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THREAT ASSESSMENT IN PUBLIC HEALTH

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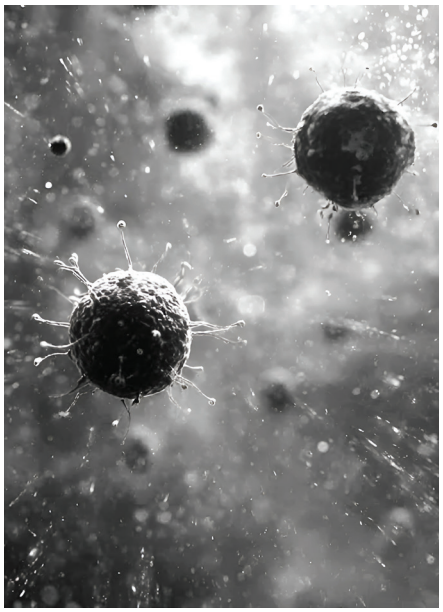

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Using a consensus-based approach to build a threat assessment tool for use in a Canadian federal public health setting

Gabrielle Brankston[1]*, Camille Dulong[1], Catherine Elliott[1], Jacqueline Middleton[1], Amrit Sandhu[1], Lindsay Whitmore[1]

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Abstract

Background: Public health intelligence activities, including assessment of emerging public health threats, are core operations for many public health agencies. Threat assessment is intended to guide public health actions proportional to the assessed threat level within the context of an evolving situation. A risk-based threat assessment framework helps clarify the overall population-level health impacts of threats, guiding appropriate public health action.

Objective: This work aimed to develop a standardized, risk-based tool for assessing public health threats that could be used across the Public Health Agency of Canada (PHAC), integrating diverse perspectives from various PHAC stakeholders to ensure the tool is applicable across the full entire spectrum of potential public health threats.

Methods: A threat assessment framework was developed to assign an overall threat level based on the assessment of three distinct threat attributes: the severity of harm to human health, the degree to which a threat is likely to impact Canada, and Canada's capacity to prevent or mitigate the threat. A Delphi-based approach was used to develop a set of qualitative criteria enabling end-users to assign a rating of high, moderate, or low for each threat attribute and the overall assessment.

Results: Three iterative surveys and two meetings led to consensus on definitions for the three threat attributes and the overall assessment, enabling a flexible framework capable of characterizing a wide range of public health threats.

Conclusion: Standardized, broadly accepted definitions for threat assessment reliably characterize and communicate public health events of importance and provide support for public health action.

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Keywords: public health intelligence, threat assessment method, Delphi, consensus

Introduction

In a global environment marked by an increasing number of high-impact public health events (1), public health systems capable of rapidly detecting and assessing the significance of potential threats are essential to support decision-making by public health officials. A public health threat can be defined as verified data indicating a potential acute risk to human health that has been assessed as having the potential to harm to the health of a population (2,3). Early detection and assessment of potential public health threats is intended to guide response planning and actions proportional to the assessed level of threat within the context of an evolving situation (4). Public health actions resulting from early assessment can limit the impact of a threat on human health.

Public health intelligence activities, including the early assessment of potential public health threats, are core operations of many national and international public health agencies (5–7). Threat assessment involves characterizing a public health threat to understand its overall severity and population health impact. There is limited information in the published and grey literature about the threat assessment methodology used by public health agencies. However, public-facing reports provide an indication of the elements considered in such assessments. These include potential public health impact, severity of health effects, likelihood of exposure or transmission, and existence of control measures (1,5–7).

At the Public Health Agency of Canada (PHAC), a formalized Coordinated Threat Assessment (CTA) process was established in May 2022 in response to recommendations from the Auditor General of Canada to strengthen PHAC's risk assessment process following an audit related to the COVID-19 pandemic (4). The CTA process sits within a spectrum of risk assessment activities, ranging from preliminary threat assessments to full, in-depth risk assessments (8). Within this spectrum, CTA coordinates technical subject-matter experts and integrates data and information from multiple sources to rapidly and systematically assess emerging public health events. This process encourages coordination of activities across PHAC and results in assessments that are standardized across programs, providing PHAC senior leadership with an overview of events that may constitute a threat to Canada and potentially require further public health action.

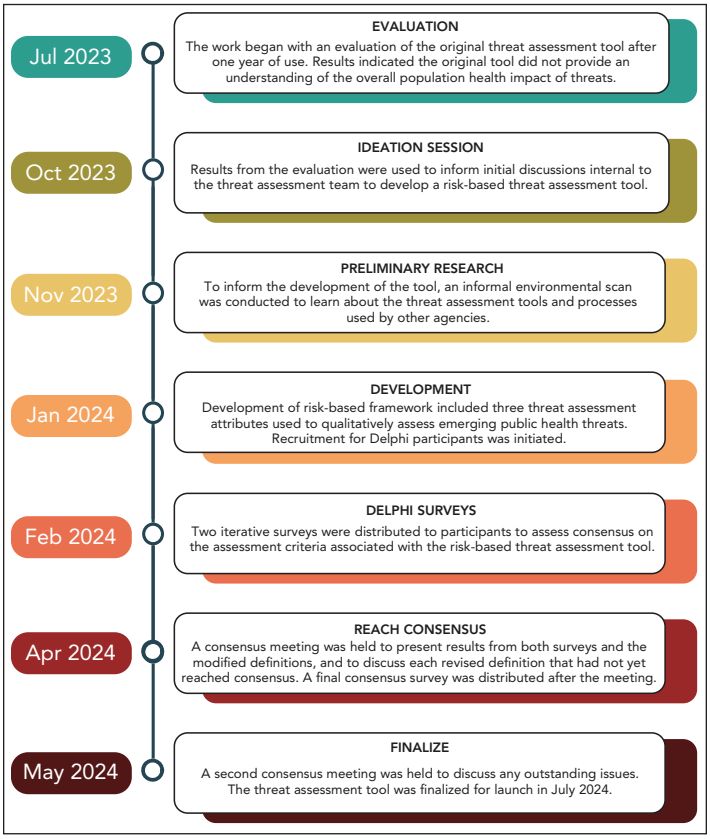
The original PHAC threat assessment method was designed as a user-friendly algorithm to characterize threats based on the type and urgency of federal public health actions required, such as monitoring, further investigation, or action within 48 hours. After a full year of use, along with feedback from an internal evaluation, the need was identified for a method that better captures the overall population health impact of threats to more effectively guide public health action. This led to the decision in 2023 to revise the threat assessment method to a risk-based approach.

The goal of this work was to develop a standardized tool that could be used across PHAC programs to characterize public health threats using a risk-based framework with high, moderate, and low threat levels for Canada. To address the challenge of designing a common tool that supports threat assessment across diverse populations and hazard types, a Delphi-based approach was used to gather perspectives from a range of PHAC stakeholders, ensuring applicability across the full spectrum of potential public health threats. This article describes the Delphi consensus process and presents the resulting threat assessment tool.

Methods

Multiple steps were taken to develop and finalize the threat assessment tool. **Figure 1** depicts the activities and timeline associated with the process. Preliminary work included internal discussions within the threat assessment team, an informal environmental scan, and engagement with internal and international colleagues.

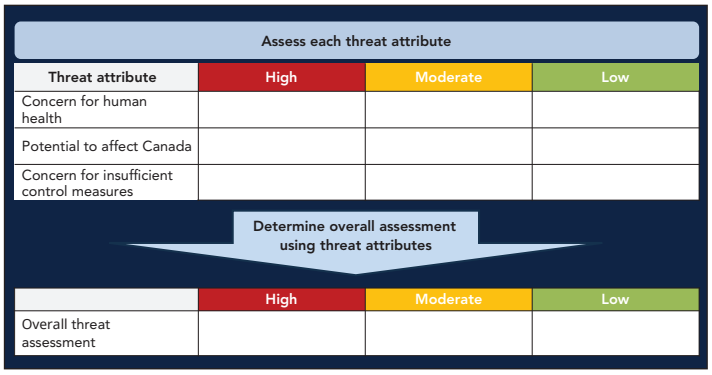
Figure 1: Timeline of engagement activities undertaken during the development of the threat assessment framework and methodology



These activities resulted in a threat assessment framework consisting of three threat attributes, each associated with three levels of assessment, and an overall assessment (**Figure 2**). The threat attributes were designed to assess the severity of harm to human health, the degree to which a threat is likely to impact Canada, and Canada's capacity to prevent or mitigate the threat.

Once the framework was developed, a Delphi-based approach was used to define each threat attribute, the overall threat assessment, and the criteria for categorizing threats as high, moderate, and low. The Delphi technique is a scientific approach that engages experts in iterative surveys and group feedback to work towards consensus on challenging topics (9). Draft threat assessment definitions were developed by the research team to populate the framework. Consensus was defined, *a priori*, as 80% of participants in agreement with each definition, as worded.

Figure 2: Public Health Agency of Canada's threat assessment framework



Participant inclusion and recruitment

Invitations to participate in the expert panel were extended to all members of PHAC's Scientific Committee for Coordinated Threat Assessment (SCCTA). The SCCTA is a group of subject matter experts with representatives from relevant disciplines within PHAC that meet weekly to assess public health threats. Participants were actively recruited to ensure representation from all stakeholder groups, reflecting the end-users of the framework for threat assessment from a national perspective.

Surveys

Agreement with definitions was assessed through three rounds of surveys conducted online using Microsoft Forms. Survey data were collected anonymously, and no directly identifying information was collected from participants. For the first two surveys, agreement with each definition was assessed using a five-point Likert scale with the following options: Yes, as currently worded; Yes, but change wording; Unsure; Probably not; and Definitely not. Respondents were also asked to provide detailed feedback or suggest alternative wording, which was used to inform modifications to the definitions.

Participants were given eight business days to complete each survey round. Two reminders were sent to participants for each survey. After each survey round, all participant feedback was considered in revising the definitions. Participants were then provided a summary of the results, reasons for changes to the definitions, and the next iteration of the definitions. Subsequent surveys and the consensus meeting included only items that had not reached 80% agreement. Following the initial consensus meeting, a third survey was conducted to formally assess agreement using a binary response format (i.e., yes/no).

Consensus meetings

Two consensus meetings were held by videoconference three weeks apart and were facilitated by a member of the research team. Results from both surveys and the modified definitions were presented at the first consensus meeting. Participants discussed each revised definition that had not reached consensus after the second survey. Areas of disagreement were explored, and definitions were further modified as needed. Consensus on each item discussed during the meeting was assessed using a post-meeting survey, with consensus defined as 80% agreement. A second consensus meeting was conducted to address outstanding areas of disagreement and to discuss the process by which the tool would be operationalized.

Data analysis

For each iteration of the survey, quantitative data were analyzed using simple descriptive statistics (i.e., the proportion of participants selecting each level of agreement) using R Studio (10). A qualitative thematic analysis (11) was used to summarize free text data into broad categories, informing feedback to participants and revisions to the definitions.

Results

Participants

A total of 26 participants were included in the consensus process. Of the 10 PHAC program areas that regularly contribute to threat assessment, representatives from eight agreed to participate, along with additional members of the SCCTA, resulting in representation from 12 programs in total. Representatives included subject matter experts in zoonotic disease (n=1), outbreak management and food safety (n=2), respiratory virus epidemiology and surveillance (including COVID-19) (n=4), risk assessment (n=8), travel health (n=3), vaccine surveillance and readiness (n=2), emergency management (n=1), biosecurity (n=1), public health measures (n=2), risk sciences and modelling (n=1), and International Health Regulations (n=1).

Surveys

Of the 26 participants, there were 23 responses to survey 1 (88.5%), 19 responses to survey 2 (73.1%), and 10 responses to survey 3 (38.5%). Over the course of the study, there was a progressive, positive shift toward consensus with iterative modifications of the definitions (**Table 1**).

No definitions achieved consensus in the first survey, two achieved consensus in the second, and all definitions assessed after the consensus meetings reached 90% to 100% agreement, exceeding the 80% target. The definitions for high, moderate, and low overall threat assessment were not assessed in the final survey however, verbal agreement amongst attendees was achieved during the second consensus meeting. Thematic analysis of the written feedback resulted in categorization by the following broad themes: wording changes, framework language, and clarifications.

