resistance to β-lactams, macrolides, tetracyclines and trimethoprim/sulfamethoxazole. Penicillin-resistant serotype 9V was among the initially described, widely disseminated antimicrobial-resistant clones defined by the Pneumococcal Molecular Epidemiology Network in 2001 (29); inclusion of this type in the first conjugate vaccine (PCV-7) decreased the incidence of IPD caused by this resistant type (7). The return of serotype 9V has also been associated with substantial MDR; 67.2% of 9V isolates were MDR, which accounted for 33.9% of the total MDR isolates collected in 2023. The inclusion of this serotype in PCV20 (but not V116) suggests it may be a more appropriate choice for both paediatric and adult immunization in jurisdictions where serotype 9V is highly prevalent. However, V116 does cover three of the five most common MDR serotypes in Canada that are not included in PCV20 (15A, 23A, 35B) in addition to 19A, suggesting that use of these vaccines in tandem could potentially prevent a substantial number of antimicrobial-resistant infections in Canada.

As Canada reaches a point where multiple PCV formulations are equally recommended for use, it will be important to monitor how the serotype distribution adjusts, both nationally and regionally, along with antimicrobial resistance rates. With provinces and territories free to choose which vaccines to offer based on procurement and epidemiological considerations, serotype distribution may vary by jurisdiction more than ever before.

Limitations

Caution should be exercised when interpreting the data presented in this report. Provinces and territories may only submit a subset of their isolates to NML for testing. Numbers of isolates submitted to NML versus information submitted to CNDSS, may differ due to differences in submission protocols from the provinces. Data for 2020 and 2021 may not be reflective of actual trends, as the COVID-19 pandemic impacted disease incidence in all age groups.

Conclusion

Incidence of IPD in Canada in 2022 increased considerably following the COVID-19 pandemic, and the high number of IPD cases collected in 2023 represents a return to pre-pandemic disease activity. Several serotypes included in previous conjugate vaccine formulations (PCV7, PCV13) were common in 2023 (serotype 3), including some that significantly increased in prevalence (serotypes 4, 9V). Continued surveillance of pneumococcal serotypes is imperative to evaluate vaccine effectiveness, particularly as new vaccine formulations are approved and integrated into immunization schedules in Canada.

Authors' statement

ARG — Formal analysis, data curation, visualization, writing−original draft, review & editing of final version
AG — Formal analysis, validation, investigation, data curation, visualization, writing−review & editing
BL — Resources, methodology, writing−review & editing
AM — Resources, methodology, writing−review & editing
GJT — Resources, methodology, writing−review & editing
JVK — Resources, methodology, writing−review & editing
JMG — Resources, methodology, writing−review & editing
JMinion — Resources, methodology, writing−review & editing
PVC — Resources, methodology, writing−review & editing
GD — Resources, methodology, writing−review & editing
DH — Resources, methodology, writing−review & editing
YY — Resources, methodology, writing−review & editing
XD — Resources, methodology, writing−review & editing
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Competing interests

None.

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Appendix

Supplemental material is available upon request to the author: alyssa.golden@phac-aspc.gc.ca

Figure S1: Number of invasive *Streptococcus pneumoniae* isolates collected in 2023, by region and serotype
Table S1: Proportion of vaccine serotypes by age group, 2019–2023

Figure S2: Invasive *Streptococcus pneumoniae* serotypes by resistance to different antimicrobial classes, 2023
Table S2: Multidrug resistance profiles of invasive *Streptococcus pneumoniae* serotypes, 2023

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EPIDEMIOLOGIC STUDY

Changing case definition: An analysis of its impact on Lyme disease surveillance in Nova Scotia

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Abstract

Background: Nova Scotia has experienced a growing number of Lyme disease (LD) cases since 2002. From 2009 to 2022, Nova Scotia adopted a LD case definition that aligned with the Public Health Agency of Canada's definition. On January 1, 2023, Nova Scotia transitioned to a LD definition that relies on laboratory evidence alone.

Objectives: To describe and compare historic trends in confirmed LD case counts and incidence under the former and current LD case definitions between 2018 and 2023 and assess the impact of the case definition change on LD surveillance.