Consensus meetings

The first and second consensus meetings were attended by 15 (57.7%) and 17 (65.4%) participants, respectively, representing 11 of the 12 participating programs. Participants discussed

Table 1: Proportion of respondents in agreement with each definition for each of three Delphi surveys

Threat assessment item	Proportion of respondents in agreement with each definition as worded		
Definition	**Survey 1 (n=23)**	**Survey 2 (n=19)**	**Survey 3 (n=10)**
Concern for human health	**43.5%**	**78.9%**	**100%**
High	52.2%	78.9%	100%
Moderate	60.9%	78.9%	100%
Low	60.9%	78.9%	100%
Potential to affect Canada	**34.8%**	**68.4%**	**90.0%**
High	39.1%	78.9%	90.0%
Moderate	34.8%	73.7%	90.0%
Low	39.1%	78.9%	90.0%
Concern for insufficient control measures	**52.2%**	**84.2%**	**N/A[a]**
High	69.6%	78.9%	90.0%
Moderate	47.8%	68.4%	90.0%
Low	73.9%	73.7%	90.0%
Overall threat assessment	**69.6%**	**84.2%**	**N/A[a]**
High	69.6%	78.9%	Not assessed
Moderate	69.6%	78.9%	Not assessed
Low	69.6%	78.9%	Not assessed

Abbreviation: n/a, not applicable
[a] Reached 80% consensus on survey 2

and refined the definitions, raised methodological questions and program-specific issues about how to apply the resulting definitions, and commented on practical considerations for applying the tool (e.g., assessing international threats not yet present in Canada). These discussions prompted group exploration of related operational challenges. Participants informally reported a deeper understanding and greater level of comfort with the tool after engaging in these conversations. The final threat assessment definitions are presented in **Table 2**.

Discussion

The new threat assessment framework was designed to assess the severity of harm to human health, the degree to which a threat is likely to impact Canada, and Canada's capacity to prevent or mitigate the threat. This article describes the Delphi consensus process used to determine a set of qualitative criteria with which users will assign a rating of high, moderate, or low for each of the three distinct threat attributes. Engaging a range of subject-matter experts led to consensus on 16 definitions in three distinct categories and one overall assessment category, resulting in a flexible framework capable of characterizing a wide range of public health threats.

The framework is aligned with other national and international health agencies in terms of the important elements to consider in public health threat assessment (5–7) and qualitative flexibility (5). Moving from the previous algorithm-based approach to a qualitative framework allows for flexibility in weighting individual threat attributes according to their relative importance in the context of a specific threat. Unlike the former algorithm-based approach, which based assessments on federal actions, the new risk-based characterization provides a clearer representation of the key information used to assess a threat and can better inform appropriate public health actions. A separate publication provides an in-depth description of the threat assessment process at PHAC and includes an example of threat assessment in practice (12).

Several strengths were associated with using a Delphi-based approach to develop definitions for a threat assessment tool. Achieving consensus among experts from multiple subject-matter areas provides confidence that the process produced a robust tool capable of appropriately characterizing public health threats and that is applicable to multiple areas of public health. Including consensus meetings allowed participants to provide verbal feedback, which resulted in greater clarification of their views than was possible with surveys alone. This collaborative process fostered understanding and acceptance of the definitions across programs. Finally, programs expressed appreciation for the opportunity to participate in this process and contribute to the development of the tool.

Limitations

The process of developing the new threat assessment tool had several limitations. The initial steps to develop the framework were conducted within the research team and, while based on feedback from programs and an international scan, may have been designed differently if a process of systematic feedback had been used. Participation declined by 57% over the course of the Delphi study, and the anonymous nature of the surveys made it impossible to assess representativeness across PHAC programs. However, participation in the consensus meetings was largely representative of the complete list of participating programs, including programs that contribute regularly to the threat report. Finally, in terms of the Delphi methodology, the statistical stability of responses was not measurable because only two rounds of surveys were conducted (13).

Conclusion

Standardized, broadly accepted definitions for threat assessment in a federal public health setting are key to reliably characterizing and communicating public health events of importance and providing support for public health action. Ongoing work in this area will lead to more reliable and valid assessments of a variety of threats in multiple public health settings. Future plans include validating and evaluating the threat assessment tool, as well as continuing to apply it to threats beyond infectious diseases.

Table 2: Final definitions for the threat assessment tool

Item	Definition
Concern for human health	**The potential severity of harm to health that the hazard poses in the population most likely to be affected, based on current knowledge.**
High	This hazard poses or is anticipated to pose severe harm to the health of the population most likely to be affected (e.g., a hazard that is typically life-threatening and/or involves permanent or long-term harmful health consequences).
Moderate	This hazard poses or is anticipated to pose moderate harm to the health of the population most likely to be affected (e.g., a hazard that is typically associated with serious but not life-threatening health effects or typically involves non-permanent or short-term harmful health consequences).
Low	This hazard poses or is anticipated to pose minor harm to the health of the population most likely to be affected (e.g., a hazard that is typically self-limiting or associated with minimal harmful health consequences).
Potential to affect Canada	**The degree to which the hazard is likely to affect the health of people in Canada, entering Canada, and/or Canadian residents abroad, based on knowledge at the time of assessment.**
High	The hazard is currently affecting or is likely to affect large numbers[a] of people in the general population or in specific subgroups in Canada, entering Canada, and/or Canadian residents abroad.
Moderate	The hazard is currently affecting or is likely to affect a moderate number[a] of people in the general population or in specific subgroups in Canada, entering Canada, and/or Canadian residents abroad.
Low	The hazard is currently affecting or is likely to affect a minimal number[a] of people in the general population or in specific subgroups in Canada, entering Canada, and/or Canadian residents abroad. OR The hazard is unlikely to affect people in Canada, entering Canada, and/or Canadian residents abroad.
Concern for insufficient control measures	**The potential that Canada has insufficient measures to detect, prevent, mitigate, prepare for, and/or respond to the hazard or associated negative health impact(s).**
High	There are currently no known mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[b]. OR There may be limited mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[b], but they are considered experimental, of unknown effectiveness, or unavailable. OR Necessary measures will require significant resources to implement.
Moderate	There are mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[b], but there may be challenges with effectiveness, availability, or deployment. OR Necessary measures may require increased resources to implement.
Low	There are effective, available, and easily deployed mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[b]. OR Routine responses are adequate (i.e., there is no need to implement additional control measures).
Overall threat assessment	**The overall evaluation of the threat posed by the hazard associated with this signal, at the time of assessment, taking into consideration 'Concern for human health', 'Potential to affect Canada', and 'Concern for insufficient control measures'.**
High	The hazard associated with this signal is assessed at a high threat level for Canada, at the time of assessment.
Moderate	The hazard associated with this signal is assessed at a moderate threat level for Canada, at the time of assessment.
Low	The hazard associated with this signal is assessed at a low threat level for Canada, at the time of assessment.

[a] There are no quantitative guidelines for this attribute. The number of people potentially or currently affected that would be considered high, moderate, or low will vary depending on the context of the event
[b] Canada refers to people living in Canada, entering Canada, and/or Canadian residents abroad

Authors' statement

The first author named is lead and corresponding author. All other authors are listed in alphabetical order. Co-author contributions are as follows:

GB — Conceptualization, methodology, investigation, formal analysis, project administration, writing–original draft, writing–review & editing
CD — Investigation, formal analysis, project administration, writing–review & editing
CE — Conceptualization, methodology, writing–review & editing, supervision

JM — Investigation, formal analysis, project administration, writing–review & editing
AS — Investigation, formal analysis, project administration, writing–review & editing
LW — Conceptualization, methodology, writing–review & editing, supervision

Competing interests
None.

ORCID numbers

None.

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Assessing public health threats: An overview of coordinated threat assessment at the Public Health Agency of Canada

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Abstract

Background: The early detection, assessment, and communication of potential public health threats are key activities in mitigating public health impacts by ensuring the timely deployment of an appropriate response. The Public Health Agency of Canada (PHAC) uses a standardized methodology to consolidate scientific and technical subject matter expertise on a weekly basis to systematically characterize and assess emerging public health signals and communicate assessments to decision-makers.

Methods: Public Health Agency of Canada's coordinated threat assessment process, and the standardized methodology used to characterize and assess threats, are described.

Results: The coordinated threat assessment methodology uses a standardized method that includes engagement with subject matter experts across PHAC to assess, document, and communicate the characterization of each threat. Three key attributes are used to assess each threat based on the concern for human health, the potential to affect Canada, and the concern that Canada has insufficient control measures to manage a specific threat. Qualitative criteria for each threat attribute are used to assess a threat based on 'high', 'moderate', or 'low' levels. An overall assessment is based on the three threat attributes and is accompanied by a narrative rationale to support the assigned threat level.

Conclusion: The standardized threat assessment methodology provides a coordinated and systematic process to characterize and assess public health threats in a consistent and timely manner. The framework reflects important elements to consider in terms of public health significance, allows for flexibility in the indicators used to characterize a public health threat, and is applicable to any threat of public health concern.

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Keywords: public health, threat assessment, tool, method, framework, public health intelligence

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Introduction

Public health intelligence is a core public health function responsible for detecting, assessing, interpreting, and communicating information for informed decision-making to protect the health of the population (1). These activities are key in mitigating public health impacts by ensuring the timely deployment of an appropriate response, and are in place in subnational, national, and international public health agencies (2–4). Some agencies follow a centralized approach, wherein a core team is responsible for all steps, including signal detection, assessment, and communication (2,4). Others follow a disseminated approach, with responsibility for these activities distributed among a variety of teams across the agency (5).

As part of the spectrum of public health intelligence activities, threat assessment is a high-level, early characterization of the public health significance associated with a specific signal or event (4) using data and intelligence from multiple sources, as well as expert opinion (6). Indicators of public health significance are measured in different ways by different public health agencies, however, factors such as population health impact, potential for exposure or transmission, and the availability of public health control measures are often considered (2–4). The threat assessment process can be challenging due to limited or emerging data, however, a standardized methodology ensures all public health threats are characterized using a consistent approach to inform a public health response that is proportionate to the threat level (6).

At the Public Health Agency of Canada (PHAC), threat assessment is standardized through the coordinated threat assessment (CTA) process, which was established in response to recommendations identified by the Auditor General of Canada in 2021 to strengthen its risk assessment process and coordination to guide public health response (7). Situated within a spectrum of risk assessment activities, CTA is a PHAC-wide approach that consolidates data, information, and subject matter expertise on a weekly basis to systematically assess emerging public health signals that may constitute a threat to Canada and potentially require further public health action. Through the CTA process, a weekly threat report is produced and shared with public health partners to document and communicate an early, high-level assessment of emerging public health threats. This article provides an overview of PHAC's CTA process and a description of the methodology used to assess threats. **Table 1** contains a list of terms associated with threat assessment and their definitions.

Table 1: Public Health Agency of Canada definitions of technical terms associated with public health threat assessment

Technical term	Definition
Hazard	Anything with the potential to cause harm (8).
Signal	Data and/or information representing a potential acute risk to human health. Signals may consist of reports of cases or deaths (individuals or aggregated) or potential exposure of human beings to hazards (9).
Event	A signal that has been assessed and verified (9).
Threat	An event that has been further assessed to have the potential (directly or indirectly) to cause harm to Canadians or individuals living in Canada and may require further action (10).
Risk	A function of the likelihood that a public health event or threat may occur and the magnitude of the impact if it were to occur (11).

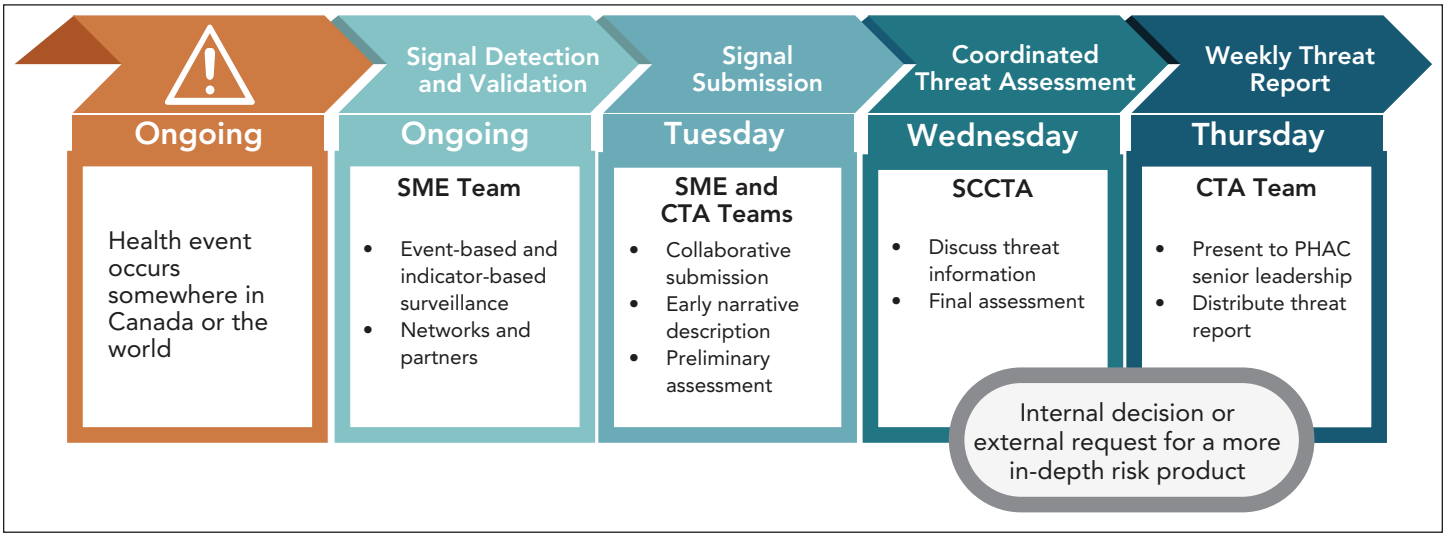
Methods

Coordinated threat assessment methods

Overall process

The threat assessment process begins when PHAC detects a signal indicating a potential hazard to human health occurring either in Canada or internationally (**Figure 1**). Signals of potential public health threats may be related to a new hazard or a change in the epidemiology of an existing hazard. This includes, but is not limited to, an increase in morbidity or mortality in animals or humans, a change in the geographical or temporal distribution of a given hazard, an unexpected cluster of cases or deaths, the emergence or re-emergence of a pathogen, and hazards that have the potential to cause substantial morbidity or mortality in humans.

Figure 1: Overview of Public Health Agency of Canada's weekly coordinated threat assessment cycle



Abbreviations: CTA, coordinated threat assessment; PHAC, Public Health Agency of Canada; SCCTA, Scientific Committee for Coordinated Threat Assessment; SME, subject matter experts

Signal detection and validation: Signals are detected through a variety of sources, including notification from subnational, national, and international partners, as well as event-based surveillance or indicator-based surveillance systems (6,12). Subject matter experts (SMEs) within PHAC validate signals to determine whether they have the potential to constitute a threat to Canada. The threat assessment process is initiated for signals that meet the specific submission criteria described in the threat assessment framework, described below.

Assessment: A preliminary threat assessment is provided by the submitting SME in collaboration with the CTA team using the standardized methodology. The final threat assessment is determined at a weekly meeting of the Scientific Committee for Coordinated Threat Assessment (SCCTA), which consists of scientific and technical public health experts with a wide breadth of expertise across PHAC. The consolidation of expert opinion using a standardized assessment tool results in a transparent and systematic measure of the public health threat level. Additional risk assessments are considered for complex threats or those identified by SMEs to require a more in-depth assessment of risk (13). Threats are reassessed on a weekly basis as a situation evolves, and more information becomes available.

Communication and documentation: Timely and clear communication of the threat level to PHAC senior leadership leads to a well-informed and common understanding of the threat to support decision-making for further action. The weekly threat report documents the signal, the assessment and rationale, as well as the public health actions undertaken by PHAC to address the threat.

A central team coordinates the process and is composed of epidemiologists and a medical director. Lead and supporting PHAC programs associated with each threat select a representative to contribute to the written submission and oral presentation at SCCTA. Subject matter experts in a variety of areas, including risk assessment, convene at SCCTA meetings to discuss and finalize the threat assessment for each submission.

Results

Threat assessment framework

Threat assessment at PHAC utilizes a standard framework that involves assessment of three threat attributes that characterize the public health significance of the event, and an overall threat level associated with the event (**Figure 2**) (14). The framework can be used to characterize threats affecting the general population or a specific subgroup, which may include populations at increased risk of severe harm due to biology (e.g., immune compromise, age), socioeconomic factors (e.g., access to care), or geography. Uncertainty in the data used to characterize a threat may elevate the assessment level of any of the attributes or the overall assessment.

Figure 2: Threat submission and assessment framework

Threat Submission Criteria

- ❑ The signal has been identified in the past 7 days.

AND

One of the following two options:

- ❑ The signal reflects a new hazard **OR**
- ❑ The signal reflects a change in incidence, location, transmission, severity, seasonality, spatiotemporal pattern, demographics, therapeutic effectiveness, or another indicator.

Threat Assessment Framework

Threat attribute	High	Moderate	Low
Concern for human health	The potential severity of harm to health that the hazard poses in the population most likely to be affected, based on current knowledge.		
Potential to affect Canada	The degree to which the hazard is likely to affect the health of people in Canada, entering Canada, and/or Canadian residents abroad, based on knowledge at the time of assessment.		
Concern for insufficient control measures	The potential that Canada has insufficient measures to detect, prevent, mitigate, prepare for, and/or respond to the hazard or associated negative health impact(s).		
	High	**Moderate**	**Low**
Overall threat assessment	The overall evaluation of the threat posed by the hazard associated with this signal, at the time of assessment, taking into consideration 'Concern for human health', 'Potential to affect Canada', and 'Concern for insufficient control measures'.		

Threat attributes

Each of the threat attributes is individually assessed and assigned a level of 'high', 'moderate', or 'low' based on the definitions in **Table 2**. These definitions allow for flexibility in the indicators used to characterize a threat and can be applied to any public health threat.

Concern for human health: Reflects the severity of harm posed to human health (Table 2). Indicators to consider for this attribute include morbidity, mortality, case fatality ratio, and burden of harm as it relates to physical, mental, or social well-being. When assessing concern for human health, the health consequences that are typically associated with the population most likely to be affected are considered. The level assigned for this attribute may vary depending on the context of the situation being assessed. For example, an outbreak of an enteric pathogen mainly involving populations at high risk of severe illness (e.g., children under the age of five years) may be assigned a higher level than the same pathogen affecting a group of young and middle-aged adults.

Potential to affect Canada: Describes the number of individuals or proportion of a population that will potentially be affected by a hazard (Table 2). Examples of indicators to consider include the transmissibility of a pathogen, the distribution of disease vectors in Canada, and the geographical range of a hazard, such as wildfire smoke. The number of people potentially or currently affected that would be considered high, moderate, or low will vary depending on the context of the event. For example, an assessment of 'high' may refer to a large proportion of a particular subgroup within Canada or a large number of people in the general population.

Concern for insufficient control measures: Relates to Canada's capacity to engage in public health activities to detect or respond to a hazard (Table 2). Activities related to detection, prevention, mitigation, preparation, or response may be applicable at different stages of an event. For example, detection refers to whether Canada has sufficient surveillance and/or laboratory capacity to detect a hazard should it enter Canada and should be considered in the assessment of threats that have not yet entered Canada. In contrast, prevention and response refers to whether Canada has mechanisms, such as vaccines, therapeutics, safety protocols, and guidelines to prevent the spread of the hazard. In addition, some control measures are dependent on knowledge of the source of the hazard prior to

Table 2: Definitions associated with each threat attribute

Threat attribute	High	Moderate	Low
Concern for human health	This hazard poses or is anticipated to pose severe harm to the health of the population most likely to be affected (e.g., a hazard that is typically life-threatening and/or involves permanent or long-term harmful health consequences).	This hazard poses or is anticipated to pose moderate harm to the health of the population most likely to be affected (e.g., a hazard that is typically associated with serious but not life-threatening health effects or typically involves non-permanent or short-term harmful health consequences).	This hazard poses or is anticipated to pose minor harm to the health of the population most likely to be affected (e.g., a hazard that is typically self-limiting or associated with minimal harmful health consequences).
Potential to affect Canada	The hazard is currently affecting or is likely to affect large numbers of people in the general population or in specific subgroups in Canada, entering Canada, and/or Canadian residents abroad.	The hazard is currently affecting or is likely to affect a moderate number of people in the general population or in specific subgroups in Canada, entering Canada, and/or Canadian residents abroad.	The hazard is currently affecting or is likely to affect a minimal number of people in the general population or in specific subgroups in Canada, entering Canada, and/or Canadian residents abroad. OR The hazard is unlikely to affect people in Canada, entering Canada, and/or Canadian residents abroad.
Concern for insufficient control measures	There are currently no known mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[a]. OR There may be limited mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[a], but they are considered experimental, of unknown effectiveness, or unavailable. OR Necessary measures will require significant resources to implement.	There are mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[a], but there may be challenges with effectiveness, availability, or deployment. OR Necessary measures may require increased resources to implement.	There are effective, available, and easily deployed mechanisms to detect, prevent, mitigate, prepare for, and/or respond to the impact(s) of this hazard on Canada[a]. OR Routine responses are adequate (i.e., there is no need to implement additional control measures).

[a] Canada refers to people living in Canada, entering Canada, and/or Canadian residents abroad

implementation. For example, concern for insufficient control measures may be assessed at a higher level for a foodborne outbreak with no known source, because deployment of a food recall, an effective control measure, is dependent on knowledge of the source of the outbreak.

Overall threat assessment

The overall threat assessment provides a single assessment that communicates the threat level, allowing decision-makers to better understand the degree to which public health action is needed for a given threat. All three attributes are taken into account when determining the overall assessment, although they may not receive equal weight. As outlined in **Table 3**, a pathogen associated with severe or fatal outcomes may receive a low overall assessment if it is unlikely to affect Canada and can be effectively managed should it occur. Recognizing the subjectivity of this approach, the final overall assessment level is made by group consensus during SCCTA meetings.

Rationale for the overall threat assessment

A narrative rationale for the overall threat assessment level provides the context within which each threat is assessed and supports the assigned threat level based on the information used to make the assessment. The rationale describes the level of each individual threat attribute, and the way it contributes to the overall assessment of the threat. This includes any nuance in the reasoning behind the level selected for the individual threat attributes and overall threat assessment, key information gaps, and associated uncertainty related to the assessment.

Discussion

The coordinated threat assessment process at PHAC was created in response to recommendations from the Auditor General of Canada's 2021 report on pandemic preparedness, surveillance, and border measures following the COVID-19 pandemic (7). The objective of PHAC's coordinated threat assessment process is to produce a quick, timely snapshot of threats for PHAC senior leadership using standardized methodology. This process provides a systematic scientific approach to assess varied threats from across PHAC programs by consolidating emerging data and SME opinion on a weekly basis. The process established at PHAC optimizes the ability to anticipate, detect, understand, and respond to potential public health threats through communication of timely assessments and corresponding actions for public health partners within PHAC and across Canada.