Methods: Confirmed LD cases were extracted from Nova Scotia's Electronic Public Health Information System, software Panorama, according to the former case definition for the years 2018–2022 and the current case definition for the years 2019–2023. As the 2018 laboratory data in Panorama was incomplete, raw data for 2018 were obtained from Nova Scotia's Provincial Public Health Laboratory Network. Confirmed case counts and incidence rates per 100,000 population were calculated by year, sex, age group and geographic zone, under both case definitions. Seasonality was determined by the reporting date of the case.

Results: From 2018–2022, the current case definition identified 4,238 cases, a substantial increase of 2,493 cases over the 1,745 reported by the former case definition, with an additional 2,058 cases in 2023 under the current case definition. This led to a clear upward trend in confirmed incidence rates with the current case definition, unlike the variable pattern seen with the former case definition. Males and individuals aged 5–14, 40–59, and ≥60 years experienced consistently higher sex and age-specific rates under both case definitions. The Western Zone consistently reported the highest incidence rates. Seasonally, both case definitions showed reporting peaks from June to September, with the peak occurring two-week later peak with the current case definition.

Conclusion: When the current LD case definition was applied to historic surveillance data, past rates of confirmed LD increased suggesting under-reporting of clinical presentation of LD to public health in high incidence jurisdictions.

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Introduction

Lyme disease (LD), the most reported tick-borne disease in North America, is transmitted to humans through the bite of a tick infected with *Borrelia burgdorferi* (1–4). In Nova Scotia, the blacklegged tick, *Ixodes scapularis*, carries this bacterium (5). The disease typically manifests with erythema migrans (EM), in approximately 80% of patients who are infected, often accompanied by other early disease symptoms such as fatigue or fever (6–8). If left untreated, dissemination of the disease may result in multiple EM lesions, along with cardiovascular (temporary atrioventricular blocks), musculoskeletal (joint swelling or arthritis) and neurologic manifestations (facial palsy, neuropathy or encephalopathy) (3,7,8).

Nova Scotia has experienced a growing number of LD cases since 2002, the Department of Health and Wellness declared the entire province of Nova Scotia an "at risk area" in 2017, defined as a location with evidence of reproducing populations of known tick vectors and the likely transmission of *B. burgdorferi* (9). In 2022, the reported incidence (confirmed and probable) of LD in Nova Scotia was almost five times greater than the national incidence (4). Furthermore, incidence of LD is projected to increase because climate change is likely to expand the abundance and distribution of tick populations (10).

Lyme disease became a nationally notifiable disease in 2009 (4). From 2009 through 2022, Nova Scotia adopted a LD case definition (CD) that aligned with the Public Health Agency of Canada's CD (11). This CD required both clinical information and laboratory evidence for a confirmatory case, and EM was captured within the probable CD (11). In 2023, Nova Scotia transitioned to a new CD, relying on laboratory evidence alone for confirmed cases (12). This approach aligns with the 2022 revised high-incidence LD CD by the Centers for Disease Control and Prevention in the United States (13). This change means that confirmed cases rely solely on laboratory evidence. Laboratory testing is not recommended in early stage LD (i.e., localized EM) due to its poor sensitivity (8,14). As such, public health will not be notified of EM with the current CD and these cases will not be included in Nova Scotia's confirmed or probable LD case counts.

Coupled with the increase in LD cases, evidence suggests that the burden of submitting clinical information for both probable and confirmed cases can result in under-reporting of LD (15). Additionally, during the COVID-19 pandemic, competing public health priorities resulted in reduced capacity for LD investigation by public health within the province (2,13,16).

The objective of this surveillance report is to describe and compare historic trends in confirmed LD counts and incidence over the period from 2018 to 2023, and to assess the impact of the CD change on LD trends.

Methods

Setting and population

This report includes all confirmed LD cases reported to public health in Nova Scotia from January 1, 2018, to December 31, 2023. Lyme disease is a notifiable disease in Nova Scotia, and any cases that met either confirmatory or probable CDs are to be reported and captured in the province's Public Health Information System, Panorama. The year 2018 was selected to align with the year that Panorama was implemented.