While different public health agencies vary in their processes and hazard priorities, many agencies employ a standard tool to characterize and assess public health threats (2–5). Public Health Agency of Canada's standardized threat assessment tool reflects three key elements to consider in terms of public health

Table 3: An example using Public Health Agency of Canada's threat assessment method

Situation summary			
Public Health Agency of Canada was notified that the Ministry of Health from Country X has reported an outbreak of hemorrhagic fever, including several deaths. The majority of cases and deaths are among health care workers from two health facilities. Additional contacts have been identified and are under follow-up. Transmission of the virus requires close contact with body fluids of an infected individual. The Government of Country X is coordinating the response, including case finding, contact tracing, implementation of infection prevention and control at health facilities, risk communication, and assessment of possible vaccines and therapeutics for clinical trials. Country X has also implemented border control measures to prevent potential cases from travelling outside the country. No approved therapeutics or vaccines exist. Public Health Agency of Canada programs have consulted travel data and find that the monthly number of travellers between Canada and Country X in the following three months is estimated to be low.			
Threat attribute	**High**	**Moderate**	**Low**
Concern for human health	☒	☐	☐
Potential to affect Canada	☐	☐	☒
Concern for insufficient control measures	☐	☐	☒
Overall threat assessment	☐	☐	☒
Rationale for the threat assessment level			
The overall threat level is assessed as low for Canada at the time of assessment. The concern for human health is assessed as 'high' because Disease X is a severe, often fatal illness in humans. The case fatality ratio ranges from 24%–88% depending on the virus strain and case management. The potential to affect Canada is assessed as 'low' because there are no cases in Canada and Country X has implemented appropriate infection prevention and control measures, including border measures, to prevent the spread of the virus outside of the affected region. In addition, travel volumes between Canada and Country X are relatively low. The concern for insufficient control measures is assessed as 'low'. There are no vaccines or treatments approved for this virus however, Canada has sufficient capacity for detection of cases and measures to limit spread if a travel-associated case is detected.			

significance, ensuring a consistent methodology is applied to a wide variety of threats with transparent outcomes.

Limitations

A critical principle of the threat assessment framework is that the application of the threat attributes is qualitative and flexible and can be applied to any public health threat of concern to Canada. Flexibility in the application of the framework is key, given the breadth of data and intelligence that may be used to inform the assessment. For example, an event associated with a pathogen will use different indicators to assign a level to individual threat attributes compared to an event associated with a natural disaster. The former may characterize concern for human health using the case fatality ratio, whereas the latter may rely on burden of harm to mental health. The rationale for the threat assessment provides context for the selected level and ensures transparency in the assessment regardless of the indicators used to arrive at the assessment level.

The qualitative nature of the threat assessment definitions can make it challenging to assign a level of 'high', 'moderate', or 'low' for each section without quantitative guidelines. However, this subjectivity allows for expert opinion influencing the assessment of threats and flexibility in weighting threat attributes based on the context of the event. The approach also allows for discordant opinions, which are discussed during SCCTA meetings and resolved by group consensus.

Some public health agencies take an all-hazards approach (2), while others are focused on infectious diseases (3,4). At the time of writing, the majority of threats assessed by PHAC have been related to infectious diseases, however, a small number of non-infectious disease threats have been submitted to the threat report (e.g., environmental hazards, mis/disinformation). While such signals are often the responsibility of other government departments, there is ongoing work to expand the scope of the CTA process to include a broader spectrum of health hazards (15,16). Recognizing the increasingly interconnected and complex nature of natural and human-induced hazards and their potential impact on health (16), an approach that includes infectious and non-infectious hazards increases efficiency by recognizing and integrating common threat assessment elements across hazard types. Accordingly, the threat assessment framework described in this paper was designed with an inclusive approach in mind and is expected to remain applicable in assessing threats associated with diverse hazard types.

Conclusion

In summary, public health intelligence, including threat assessment, is a key component of public health infrastructure. Early assessment of threats can be challenging with limited and emerging information, however, a standardized methodology ensures all public health threats are characterized using a consistent approach. The implementation of CTA across PHAC has improved the process and transparency of risk assessment activities and fosters relationships by sharing results with public health partners.

Authors' statement

GB — Conceptualization, project administration, writing–original draft, writing–review & editing
EB — Writing–original draft, writing–review & editing
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Competing interests

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Laboratory diagnosis of pertussis: A survey on provincial public health laboratory methods

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Abstract

Background: Pertussis, a vaccine preventable respiratory illness caused by the bacterium *Bordetella pertussis* (*B. pertussis*), has been a nationally reportable disease in Canada for over 100 years; however, cases resurged in Canada and globally in 2023–2024.

Objective: To examine the breadth and depth of pertussis strain surveillance currently being carried out across Canada.

Methods: A survey was sent to all ten provincial public health laboratories inquiring how pertussis was diagnosed or identified in the laboratory, including the polymerase chain reaction (PCR) diagnostic methods, bacteriological culture, identification and strain characterization such as molecular typing and antibiotic susceptibility testing.

Results: Nine of the ten provincial laboratories provided responses. Five provincial laboratories reported performing bacteriological culture, and some only from specimens that tested positive by PCR. Long-term storage of submitted and historical specimens took place in six laboratories. Identification of *B. pertussis* was commonly done through matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis, though immunochemical and PCR-based methods were also used. One laboratory conducted antibiotic susceptibility testing in specific circumstances. No laboratory performed fimbriae serotyping or examined expression of other pertussis vaccine antigens. One laboratory used whole-genome sequencing for outbreak investigation. The PCR diagnostics were performed in eight of the responding laboratories and always include IS481 and pIS1001 gene targets. Some laboratories also reported using other gene targets to identify and distinguish between *B. pertussis*, *B. parapertussis*, *B. holmesii* and *B. bronchiseptica*.

Conclusion: Given the global increase in pertussis, with the emergence of macrolide-resistant and pertactin-deficient strains, strain characterization should be added to the Canadian national pertussis surveillance program.

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Introduction

Pertussis, which is commonly referred to as whooping cough, is caused by the bacterium *Bordetella pertussis* (*B. Pertussis*) (1). Pertussis has been a notifiable disease in Canada since 1924 (2). Surveillance of pertussis is done by provinces and territories and they in turn voluntarily report cases to the Public Health Agency of Canada (PHAC)'s Canadian Notifiable Disease Surveillance System. Data collected and validated by the Canadian Notifiable Disease Surveillance System are published annually online in the

Notifiable Diseases Online website (3). The PHAC also supports the Canadian Immunization Program ACTive (IMPACT) to carry out hospital-based surveillance of paediatric pertussis cases (4).

For control of pertussis, an inactivated whole-cell vaccine was introduced in Canada in 1943, which was subsequently replaced by the adsorbed whole-cell vaccine from 1981 to 1985. Eventually, acellular pertussis vaccine was introduced in 1997 because of its less reactogenic nature (5). Despite having a vaccine, pertussis continues to cause disease in infants, young children, adolescents and adults for various reasons related to vaccine hesitancy, waning of vaccine-induced protective immunity and divergence of current circulating and vaccine strains (6).

Between 2020 and 2022, COVID-19 pandemic restrictions caused disruptions in social gatherings, which resulted in lower numbers of different respiratory infections, including pertussis (7). As with other respiratory infections (8,9), pertussis appears to have re-emerged after the pandemic to cause more cases than before the pandemic (10,11). Data from 29 European Economic Area countries reported 1,578 and 2,623 cases of pertussis in 2021 and 2022, respectively (12,13). In 2023, the number of pertussis cases reported by these countries jumped to over 25,000 cases; and in the first three months of 2024, more than 32,000 cases were reported (14). In China, pertussis increased in 2022 and 2023 with 39,781 and 38,205 cases reported, respectively (15). In the first two months of 2024, 32,380 cases, including 13 deaths, were recorded (16). Furthermore, the disease has shifted from mainly affecting infants to older children, and a new strain showing macrolide resistance and pertactin deficiency emerged (17). In South Korea, a national epidemic was described in 2024 with the highest incidence rate found in those aged 13 years, with 526.2 cases per 100,000 population (18). In addition, the macrolide-resistant strain appeared to have spread to some Asian countries (19). Besides monitoring for susceptibility to macrolides, the European Centre for Disease Prevention and Control (ECDC) also recommends performing serotyping, multi-locus antigen sequence typing and vaccine antigen expression by enzyme-linked immunosorbent assay (ELISA) or gene sequencing (20). Similar strain surveillance programs are also available at the United States (US) Centers for Disease Control and Prevention and the United Kingdom Health Security Agency.

In 2024, the Pan American Health Organization also reported increases in pertussis in multiple countries within the Americas including the US, Brazil, Mexico and Peru (21). For example, preliminary data in the US show that reported cases of pertussis in 2024 increased six-fold when compared to 2023 (22). Canada was no different from other nations, reporting increases in pertussis cases in multiple jurisdictions leading to significant case numbers not seen since prior to the introduction of the pertussis vaccines. The increases in pertussis cases occurred in nearly all provinces and territories (23–29) (*personal communication Dr. Paul Van Caeseele, March 31, 2025*). For the first eleven months in 2024, Public Health Ontario reported 1,634 pertussis cases, with 1,396 as confirmed and 239 probable cases. This led to the highest incidence rates since 2017 in those younger than one year old and those between the ages of 10 and 14 years old (74.2 and 55.2 per 100,000, respectively). According to Québec public health, 16,130 cases of whooping cough were recorded January 1–October 9, 2024. In Newfoundland and Labrador, 230 confirmed cases of pertussis were recorded throughout the province by September 10, 2024.

Given the global resurgence of pertussis after the COVID-19 pandemic, with the emergence of macrolide-resistant and vaccine antigen-deficient strains (30,31), the capacity in Canada for a national surveillance program that includes strain characterizations and antibiotic susceptibility testing must be re-examined. It is with this understanding that the National Microbiology Laboratory Branch of the PHAC is working with provincial and territorial public health laboratory partners to examine how pertussis is diagnosed and characterized in Canada in order to understand the breadth and depth of pertussis surveillance in the country.

Methods

This study was intended to obtain details on strain characterization work, which can contribute to the Canadian national surveillance of pertussis. Strain characterizations are often done at the provincial public health laboratories, which also serve as reference laboratories for their provinces as well as neighboring territorial governments. The PHAC's National Microbiology Laboratory Branch has a close working relationship with the public health agencies in all provinces and territories as partners in public health microbiology issues. This relationship is formalized as a national association of public health laboratory professionals, established in 2001 as the Canadian Public Health Laboratory Network, with a role to provide rapid, coordinated and unified laboratory response to emerging and re-emerging infectious diseases (32). As such, frontline and hospital laboratories as targets of the survey were not included.

Therefore, on November 17, 2024, an e-mail was sent to the medical microbiologists or medical directors of ten provincial public health laboratories explaining the purpose of the survey and a questionnaire with questions covering bacteriological culture of *B. pertussis*, polymerase chain reaction (PCR) diagnostic method and strain characterization. For strain characterization, the following questions were asked: 1) how long are cultures preserved; 2) how cultures are identified and characterized including serotyping (for expression of fimbriae antigens); 3) expression of other vaccine antigens; 4) molecular typing, and 5) antibiotic susceptibility testing. For PCR diagnostic methods, details of the method used (commercial kit/platform or laboratory developed method), the gene targets detected in the PCR assays and positivity cut-off values were included in the

questionnaire. A copy of the survey questionnaire can be found in the **Appendix** and participants had up to December 31, 2024 to respond voluntarily.

Since the survey did not request any personal information and was done within the autonomy of the Canadian Public Health Laboratory Network for public health purposes, institutional research ethics approval was not sought nor was informed consent necessary as the response was voluntary. Data protection was only applied with laboratories identified by numbers instead of naming the laboratory linked to the data captured in the survey. The survey questions were based on questions received by the National Microbiology Laboratory Branch from public health practitioners across the country, such as antibiotic resistance patterns and strain types found.

Results

Responses to the questionnaire were received from nine of the ten provincial public health laboratories. One provincial public health laboratory did not respond to the survey.

Culture of *Bordetella pertussis* and subsequent testing on *Bordetella pertussis* isolates

Five provincial public health laboratories performed bacteriological culture of primary specimens for isolation of *B. pertussis*, although one of them reported doing so only rarely in recent years. Three of these five provincial laboratories disclosed that only specimens tested positive by PCR for *B. pertussis* were subjected to culture, including one of these laboratories only performed culture on specimens that were PCR-positive with low cycle threshold (Ct) values. Six provincial laboratories reported long term (on the scale of years) storage of *B. pertussis* isolates; although some laboratories had stopped performing primary cultures, historical isolates were preserved and stored. Two provincial laboratories also reported storage of primary specimens submitted for *B. pertussis* testing at −80°C.

Among those performing primary bacteriological culture and/or performing bacterial identification as a provincial public health reference laboratory, six laboratories (including one laboratory that did not provide primary culture service but received samples for reference diagnostic identification testing) identified *B. pertussis* by matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF). One of these six laboratories also used biochemical tests such as oxidase, motility, growth on MacConkey agar, and genetic sequencing for identification of *B. pertussis* and other uncommon *Bordetella* species, while another laboratory also used bacterial agglutination and fluorescent antibody tests for identification of *B. pertussis* and *B. parapertussis*.

Only one laboratory reported performing antibiotic susceptibility testing for *B. pertussis* specimens when requested by clinicians. No laboratory was reporting any phenotypic or genetic typing, including looking at expression of vaccine antigens or sequencing of vaccine antigen genes. Only one laboratory reported performing whole-genome sequencing on *B. pertussis* and *B. parapertussis* for outbreak investigation. The scope of bacteriological culture from primary specimens, and the subsequent testing to characterize the strains in the different provincial public health laboratories are summarized in **Table 1**.

Table 1: Primary culture of *Bordetella pertussis* from clinical specimens, identification method, antibiotic susceptibility testing and routine typing provided across provincial public health laboratories in Canada

Laboratories	Primary culture	Identification method	Antibiotic susceptibility testing	Routine typing for strain characterization	Culture preservation	Comments
1	Yes	MALDI-TOF plus PCR	No	No	Yes, years	-
2	Yes[a]	MALDI-TOF	Yes[b] E-test	No	Yes, years	Whole-genome sequencing for outbreak investigation
3	Yes	MALDI-TOF	No	No	Yes, more than 10 years	-
4	Yes[c]	MALDI-TOF	No	No	Yes, years	-
5	Yes[d]	MALDI-TOF plus agglutination and FA[e]	No	No	Yes, years	-
6	No[f]	MALDI-TOF plus biochemical testing (16S rRNA sequencing if necessary)	No	No	Yes[g], years	-
7	No	N/A	No	No	No	-
8	No	N/A	No	No	No	-
9	No	N/A	No	No	No	-
10	NA	N/A	N/A	N/A	N/A	No response

Abbreviations: FA, fluorescent antibody; MALDI-TOF, matrix-assisted laser desorption/ionization time-of-flight; N/A, not applicable; PCR, polymerase chain reaction; -, no comment
[a] Only on PCR-positive samples
[b] Only when requested by clinicians
[c] Only when submitted on appropriate culture collection and transport media
[d] Only on PCR-positive samples with low cycle threshold (Ct) values
[e] Fluorescent Antibody Test
[f] However, receives suspected *Bordetella* specimens as a provincial reference laboratory for identification
[g] Received suspected *Bordetella* specimens for identification purpose

Polymerase chain reaction diagnosis of pertussis

Three provincial public health laboratories used commercially available test kits or platforms for the laboratory diagnosis of pertussis: the R-Biopharm AG RIDA®GENE Bordetella (33), the Diasorin Simplexa™ Bordetella Direct Test (34) and the QuidelOrtho Corporation's Solana® Bordetella Complete Assay (35). Five other provincial laboratories used laboratory developed tests (LDT), and while the gene targets detected by specific primer-probe sets in these LDTs may differ, they invariably included IS481 and pIS1001 (for the simultaneous detection and differentiation or identification of *B. pertussis* and *B. parapertussis*). Some laboratories also employed additional gene targets such as hIS1001 (for detection of *B. holmesii*), BHrecA (for detection of *B. holmesii*), bfrZ (for detection of *B. bronchiseptica*) and IS1002 (for detection of *B. parapertussis*). The gene targets used in the PCR assays by the various laboratories and their ability to identify and differentiate common *Bordetella* species are summarized in **Table 2**. Five laboratories that used LDTs also reported using Ct values to interpret the PCR results. Positive PCR results for pertussis were defined by Ct values ranging from less than or equal to 35 to less than 45 (Table 2).

Table 2: Polymerase chain reaction gene targets for molecular detection/diagnosis of *Bordetella pertussis* and other *Bordetella* species

Laboratories and PCR method	IS481	IS1001	IS1002	hIS1001 (*B. holmesii*)	bfrZ	BHrecA (*B. holmesii*)	Ct values for defining positive PCR results	Comments
1[a]	√	√	-	√	√	-	≤35	Can identify all four species including *B. bronchiseptica* with species-specific PCR; however, may not identify co-infection of Bp and Bh.
2[b]	√	√	-	√	-	-	N/A	Can identify Bp accurately most of the time; but may not identify co-infection of Bp and Bh; cannot differentiate between *B. para* and Bb.
3[a]	√	√	-	√	-	-	<45	Can identify Bp accurately most of the time; but may not identify co-infection of Bp and Bh; cannot differentiate between *B. para* and Bb.
4[c]	√	√	-	-	-	-	Built-in cut off values[d]	Can identify and differentiate between Bp and *B. para* accurately most of the time; however, *B. para* and Bb may be misidentified; also Bp and Bh may be misidentified.
5[a]	√	√	-	-	-	√	≤36	Method described in J Clin Microbiol 2010;48 (4):1435–7.
6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Not applicable or do not offer PCR diagnostic service at the provincial public health laboratory.
7[a]	√	√	-	√	-	-	40	Can identify Bp accurately most of the time; but may not identify co-infection of Bp and Bh; cannot differentiate between *B. para* and Bb.
8[a]	√	√	√	-	-	-	40	Can identify Bp and *B. para*; but in IS481+/ IS1001−/IS1002− samples, differentiation between Bp and Bh/Bb is not possible (due to Bb may contain low copy numbers of IS481). In IS1001+/IS1002− samples, differentiation between *B. para* and Bb is not possible (due to Bb possibly containing low copy numbers of IS1001).
9[c]	√	√	-	-	-	-	Built-in cut off values[e]	Can identify and differentiate between Bp and *B. para* accurately most of the time; however, *B. para* and Bb may be misidentified; also Bp and Bh may be misidentified.
10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	No response

Abbreviations: Bb, *Bordetella bronchiseptica*; Bh, *Bordetella holmesii*; Bp, *Bordetella pertussis*; *B. para*, *Bordetella parapertussis*; Ct value, cycle threshold value; N/A, not applicable; PCR, polymerase chain reaction; -, not tested in this laboratory

[a] Laboratory-developed test
[b] Commercial diagnostic test kit
[c] Commercial diagnostic test platform
[d] Approximately 37
[e] Not given, measured and interpreted fluorescent signal

Discussion

Nine of the ten provincial public health laboratories responded to this survey and the data obtained formed the basis of this report. Of the eight provincial public health laboratories that provide diagnostic PCR assays, five are able to detect *B. pertussis*, *B. parapertussis* and *B. holmesii*, and three were able to detect only *B. pertussis* and *B. parapertussis*. Thus, not all laboratories could definitively identify these three most important species by PCR. Bacteriological culture to recover viable *B. pertussis* from clinical specimens was only performed in five of the responding laboratories, and often only on PCR-positive clinical samples. The MALDI-TOF was the most common method used to identify *B. pertussis* cultures (used by all laboratories that provide this service of reference diagnostic/identification); however, only one laboratory carried out antibiotic susceptibility testing by E-test when requested by clinicians. Furthermore, none of the laboratories carried out routine typing of isolates to understand characteristics of the circulating *B. pertussis* strain. Therefore, current laboratory results do not contribute additional information towards the understanding of how strain characteristics may alter the epidemiology of pertussis in Canada.

At this time, the national surveillance of pertussis depends on provinces and territories reporting cases with minimal demographic information, including age and gender. The IMPACT surveillance of pertussis focuses on hospitalized cases with some additional clinical information (4). One deficient area is the lack of information on the *B. pertussis* bacteria currently circulating in Canada, which is needed to understand if the increase in Canadian pertussis cases in 2024 was due to expansion of a clonal strain or to diverse strain types. Resistance to oral macrolide antibiotics, such as erythromycin or clarithromycin, has been reported elsewhere and may also have emerged in circulating Canadian strains. It is with this understanding that the laboratory methods currently being used by our provincial partners for the surveillance of this highly contagious bacterial disease was reviewed.

Like for other common pathogens, strain characterization is an important component to an overall understanding of the evolving nature of the changing epidemiology of pertussis in Canada and globally. For example, once mainly a childhood disease, it now appears that depending on the locality, a noticeable proportion of cases occur either in older children, adolescent, adults or elderly. Several studies in the late 1990s and in early 2000s have described genetic polymorphisms in the vaccine antigen genes (e.g., pertactin and pertussis toxin) leading to the suggestion of divergence between current circulating *B. pertussis* strains and the strains used to manufacture vaccines (36–40). Genetic polymorphisms in the fim3 gene that encode fimbriae 3 or serotype 3 antigen have also been observed. In Canada, since the 1970s, the majority of *B. pertussis* isolates examined expressed the fimbriae 3 antigen but rarely the fimbriae 2 antigen. Additionally, non-synonymous mutations of the fim3 gene resulted in amino acid changes on a surface epitope of the fimbriae antigen led to the postulation that the polymorphisms may be subjected to immune pressure or selection from vaccine induced or naturally occurring immune response (41). Recent studies have also shown that genetic changes that favour the increase production of pertussis toxin (such as having the ptxP3 allele) have been associated with pertussis resurgence (42). Also, recent global *B. pertussis* isolates are frequently deficient in the expression of the pertactin antigen, including isolates in Canada (43–48). Furthermore, over a period of nine years, *B. pertussis* samples recovered from one province had the potential to fluctuate between different genotypes and expression of the vaccine antigen pertactin (49).

Although it is not fully understood 1) how these genetic polymorphisms within the vaccine antigen genes or 2) how strains not expressing certain vaccine antigens (such as Canadian isolates not expressing fimbriae 2 and pertactin antigens) would affect vaccine efficacy, it is expected that further antigenic drift away from the *B. pertussis* vaccine strains and their encoded antigens will negatively affect vaccine efficacy. Therefore, this highlights the importance of incorporating strain characterization into the overall pertussis surveillance program in Canada. Strain characterization may also mitigate potential emergence of antibiotic resistance, as in the case of a large increase in the number of pertussis cases due to the emergence of an erythromycin-resistant *B pertussis* strain in China (50).

In Canada, as in many other countries, most pertussis cases are diagnosed in the laboratory by PCR. This is likely because *B. pertussis* is a nutritionally fastidious bacteria that requires specialized and enriched culture media to support growth. The commonly used culture media for bacteriological isolation from primary specimens include both the Bordet-Gengou agar and the Regan-Lowe charcoal blood agar, which contain starch and/or charcoal to neutralize toxic fatty acids and peroxides, defibrinated horse or sheep blood, and sometimes antibiotics such as cephalexin to inhibit normal flora present in the nasopharynx. Also, bacteria can only be recovered during the first two weeks of cough, while PCR would remain positive for up to three or four weeks after disease onset. As such, bacterial culture has become less popular in frontline laboratories, which are increasingly adopting PCR assays that can simultaneously detect and identify a number of respiratory pathogens (e.g., BioFire Respiratory Panel [RP]2.1-EZ, which can detect up to 19 respiratory pathogens including *B. pertussis* and *B. parapertussis*). Also, the practice of PCR diagnostics for pertussis may varies by province (e.g., more reliance on provincial public health laboratory to provide this service in some provinces versus decentralized testing in others). Similarly, the ability to detect *Bordetella* species (e.g., *B. holmesii* and *B. bronchiseptica*) that may also cause cough symptoms varies across the country.