Case definitions and detection

Between January 1, 2018 and December 31, 2022, a confirmatory case of LD required both clinical evidence and laboratory confirmation (11). Probable cases required EM rash (determined by clinical presentation without laboratory tests) or clinical evidence of illness with laboratory evidence of infection, without history of residence in or visit to a LD risk area (national case definition) (11). As of January 1, 2023, a confirmed case of LD must have confirmatory laboratory evidence; however, clinical evidence is no longer required (17). Individuals presenting with localized EM will not receive laboratory testing given the high likelihood of a false negative serology test in early stage LD (8,14).

Probable cases are those with only presumptive laboratory evidence (i.e., positive IgG immunoblot); EM (i.e., clinical criteria) is no longer captured in the probable CD (Nova Scotia case definition). Full CDs are in the **Appendix**, as Supplemental material (Table S1).

On April 1, 2021, the modified two-tier test (MTTT) for serologic testing of LD was introduced in Nova Scotia, replacing the standard two-tier test (STTT). The MTTT has approximately 25% greater sensitivity in the detection of early LD (11,12,14,18). Both STTT and MTTT are included as confirmatory laboratory evidence of infection in the CD.

Data sources

Reported LD cases were obtained from Panorama. All reported cases meeting the Nova Scotia LD CD between 2018 and 2022 were obtained using investigations in Panorama. Investigations are conducted by public health nurses and include clinical evidence from physicians as well as additional demographic, risk factor and geographic data. To retrospectively apply the current CD, we assessed the stand-alone laboratory results (i.e., those with no associated case investigation ID attached). These were extracted directly from Panorama (2019–2023) and from raw data from Nova Scotia's Provincial Public Health Laboratory Network for 2018. The current CD was applied to the data to determine the number of cases meeting the new CD. Population characteristics were extracted from Statistics Canada's annual (July 1) population estimates for each year (2018–2023). The Statistics Canada annual population estimate corresponded with the year the case occurred.

Analysis

Confirmed case counts and incidence rates per 100,000 population were calculated by year, sex and age group under the former and current Nova Scotia CD using confirmed cases as the numerator and the census population estimates from Statistics Canada data for 2018–2023 as the denominator (19). The current confirmed LD CD was applied to analyze geographic trends using the client's active address at the time of specimen collection. Four geographic areas were used to correspond to Nova Scotia administrative health zones (Northern, Eastern, Central, Western). For 2018, the raw data included age at the time of data extraction and date of specimen collection but did not include age at diagnosis, date of birth or geography. Age at diagnosis was determined by manually extracting and reviewing the records in Panorama or the Provincial Public Health Laboratory Network. If age at diagnosis was still unavailable, it was estimated by applying the average age difference between age at data extraction and specimen collection date. Age groups were selected to align with Nova Scotia provincial Notifiable Disease reporting and were collapsed in accordance with incidence trends provincially and nationally. Seasonality was determined by the case reporting date, which, under the former CD, could be the first clinical diagnosis, symptom onset, or laboratory collection date; under the current CD, it is the laboratory collection date.

We performed a sensitivity analysis to account for the increased number of cases expected with the new MTTT methodology compared to the STTT. This analysis assumed the MTTT was not introduced and involved applying a 25% decreased sensitivity to incident cases after 2020.

Results

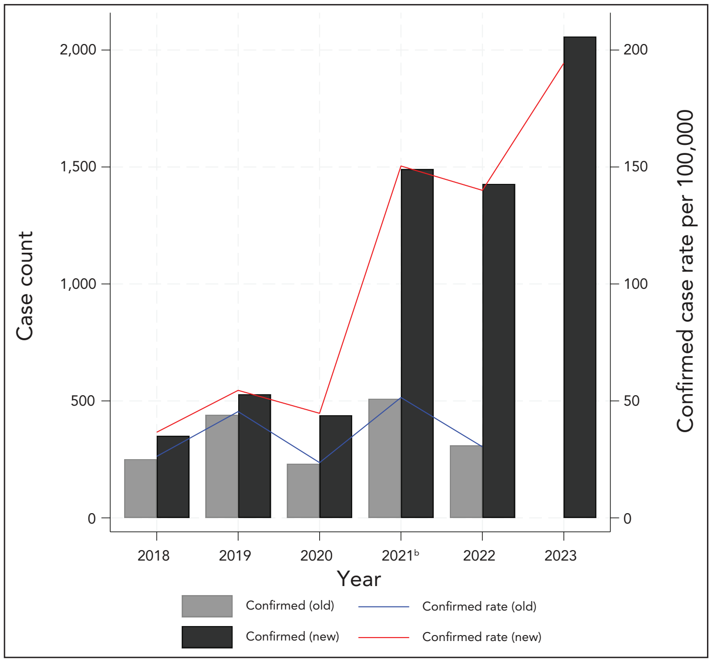
Lyme disease trends over time under the former and current Nova Scotia confirmed case definition

Figure 1 shows the confirmed case counts and incidence rate of LD over time using the former and current CD. Nova Scotia reported 1,745 confirmed cases of LD between 2018 and 2022 using the former CD. After retrospectively applying the current CD, a total of 4,238 cases would have met CD between 2018 and 2022 (+2,493). An additional 2,058 confirmed cases were reported in 2023 under the current CD. Confirmed case counts were higher each year when the current CD was retrospectively applied. Moreover, the confirmed incidence rates over time exhibited a clear upward trend with the current CD whereas the confirmed case rates showed year to year variability and no clear directional trend with the former CD. In 2018, the percent difference in confirmed LD cases between CD was 33%, dropping to 18% in 2019, but rising sharply from 62% in 2020 to 129% in 2022.

Demographic characteristics of confirmed cases

Complete demographic information was available for all reported cases of LD obtained from the investigations (former CD) and 54% of age-data from 2018 laboratory records had to be estimated (current CD). **Figure 2** presents sex-specific rates. Males experienced higher sex-specific incidence rates of

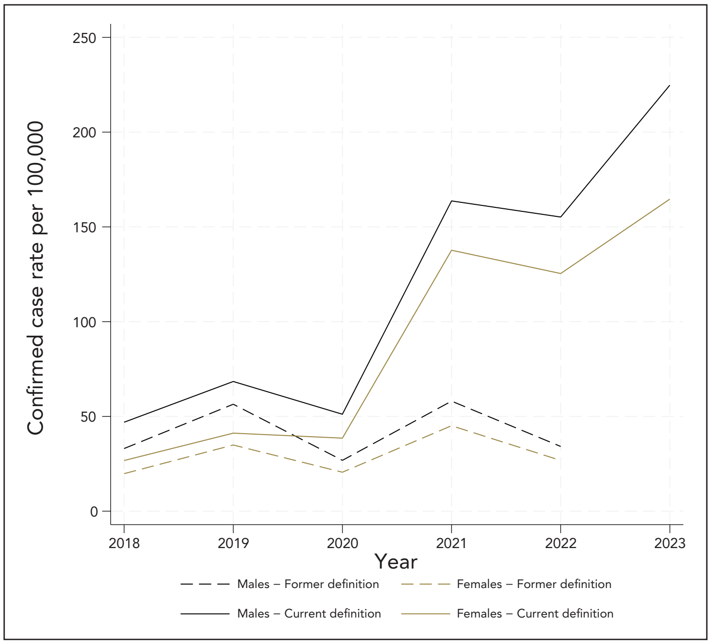
Figure 1: Reported confirmed Lyme disease counts and incidence rate[a], with the former and current definitions, 2018–2023[b]



[a] Denominators for yearly rates per 100,000 population were obtained from Statistics Canada, population estimates on July 1

[b] April 1, 2021 modified two-tier test introduced, replacing the standard two-tier test