Not all the commercially available test kits and platforms or LDT for detection of pertussis by nucleic acid amplification testing (NAAT) can detect and differentiate between pertussis-causing *B. pertussis* and pertussis-symptoms like causing *B. parapertussis* and *B. holmesii*. To detect and differentiate these three *Bordetella* species, a NAAT needs to have specific primers and/or probes that target these three species separately (51,52). One such specific gene target for *B. pertussis* is ptxA. *Bordetella bronchiseptica* may also cause respiratory infections with cough in immunocompromised individuals (53). For detection and identification of *B. bronchiseptica*, yet another set of primers and/or probes would be required (54,55). The challenge in using NAAT with minimum numbers of primer pairs and probes is due to the fact that, for example, *B. holmesii* has been reported to harbor low copy numbers of IS481 (56) while *B. bronchiseptica* has been reported to harbor low copy numbers of IS481 and IS1001 (57). The IS481 and IS1001 are often used in PCR assays to detect *B. pertussis* and *B. parapertussis*, respectively.

While NAAT may be able to detect and differentiate or identify important *Bordetella* species involved in causing respiratory infections in human, the sensitive nature of this laboratory method may require some additional considerations in the interpretation of the test result. First, results from a NAAT for pertussis must be interpreted in the context of the clinical setting. For example, in Canada, a laboratory-confirmed case of pertussis is defined either by bacteriological isolation of *B. pertussis* or by detection of *B. pertussis* DNA from an appropriate clinical specimen, together with at least one compatible clinical findings of either cough lasting for two weeks or longer, paroxysmal cough of any duration, cough with inspiratory "whoop" or cough ending in vomiting or gagging, which may be associated with apnea (58). Secondly, contamination from the environment with the organism or its DNA may introduce potential false positive results. For example, pseudo-outbreaks of pertussis have been described in the literature (59–61). Therefore, the US Centers for Disease Control and Prevention also recommends that culture confirmation of at least one case should occur during the setting of a suspected pertussis outbreak (62).

In summary, maintaining *B. pertussis* culture capacity as well as strain identification and characterization including antibiotic susceptibility testing should remain available at either the provincial and/or national level pending further discussions on the most cost-effective surveillance program that meets the need of Canadian public health. Previously National Microbiology Laboratory has performed serotyping using monoclonal antibodies to *B. pertussis* fimbriae 2 and fimbriae 3, western immunoblot to detect the expression of vaccine antigen pertactin and genotyping of vaccine antigens genes, including pertussis toxin subunit A and pertussis toxin promoter region, fimbriae 3, pertactin and filamentous hemagglutinin (41,43,49).

In 2002, the Government of Canada organized a national consensus conference on pertussis with recommendations concerning laboratory diagnosis and surveillance (63). As a follow up, the National Microbiology Laboratory gathered Canadian experts on the subject of pertussis in a workshop to discuss the recommendations on laboratory diagnosis and surveillance from the national consensus conference. One of the action plans from this workshop was to set up a Working Group to discuss implementing a national strain characterization program (64). Due to competing priorities, this plan was put on hold, but in view of global resurgence of pertussis, the concern of antibiotic resistance and circulation of strains not expressing vaccine antigens, it may be time to re-examine this plan and put it into action.

Limitations

Limitations of this study include not sending this survey to frontline laboratories (including private medical laboratories), hospital laboratories and regional public health laboratories. Therefore, important laboratories may have been missed that may be providing bacteriological cultures for the laboratory diagnosis of pertussis, and also the overall PCR technology being offered for detection of pertussis, including the popular molecular diagnostic platform like the BioFire Respiratory Panel [RP]2.1-EZ for simultaneous detection and identification of 19 respiratory viral and bacterial pathogens including *B. pertussis* and *B. parapertussis*. To reach out to all the frontline medical and hospital laboratories would have been a big undertaking. Nevertheless, six regional laboratories were contacted through one provincial public health laboratory to gather frontline information for comparison. None of these six responding laboratories reported providing bacteriological culture for pertussis; two laboratories use BioFire for the detection of *B. pertussis* and *B. parapertussis* (including one of these two laboratories also having an LDT) and one laboratory uses a LDT that targets only IS481. None of these six laboratories provided any testing to identify, type or determine antibiotic susceptibility for *B. pertussis*. This is likely because, at least in some provinces, testing for *B. pertussis* may be regarded as specialized testing and therefore perceived as best handled at the provincial public health reference laboratories.

Conclusion

This survey has reviewed the current situation of pertussis in Canada and elsewhere globally, summarized the laboratory diagnostic procedures used in the Canadian Public Health Laboratory Network, identified some gaps in the national surveillance system and made recommendations to eliminate gaps identified. While PCR assays to detect *B. pertussis* is widely available across the country, culture capability may be more limited to some larger provinces. Routine strain typing that can inform strain characteristics such as expression of vaccine antigens, genetic polymorphisms that may affect a mismatch between the vaccine strains and current circulating strains and

antimicrobial resistance data are currently lacking. Maintaining some bacteriological culture and strain characterization capability is essential for understanding effects of vaccine induced immune pressure on *B. pertussis*. A system to collect data representative of national distribution of strain types (including antimicrobial resistance) is essential to understand the evolving nature of pertussis and to prepare for potential need of newer vaccine strain. A sentinel surveillance system including collection of strain typing data coupled with epidemiological information is recommended for a comprehensive understanding of the current epidemiology of pertussis in Canada. Moving forward, strain collection and characterization with antibiotic susceptibility monitoring should be included in a sentinel surveillance system to understand the evolving nature of *B. pertussis* under national infant, adolescent and maternal pertussis immunization programs.

Authors' statement

CM — Writing–original draft, writing–review & editing, investigation, data curation
JG — Resources, writing–review & editing, methodology
GT — Resources, writing–review & editing, methodology
JM — Resources, writing–review & editing, methodology
PVC — Resources, writing–review & editing, methodology
JK — Resources, writing–review & editing, methodology
BL — Resources, writing–review & editing, methodology
TH — Resources, writing–review & editing, methodology
GD — Resources, writing–review & editing, methodology
LJ — Resources, writing–review & editing, methodology
HP — Resources, writing–review & editing, methodology
RT — Conceptualization, methodology, writing–original draft, writing–review & editing, investigation, supervision

Competing interests

None declared.

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Appendix

List 1: Questionnaire on laboratory diagnosis of *Bordetella pertussis* infection

1. Does your laboratory (province) perform bacterial culture of *Bordetella pertussis* and other *Bordetella* species? Yes ____; No ____
2. a) Describe the PCR method (and PCR targets) your laboratory (province) performs for detection of pertussis? _____
   b) Is the assay able to differentiate between *B. pertussis*, *B. parapertussis*, and *B. holmesii*? _____
   c) If your laboratory is performing qPCR: Yes ___; No ___; what is the Ct value used to determine a positive result (presence of pertussis)? _____
3. a) Subsequent to culture, what method do you use to identify it as *B. pertussis* and not other *Bordetella* species? _____
   b) Does your laboratory (province) perform phenotypic and/or molecular typing: Yes _____; No _____
   c) Does your laboratory test for antibiotic susceptibility? Yes _____; No _____
      i. If yes, by what method: disk diffusion ( ); E-test ( ); micro-broth dilution method for MIC ( ); agar dilution method for MIC ( ).
   d) How long do you keep your positive cultures? _____ Months; _____ Years

Device and surgical procedure-related infections in Canadian acute care hospitals, 2020–2024

Canadian Nosocomial Infection Surveillance Program[1]*

Abstract

Background: Healthcare-associated infections (HAIs) are a significant healthcare burden in Canada. National surveillance of HAIs at sentinel acute care hospitals is conducted by the Canadian Nosocomial Infection Surveillance Program.

Objective: To describe device and surgical procedure-related HAI epidemiology in Canada from 2020 to 2024.

Methods: Data were collected from up to 67 Canadian sentinel acute care hospitals between January 1, 2020 and December 31, 2024 for intensive care unit central line-associated bloodstream infections (ICU-CLABSIs), hip and knee surgical site infections (SSIs), cerebrospinal fluid (CSF) shunt SSIs and paediatric cardiac SSIs. Case counts, rates, patient and hospital characteristics, pathogen distributions and antimicrobial resistance data are presented.

Results: Between 2020 and 2024, 1,846 device-related infections and 1,014 surgical procedure-related infections were reported. Rates of ICU-CLABSIs, hip and knee SSIs, CSF shunt SSIs and paediatric cardiac SSIs fluctuated throughout the study period, with no significant trends observed. The most commonly identified pathogens were coagulase-negative staphylococci (37%) in ICU-CLABSIs and *Staphylococcus aureus* (41%) in SSIs.

Conclusion: Epidemiological and microbiological trends among selected device and surgical procedure-related HAIs are essential for benchmarking infection rates nationally and internationally, identifying any changes in infection rates or antimicrobial resistance patterns and helping inform hospital infection prevention and control and antimicrobial stewardship policies and programs.

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Keywords: hospital-associated infection, acute care, surveillance, antimicrobial resistance, device-associated infection, surgical procedure-related infection, surgical site infection, ICU-CLABSI, central line-associated bloodstream infection, hip and knee arthroplasty surgical site infection, cerebrospinal fluid shunt surgical site infection, paediatric cardiac surgical site infection, Canada

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Introduction

Healthcare-associated infections (HAIs) are a common outcome of healthcare delivery and among hospitalized patients prolong hospital stays and require additional treatment (1,2). Healthcare-associated infections can result from the use of invasive medical devices and surgical procedures (3) and are commonly reported in Canadian hospitals, where they are significantly associated with hospital readmissions and all-cause mortality, compared with surgical patients without an associated infection (4).

A point prevalence study conducted in 2024 in Canadian sentinel acute care hospitals revealed that one third (33%) of all reported HAIs were device associated (5). Among all adult inpatients, the prevalence of surgical site infections (SSIs) in this study was 1.6% and the prevalence of central line-associated bloodstream infections (CLABSIs) was 0.7% (5). The risk of device and surgical procedure-related infections is associated with factors including patient demographics, prior surgeries and the duration of hospital stay, in addition to the type of hospital in which the patient received care (6–8).

Understanding the epidemiology of HAIs related to medical devices and surgical procedures is crucial for establishing benchmark rates over time. These benchmarks support the development of effective antimicrobial stewardship programs and guide infection prevention and control strategies. Collecting and analyzing antimicrobial susceptibility data are crucial for guiding appropriate antimicrobial use and combating antimicrobial resistance (9). This report presents an epidemiological summary of specific device and surgical procedure-related HAIs reported between 2020 and 2024 across 67 hospitals participating in the Canadian Nosocomial Infection Surveillance Program (CNISP).

Methods

Design

Since its establishment in 1994, CNISP has conducted national HAI surveillance at sentinel acute care hospitals across Canada, in collaboration with the Public Health Agency of Canada and the Association of Medical Microbiology and Infectious Disease Canada. Data are presented for device-related infections including intensive care unit (ICU)-CLABSIs, and surgical procedure-related HAIs including hip and knee arthroplasty SSIs, cerebrospinal fluid (CSF) shunt SSIs, and paediatric cardiac SSIs.

Case definitions

Device and surgical procedure-related HAIs were defined according to standardized protocols and case definitions (see **Appendix**). Complex infections, defined as deep incisional and organ/space, were included in hip and knee SSI surveillance. Central line-associated bloodstream infections identified in ICU settings were included in CLABSI surveillance. The adult mixed patient ICU, adult cardiovascular surgery intensive care unit (CVICU), paediatric intensive care unit (PICU) and neonatal intensive care unit (NICU) were included as eligible ICU settings. Adult mixed ICUs included any adult ICU with a mix of patient types as part of the ICU patient mix (i.e., medical/surgical, surgical/trauma, burn/trauma, medical/neurosurgical).

Data source

Epidemiological data for device and surgical procedure-related infections identified between January 1, 2020 and December 31, 2024 (using surgery date for SSIs and date of positive blood culture for CLABSIs) were submitted by participating hospitals using standardized data collection forms. Hospital participation varied by surveillance project and year. Data submission and case identification were supported by training sessions and periodic evaluations of data quality.