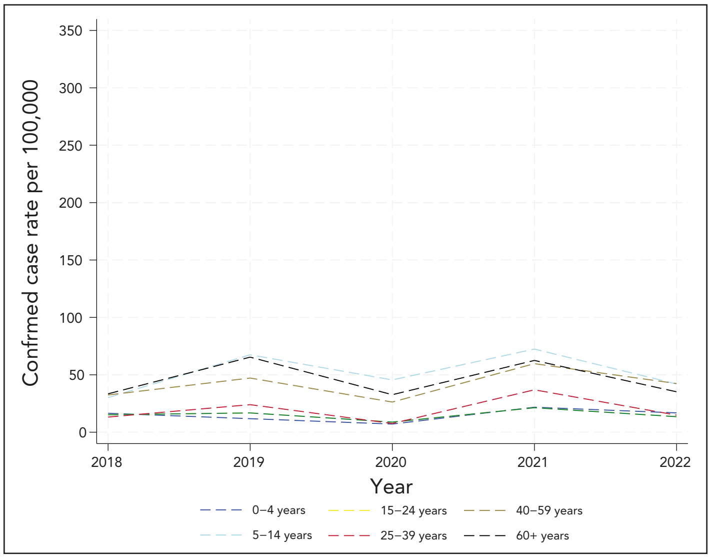
Figure 2: Confirmed incidence rate[a] of reported Lyme disease cases by sex, with the former and current case definition, 2018–2023



[a] Denominators for yearly rates per 100,000 population were obtained from Statistics Canada, population estimates on July 1

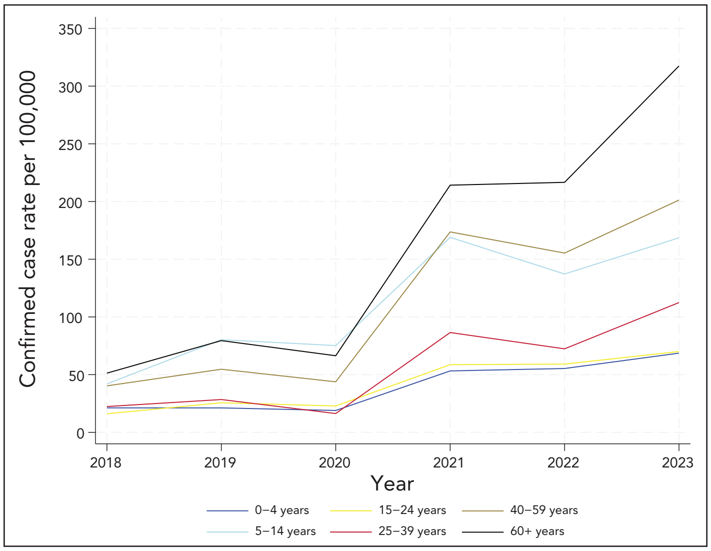
confirmed LD compared with females. The sex-specific trends were similar to the overall population trends. **Figure 3** and **Figure 4** show age-specific incidence rates over time in the former and current CD, respectively. Cases ranged in age from birth to 97 years. Individuals aged 5–14 years, 40–59 years and 60 years and older consistently experienced higher age-specific rates of confirmed LD across all years under both CD.

Figure 3: Confirmed incidence rate[a] of reported Lyme disease cases by age group, with the former definition, 2018–2022



[a] Denominators for yearly rates per 100,000 population were obtained from Statistics Canada, population estimates on July 1

Figure 4: Confirmed incidence rate[a] of reported Lyme disease cases by age group, with the current definition, 2018–2023

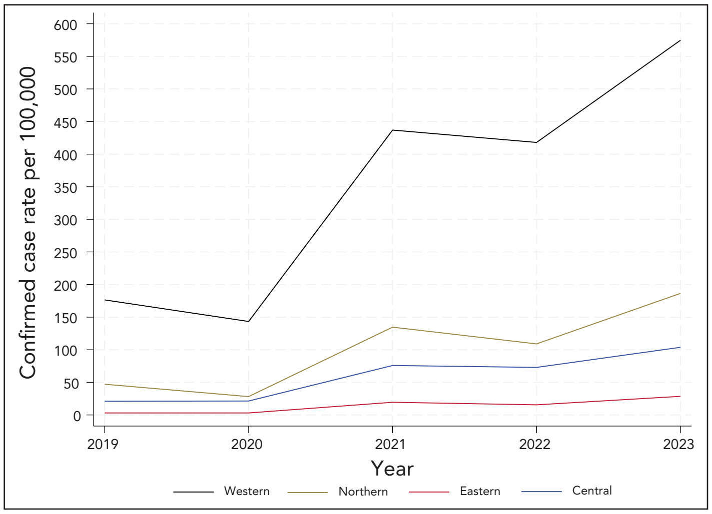


[a] Denominators for yearly rates per 100,000 population were obtained from Statistics Canada, population estimates on July 1 of each year (2018–2023)

Geographic distribution of confirmed cases

Information on location was available for 5,886 (98.8%) cases under the current CD, from 2019 onwards and was unavailable from 2018 laboratory data. **Figure 5** displays the incidence rate of LD by zone using the current CD. The incidence rate was consistently highest in Western Zone. Under the former CD, most Nova Scotia confirmed cases were in the Western Zone in 2018 to 2020. In 2021 and 2022, Western Zone made up 15% or less of all cases in Nova Scotia. When applying the current CD, the majority of cases were in Western Zone in all years (Figure S1).

Figure 5: Confirmed incidence rate[a] of reported Lyme disease cases by zone, with the current case definition, 2019–2023



[a] Denominators for yearly rates per 100,000 population were obtained from Statistics Canada, population estimates on July 1

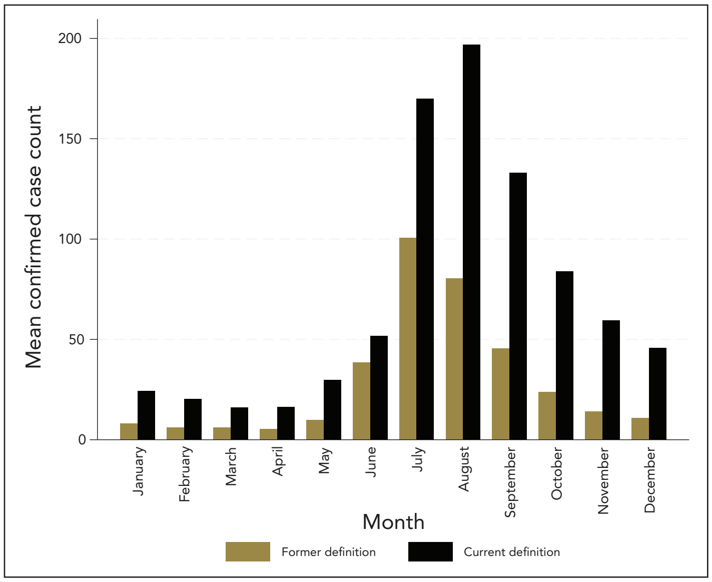
Seasonal distribution

Figure 6 shows the seasonality of confirmed cases of LD. Reporting dates peaked from June to September with both LD CDs. July was the peak month under the former LD CD, while August was the peak month under the current LD CD. On average, the peak reporting date with the current LD CD occurred two weeks later than with the former CD.

Impact of serologic testing on Lyme disease trends

An increase in serologic testing volume for LD over time was observed using crude laboratory LD test volume counts from the Provincial Public Health Laboratory Network. The trend in testing volume mirrored the trend in reported case counts with the current LD CD (Figure S2).

Figure 6: Mean number of confirmed Lyme disease cases by month, based on reporting date[a], with the former and current case definitions, 2018–2022



[a] The date of the first clinical diagnosis, symptom onset, or the laboratory collection date for the former Lyme disea definition OR the laboratory collection date for the current Lyme disease definition

After applying a sensitivity analysis to account for the introduction of MTTT in 2021, a similar trend of increased confirmed cases over time remained with lower year specific rates (Figure S3 and Figure S4).

Discussion

Comparison of trends with the former and current Lyme disease case definitions

To optimize public health resources and strengthen surveillance, surveillance systems should be periodically evaluated, focusing on attributes such as data quality, acceptability and positive predicative value (20).