Statistical analysis

To calculate hip and knee SSI, CSF shunt SSI and paediatric cardiac SSI rates, the number of cases were divided by the number of surgical procedures performed (multiplied by 100). To calculate ICU-CLABSI rates, the number of cases was divided by line day denominators (multiplied by 1,000). Neonatal ICU-CLABSI rates were also calculated per 1,000 line days by birth weight category (750 g or less, 751 g–1,000 g, 1,001 g–1,500 g, 1,501 g–2,500 g and more than 2,500 g). To calculate ICU-specific catheter utilization, the total number of ICU patient central line days was divided by the total number of ICU patient days. To calculate proportions of pathogens, the number of pathogens were divided by the total number of identified pathogens. Denominators may vary, as missing and incomplete data were excluded from analyses. Median and interquartile ranges (IQRs) were calculated for continuous variables. Trends over time were tested using the Mann-Kendall test. The chi-square test was used to compare two categorical variables. Significance testing was two-tailed, and differences were considered significant at a p-value of ≤ 0.05. Analyses were conducted using R version 4.4.3.

Results

Between 2020 and 2024, up to 67 unique hospitals submitted device and surgical procedure-related infection data to CNISP. In the most recent year of surveillance data available, 2024, 67 hospitals submitted these data (**Table 1**), with the majority of participating hospitals located in the Western (British Columbia, Alberta, Manitoba and Saskatchewan; n=29, 43.3%) and Central (Ontario and Québec; n=28, 41.8%) regions. Additionally, the majority of hospitals served an adult-only (n=26, 38.8%) or mixed adult-paediatric (n=22, 32.8%) population and were medium-sized (201–499 beds; n=29, 43.3%) (Table 1). Overall, 1,846 ICU-CLABSIs and 1,014 surgical procedure-related infections were reported (**Table 2**) between 2020 and 2024. Among all SSIs reported, hip and knee infections represented 70.2% (n=712) of these types of infections (Table 2).

A total of 3,111 pathogens were identified from device-related infections and 1,072 pathogens from surgical procedure-related cases between 2020 and 2024 (**Table 3**). Of the identified pathogens for ICU-CLABSIs, 59.6% were gram-positive, 24.7% were gram-negative and 15.7% were fungal. Coagulase-negative staphylococci (CoNS) and *Enterococcus* spp. were most frequently identified in cases of ICU-CLABSIs. Of the identified pathogens for SSIs, 79.6% were gram-positive, 19.1% were gram-negative and 1.3% were fungal. Coagulase-negative staphylococci and *Staphylococcus aureus* were the most common pathogens associated with SSIs (Table 3). From 2020 to 2024, the proportion of *S. aureus* that was methicillin-resistant (MRSA) was 16.7% for ICU-CLABSIs and 9.9% for SSIs (data available on request).

Intensive care unit central line-associated bloodstream infections

Infection characteristics: Between 2020 and 2024, a total of 2,801 CLABSIs were reported. Most infections occurred in

Table 1: Characteristics of acute care hospitals participating in device and surgical procedure-related healthcare-associated infection surveillance, 2024

Characteristic of hospitals	CLABSI-adult mixed ICU	CLABSI-adult CVICU	CLABSI-PICU	CLABSI-NICU	CSF shunt SSI	Paediatric cardiac SSI	Hip and knee SSI	Total unique hospitals
Total number of participating hospitals	40	9	12	20	11	6	30	67
Region[a]								
Western	17	4	5	8	4	1	16	29
Central	19	4	6	9	5	4	7	28
Eastern	4	1	1	3	2	1	7	10
Northern	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hospital type								
Adult[b]	22	4	N/A	N/A	2	N/A	12	26
Adult-NICU	6	2	N/A	3	N/A	N/A	2	6
Mixed[c]	12	3	1	5	2	N/A	16	22
Paediatric[d]	N/A	N/A	8	8	7	4	N/A	99
Paediatric-OB	N/A	N/A	3	4	N/A	2	N/A	4
Hospital size								
Small (1–200 beds)	4	1	7	9	5	4	6	19
Medium (201–499 beds)	20	3	4	7	3	2	14	29
Large (500 and more beds)	16	5	1	4	3	N/A	10	19

Abbreviations: CLABSI, central line-associated bloodstream infection; CSF, cerebrospinal fluid; CVICU, cardiovascular surgery intensive care unit; ICU, intensive care unit; N/A, not applicable; NICU, neonatal intensive care unit; PICU, paediatric intensive care unit; SSI, surgical site infection

[a] Western region includes British Columbia, Alberta, Manitoba and Saskatchewan; Central region includes Ontario and Québec; Eastern region includes New Brunswick, Nova Scotia, Prince Edward Island and Newfoundland and Labrador; Northern region includes Yukon, Northwest Territories and Nunavut

[b] Adult standalone hospitals excluding adult facilities with a neonatal intensive care unit

[c] Mixed hospitals provide both adult and paediatric care

[d] Paediatric standalone hospitals excluding mixed facilities with women's and obstetric wards

Table 2: Number of device and surgical procedure-related healthcare-associated infection, by type and year, 2020–2024

Infection type	2020	2021	2022	2023	2024	Total 2020–2024
ICU-CLABSI	273	416	356	435	366	1,846
CSF shunt SSI	22	20	28	14	19	103
Paediatric cardiac SSI	37	35	25	52	50	199
Hip and knee SSI	85	126	166	165	170	712
Total infections	417	597	575	666	605	2,860

Abbreviations: CLABSI, central line-associated bloodstream infections; CSF, cerebrospinal fluid; ICU, intensive care unit; SSI, surgical site infection

adult mixed ICUs (65.9%, n=1,846) and NICUs (17.3%, n=484), reflecting higher site participation in CLABSI surveillance in these ICU settings. Patient demographics and outcomes for ICU-related CLABSIs are summarized in **Table 4**. Among patients with CLABSIs in adult ICUs, the median age was older in the adult CVICU compared to adult mixed ICUs ($p<0.001$). Across all ICU settings, the majority of those with CLABSIs were male, ranging from 57.4% in the PICU to 68.2% in the adult CVICU. The median time from ICU admission to infection was longest in the PICU (28 days, IQR: 12–66 days) while shorter time periods were reported in all other ICU settings, ranging from 10–14 days ($p<0.001$).

Trends over time: From 2020 to 2024, adult mixed ICUs had the highest overall CLABSI rates (1.89 infections per 1,000 line days), followed by PICUs (1.88 infections per 1,000 line days), NICUs (1.66 infections per 1,000 line days) and adult CVICUs (0.97 infections per 1,000 line days) (Appendix, **Table A1**). From 2020 to 2024 in adult ICU settings, CLABSIs rates fluctuated for adult mixed ICUs (1.74–1.82 infections per 1,000 line days, $p=0.45$) and adult CVICUs (0.80–1.19 infections per 1,000 line days, $p=0.57$) (**Figure 1**). Both adult mixed ICU CLABSI and adult CVICU rates peaked in 2021 with a rate of 2.14 and 1.27 infections per 1,000 line days, respectively. Catheter utilization from 2020 to 2024 ranged from 70.1%–74.2% in adult mixed ICUs and 66.4%–87.0% in adult CVICUs (data available on request).

Table 3: Distribution and rank of the most frequently reported gram-negative, gram-positive and fungal pathogens, 2020–2024[a]

Pathogen category	Rank	Pathogen	ICU-CLABSI N=3,111		Hip and knee N=805		CSF shunt N=111		Paediatric cardiac N=156	
			n	%	n	%	n	%	n	%
Gram-positive	1	Coagulase-negative staphylococci[b]	678	21.8	139	17.3	33	29.7	22	14.1
	2	*Enterococcus* spp.	666	21.4	50	6.2	2	1.8	1	0.6
	3	*Staphylococcus aureus*[c]	305	9.8	315	39.1	32	28.8	92	59.0
	4	*Streptococcus* spp.	65	2.1	70	8.7	4	3.6	11	7.1
	Other gram-positive[d]		139	4.5	59	7.3	15	13.5	8	5.1
	Total gram-positive		1,853	59.6	633	78.6	86	77.5	134	85.9
Gram-negative	1	*Klebsiella* spp.	173	5.6	14	1.7	8	7.2	4	2.6
	2	*Escherichia coli*	132	4.2	25	3.1	3	2.7	0	0.0
	3	*Enterobacter* spp.	129	4.1	34	4.2	4	3.6	6	3.9
	4	*Pseudomonas* spp.	95	3.1	28	3.5	3	2.7	0	0.0
	5	*Serratia* spp.	58	1.9	14	1.7	2	1.8	2	1.3
	Other gram-negative[e]		182	5.9	52	6.5	3	2.7	3	1.9
	Total gram-negative		769	24.7	167	20.7	23	20.7	15	9.6
Fungi	1	*Candida albicans*	259	8.3	4	0.5	0	0.0	0	0.0
	2	Other *Candida* spp.[f]	215	6.9	1	0.1	2	0.9	7	4.5
	Other fungi[g]		15	0.5	0	0.0	0	0.0	0	0.0
	Total fungal		489	15.7	5	0.6	2	1.8	7	0.0
Total			3,111	100	805	100	111	100	156	100

Abbreviations: CLABSI, central line-associated bloodstream infections; CSF, cerebrospinal fluid; ICU, intensive care unit
[a] The number of pathogens may not equal the number of infections as each case of device-related and surgical site infection may include multiple pathogens
[b] Coagulase-negative staphylococci included *S. lugdunensis*, *S. haemolyticus*, *S. epidermidis*, *S. capitis*, *S. hominis* and *S. warneri*
[c] *Staphylococcus aureus* includes methicillin-resistant *S. aureus*, methicillin-susceptible *S. aureus* and unspecified *S. aureus*
[d] Other gram-positive pathogens included anaerobic gram-positive cocci, *Finegoldia magna*, *Clostridioides* spp., *Lactobacillus* spp. and others
[e] Other gram-negative pathogens included *Stenotrophomonas* spp., *Morganella morganii*, *Proteus mirabilis*, *Pantoea* spp., *Prevotella* spp., *Bacteroides fragilis* and others
[f] Other *Candida* spp. included *C. dubliniensis*, *C. glabrata*, *C. krusei*, *C. lusitaniae*, *C. parapsilosis* and *C. tropicalis*
[g] Other fungi included *Aspergillus* spp., *Trichophyton tonsurans* and unspecified fungi

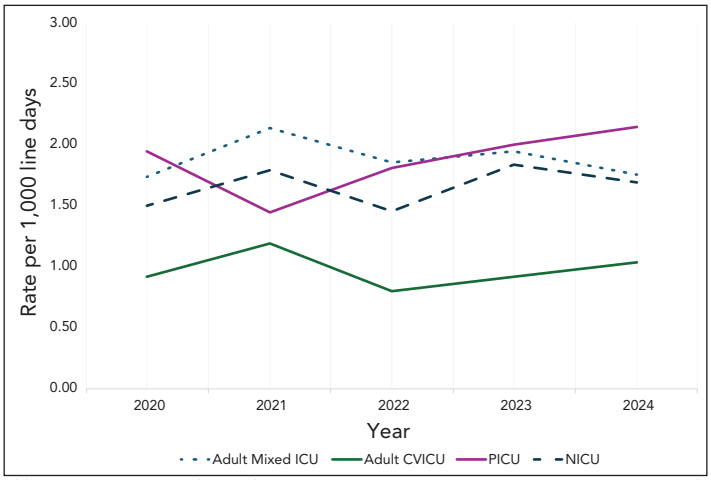
Table 4: Patient characteristics and outcomes of intensive care unit central line-associated bloodstream infections, 2020–2024

Characteristic	Adult mixed ICU (N=1,846)	Adult CVICU (N=182)	PICU (N=289)	NICU (N=484)
Age, median (IQR)	59 years (46 years–68 years)	65 years (52 years–72 years)	6 months (3 months–24 months)	21 days (9 days–52 days)
Sex, female/total (%)	582 (31.5%)	55 (30.2%)	123 (42.6%)	184 (38.0%)
Birthweight (g), median (IQR)	N/A	N/A	N/A	947 (IQR: 669–2,130)
Gestational age (weeks), median (IQR)	N/A	N/A	N/A	27.0 (IQR: 24.1–34.0)
Days from ICU admission to infection, median (IQR)	11 (IQR: 6–21)	10 (IQR: 6–18)	28 (IQR: 12–66)	15 (IQR: 8–38)
Deaths, thirty-day all cause (%)	606 (32.9%)	58 (31.9%)	28 (9.7%)	51 (10.6%)