Applying the current Nova Scotia LD CD retrospectively to reported LD cases from 2018–2022 increased the number of reported confirmed cases from 1,745 to 4,238. The key distinction in the current CD is the removal of the requirement for clinical evidence to confirm a case. Clinical evidence may have been a barrier to submitting LD case data, resulting in under-reporting. This could be particularly true when the number of cases is high, as we would expect in a high-incidence jurisdiction.

There has been discourse around the potential underreporting of LD cases in human surveillance, highlighted in literature from Canada and the United States (15,21). While more research is needed to understand possible reasons for under-reporting, clinicians may not be reporting clinical symptoms because of the additional time burden, or they fail to see value in reporting since clinical evidence does not provide information that could be used to prevent cases of LD (6,13). This may be the result of low acceptability of the former CD.

It is also possible that a true absence of symptoms that meet CD, rather than under-reporting of symptoms, explains some of the difference between the number of cases in the former and current CD. If symptoms were not present, there is a greater likelihood of including false positives with the current CD. Nonetheless, while clinical information improves LD pre-test probability and influences the positive predictive value, in a high incidence jurisdiction, the proportion of people who test positive who are truly positive is higher than a low incidence jurisdiction. This is supported by two LD studies showing LD seropositivity rates in Nova Scotia increasing from 1% to 1.6% from 2012 to 2023 (22,23).

The former and current LD CDs showed similar trends for both sex-specific and age-specific rates of LD. Males experienced higher rates of confirmed LD and those aged 5–14 years, 40–59 years and 60 years and older experienced the highest age-specific rates of LD. These demographic trends mirror historical patterns of LD distribution in Nova Scotia. The Western Zone experienced the highest zone-specific rates of confirmed LD, followed by the Northern Zone. This also follows environmental and historical trends in LD risk areas, where South-Western Nova Scotia was the earliest LD endemic area (5). Before the change LD CD, varying workload demands and clinician reported behaviour may have resulted in inconsistent reporting methods between zones. As a result, geographic trends based on the former CD may not accurately reflect the burden of disease within the zones and were therefore omitted from the main geographic analysis.

When considering both LD CD, cases peaked from late spring until the end of summer, with the highest number of cases falling within the months of June, July, and August. The former CD required clinical information to be collected, resulting in reporting dates encompassing date of symptom onset or clinical diagnosis. The time lag in reporting date, when applying the current CD likely reflects the expected lag time between symptom onset and presenting for assessment and testing contributing to the later reporting dates (13).

Additional factors influencing Lyme disease case trends

Other factors that may have contributed to the LD trends observed include 1) the COVID-19 pandemic, 2) climate change and 3) increased awareness and testing.

The COVID-19 pandemic led to the disruption in public health follow-up on positive laboratory tests, which resulted in an overall decrease in reported LD cases in 2020. Further, a sustained greater reduction in reported cases in 2021 and 2022, relative to laboratory-confirmed cases under the current CD, may reflect reduced public health capacity during those years. Following the pandemic, public health follow-up for LD never fully returned to its pre-pandemic level. Behaviour changes, such as time spent outdoors, may have been influenced by the pandemic, possibly impacting LD cases. Further, the inability to access primary care or delay in primary care delivery may have decreased the number of LD cases diagnosed and reported (24,25). The exact magnitude and direction of these effects are unclear.

The consequences of climate change, including increasing temperatures, may contribute to the expansion of habitat and host populations for infected ticks and to increased outdoor human activity—increasing tick abundance and potential for LD transmission (4,10,26). In Nova Scotia, compared to the 30 year climate stable period from 1961 to 1990, the subsequent 30 years from 1990 to 2020 have seen a statistically significant increase in the overall mean temperature across all months of the year (27). Additionally, there has been a decline in the number of frost days in both spring and autumn, with frost ending earlier in the spring and starting later in the autumn, resulting in an increase in number of days that ticks could be active (27).

As the number of LD cases has increased, so has both clinical and public awareness, potentially contributing to increased health-seeking behaviours and clinician suspicion for LD (4). An increase in serologic testing volume for LD over time was observed using crude laboratory LD test volume counts from the Provincial Public Health Laboratory Network. An increase in test volume provides the opportunity for more frequent detection and reporting of LD.

Introduced April 1, 2021, the MTTT has shown to be approximately 25% more sensitive for detection of early LD with equivalent specificity to the STTT (14,18); however, sensitivity to early stages of LD is estimated to still be relatively low, at approximately 70% (18). It is likely that the increase in cases observed after April 1, 2021, could be partly attributed to increased sensitivity in detecting earlier cases of LD, thus capturing cases in people with early infection. Although healthcare workers are encouraged to treat cases of EM without testing for LD, not all patients with early infection present with an EM rash, leading to testing for atypical presentations.

Like the STTT, the MTTT is unable to distinguish between active and past LD infections as the antibody response to the bacteria may persist for years after initial infection; therefore, a positive laboratory result may reflect previous rather than current infection. The impact of this may increase over time as the prevalence of LD increases (14).

Limitations

Crude laboratory data from 2018 were used, applying the current LD CD retrospectively. Thus, a positive enzyme immunoassay and subsequent positive IgG or IgM, were considered as confirmatory, regardless of negative IgM or IgG results, in line with the current Nova Scotia LD CD. Age data for 54% of individuals in 2018 were approximated; however, given the broad age categories, this likely had minimal impact on observed trends. Furthermore, published 2022 population estimates were applied to 2018–2022 and the 2023 geographic zone analysis; at the time of analysis, Statistics Canada 2023 zone population estimates were not available. Since population changes from 2022 to 2023 were minimal, the impact on the calculated rates in this analysis are likely minor.

Conclusion

After retrospectively applying Nova Scotia's current CD to historic surveillance data, there was a clear increase in the number of cases of LD identified and an upward trend in LD. While the overall upward trend observed with the current LD CD aligns with historical patterns of LD expansion in Nova Scotia (2009–2018), the change in CD inherently limits direct numerical comparisons with data collected under the former definition or with other jurisdictions using different criteria.

Relying on a laboratory-based CD strengthens the surveillance system's ability to meet system goals and monitor the burden of LD and trends in LD in the province. Moreover, using only laboratory evidence to monitor LD reduces the burden of investigations on front-line public health staff, freeing resources that can be redirected towards LD awareness campaigns to prevent tick bites and promote appropriate LD management.

Nova Scotia has worked with provincial and federal partners on knowledge translation efforts. Effective communication strategies, including data notes in surveillance reports and engagement with healthcare providers, are crucial to explain the reasons behind the observed increase in reported cases and prevent misinterpretation of LD trends.

Under-reporting is a substantive limitation in high incidence jurisdictions, like Nova Scotia, and the laboratory-based approach improves the accuracy, timeliness, flexibility and acceptability of LD surveillance.

Authors' statement

KN — Conceptualization, methodology, formal analysis, writing–original draft, writing–review & editing, visualization
JC — Conceptualization, methodology, writing–review & editing, visualization, management
CR — Conceptualization, methodology, writing–review & editing, visualization, management

KM — Conceptualization, methodology, writing–review & editing, visualization, management
AK — Methodology, validation, writing–review & editing
TFH — Methodology, writing–review & editing
SLD — Conceptualization, writing–review & editing
LP — Writing–review & editing
MT — Methodology, writing–review & editing

Competing interests

None.

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Appendix

Supplemental material is available upon request to the author: surveillancedhw@novascotia.ca

Table S1: Lyme disease case definitions
Figure S1: Confirmed incidence rate of reported Lyme disease cases by zone, with the former case definition, 2018–2022
Figure S2: Nova Scotia Lyme disease serology testing volume and rate, 2018–2023
Figure S3: Sensitivity analysis of reported confirmed Lyme disease counts and incidence rate, with the former definition, 2018–2022
Figure S4: Sensitivity analysis of reported confirmed Lyme disease counts and incidence rate, with the current definition, from 2018–2023

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CANADA COMMUNICABLE DISEASE REPORT

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