Abbreviations: CVICU, cardiovascular surgery intensive care unit; ICU, intensive care unit; IQR, interquartile ranges; NICU, neonatal intensive care unit; N/A, not applicable; PICU, paediatric intensive care unit

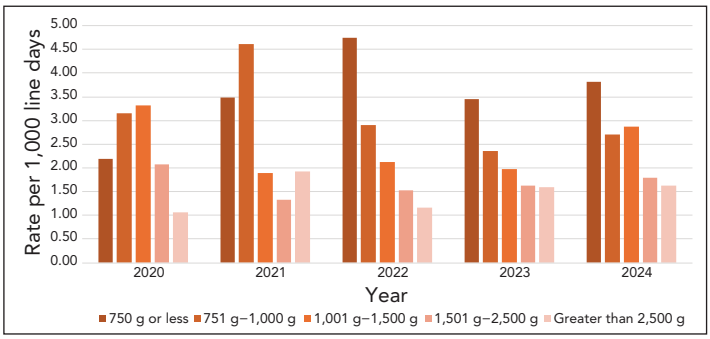
In paediatric ICUs, NICU and PICU CLABSIs fluctuated from 2020 to 2024, with NICU CLABSI rates ranging between 1.46 to 1.84 infections per 1,000 line days (Figure 1). In addition, PICU CLABSIs were lowest in 2021 (1.45 infections per 1,000 lines days), followed by increases in each year from 2022 to 2024 (Figure 1). Of the 65.7% (n=318/484) of NICU CLABSI cases from participating sites with birthweight-specific data, rates of CLABSIs in the NICU per 1,000 line days were highest among the infants with lower birthweight (1,000 g or less) from 2020 to 2024, peaking in 2022 for 750 g or less (4.75 infections per 1,000 lines days), with rates generally decreasing as birthweight increased (**Figure 2**). Catheter utilization in PICUs ranged from

Figure 1: Rate of central line-associated bloodstream infection per 1,000 line days by intensive care unit type, 2020–2024



Abbreviations: CVICU, cardiovascular intensive care unit; ICU, intensive care unit; NICU, neonatal intensive care unit; PICU, paediatric intensive care unit

Figure 2: Rate of neonatal intensive care unit central line-associated bloodstream infections per 1,000 line days by birthweight, 2020–2024



58.9%–66.6% from 2020 to 2024 while NICU had the lowest catheter utilization overall during the same time period, ranging from 28.1%–29.5% (data available on request).

All-cause mortality at thirty days was highest in the adult mixed ICU and adult CVICU at 32.8% and 31.9%, respectively, while thirty-day all-cause mortality ranged from 9.7%–10.6% in paediatric and neonatal ICU settings. The most commonly identified pathogens among ICU-CLABSIs overall were CoNS (21.8%) and *Enterococcus* spp. (21.4%), which aligned with the most commonly identified pathogens among adult mixed ICUs and adult CVICUs. Among PICU and NICU CLABSIs, the most commonly identified pathogens were CoNS and *S. aureus* (data available on request).

Hip and knee surgical site infections

Infection characteristics: Between 2020 and 2024, a total of 712 complex hip and knee SSIs were reported, with hip arthroplasties accounting for most of the cases (n=440, 61.8%). Among these SSIs, 51.8% (n=369) were organ/space infections, while 48.2% (n=343) were deep incisional infections (**Table 5**). The median patient age was 69 years (IQR: 60–77 years) for hip SSIs and 67 years (IQR: 61–75 years) for knee SSIs. The median time from procedure to infection onset was 23 days (IQR: 16–36 days) for hip SSIs and 24 days (IQR: 18–37 days) for knee SSIs. The median length of stay was two days for hip (IQR: 1–7.5 days) and one day for knee (IQR: 1–3 days) SSIs.

Table 5: Frequency of hip and knee surgical site infections by year and infection type, 2020–2024

Year	Deep incisional SSI		Organ/space SSI		All cases
	n	%	n	%	n
Hip arthroplasty					
2020	22	45.8	26	54.2	48
2021	44	49.4	45	50.6	89
2022	48	46.2	56	53.9	104
2023	47	52.2	43	47.8	90
2024	54	49.5	55	50.5	109
Overall	215	48.9	225	51.1	440
Knee arthroplasty					
2020	14	37.8	23	62.2	37
2021	23	62.2	14	37.8	37
2022	34	54.8	28	45.2	62
2023	34	45.3	41	54.7	75
2024	23	37.7	38	62.3	61
Overall	128	47.1	144	52.9	272

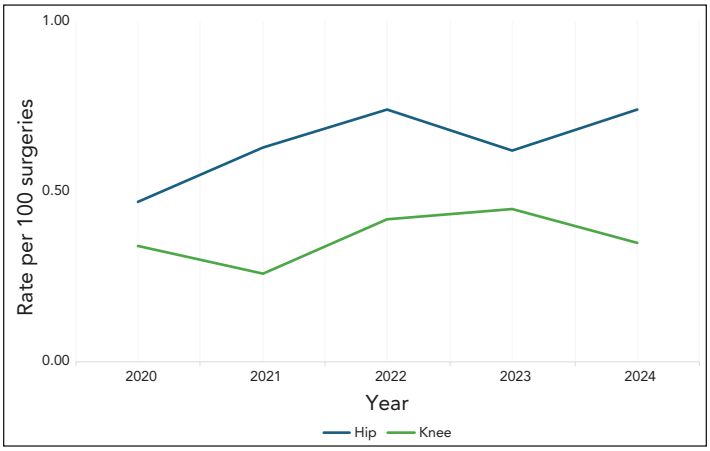
Abbreviation: SSI, surgical site infection

Trends over time: Between 2020 and 2023, knee SSI rates increased non-significantly by 32.4% (0.34–0.45 infections per 100 surgeries, p=0.31), before decreasing to a rate of 0.35 infections per 100 surgeries in 2024. Hip SSI rates fluctuated between 0.47 and 0.74 infections per 100 surgeries (p=0.31) (**Figure 3**; Appendix, **Table A2**). Most patients (74.0%, n=527/712) with a hip or knee SSI were readmitted and 65.3% (n=465/712) required revision surgery. Within 30 days after the first positive culture, 15 all-cause deaths (3.5%, n=15/440) were reported among patients with a complex SSI following a hip arthroplasty, while no deaths were reported among knee arthroplasty SSI patients. The most common pathogens identified among hip and knee SSIs were *S. aureus* (39.1%) and CoNS (17.3%) (Table 3), with no significant differences by infection type.

Cerebrospinal fluid shunt surgical site infections

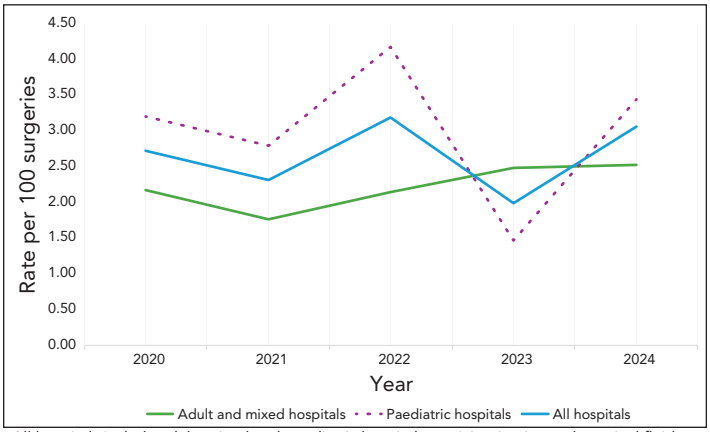
Infection characteristics: Between 2020 and 2024, a total of 103 CSF shunt SSIs were reported. The median patient age was 49 years (IQR: 34–66 years) for adult patients and two years (IQR: 0.3–11 years) for paediatric patients. The median time from procedure to infection onset was 19 days (IQR: 8–40 days). More than half of CSF shunt SSIs (54.4%, n=56/103) were identified from new surgeries, while 45.6% (n=47/103) were from revision surgeries. Women represented 46.6% (n=48/103) of cases.

Figure 3: Rate of hip and knee surgical site infections per 100 surgeries, 2020–2024



Trends over time: The overall rate of CSF shunt SSIs was 2.64 infections per 100 surgeries (range: 1.99–3.19 infections per 100 surgeries; Appendix, **Table A3**). Paediatric and adult/mixed hospitals infection rates were not significantly different at 3.07 and 2.18 infections per 100 surgeries, respectively (p=0.15). From 2020 to 2024, no significant trend was observed in CSF shunt SSI rates for adult and mixed hospitals (range: 1.76–2.53 infections per 100 surgeries, p=0.88), paediatric hospitals (range: 1.47–4.18 infections per 100 surgeries, p=0.11) and all hospital types combined (p=0.50) (**Figure 4**). The most common pathogens identified from CSF shunt SSIs were CoNS (29.7%) and *S. aureus* (28.8%) (Table 3). Outcome data were not collected for CSF shunt SSI surveillance.

Figure 4: Cerebrospinal fluid shunt surgical site infection rates per 100 surgeries by hospital type[a], 2020–2024



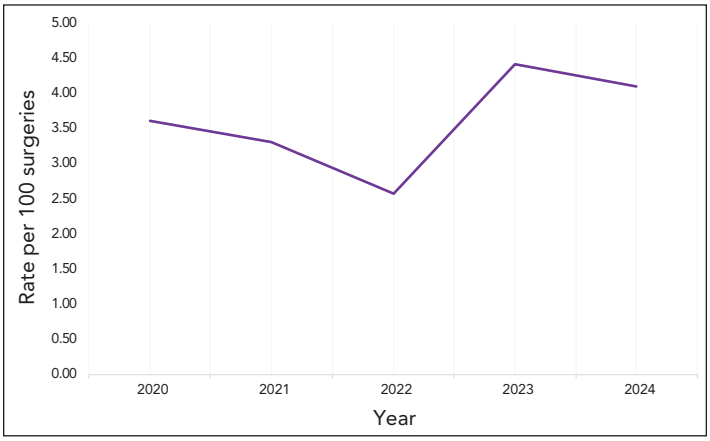
[a] All hospitals include adult, mixed and paediatric hospitals participating in cerebrospinal fluid shunt surgical site infection surveillance

Paediatric cardiac surgical site infections

Infection characteristics: Between 2020 and 2024, a total of 199 paediatric cardiac SSIs were reported (**Table 6**). Most infections were superficial incisional SSIs (68.8%), followed by organ/space infections (21.1%) and deep incisional infections (10.1%). The median patient age was 69 days (IQR: 8–365 days) and the median time from surgery to infection onset was 14 days (IQR: 8–22 days) (data available on request). The proportion of deep incisional infections increased from 5.4% in 2020 to 15.4% in 2023, followed by a decrease to 8.0% in 2024; however, the increase observed between 2020 and 2023 was not significant (p=0.09, Table 6).

Trends over time: The overall paediatric cardiac SSI rate was 3.61 infections per 100 surgeries, with annual rates fluctuating between 2.59 and 4.43 infections per 100 surgeries (**Figure 5**; Appendix, **Table A4**). No significant trend was observed during this five-year period. From 2020 to 2024, at 30 days post-infection, 70.0% of patients had been discharged. Five deaths (2.5% of cases) were reported within 30 days of infection onset, including one death indirectly attributable to the paediatric cardiac SSI (data available on request). The most common pathogens identified among paediatric cardiac SSIs were *S. aureus* (59.0%) and CoNS (14.1%).

Figure 5: Paediatric cardiac surgical site infection rates per 100 surgeries, 2020–2024



Antibiogram

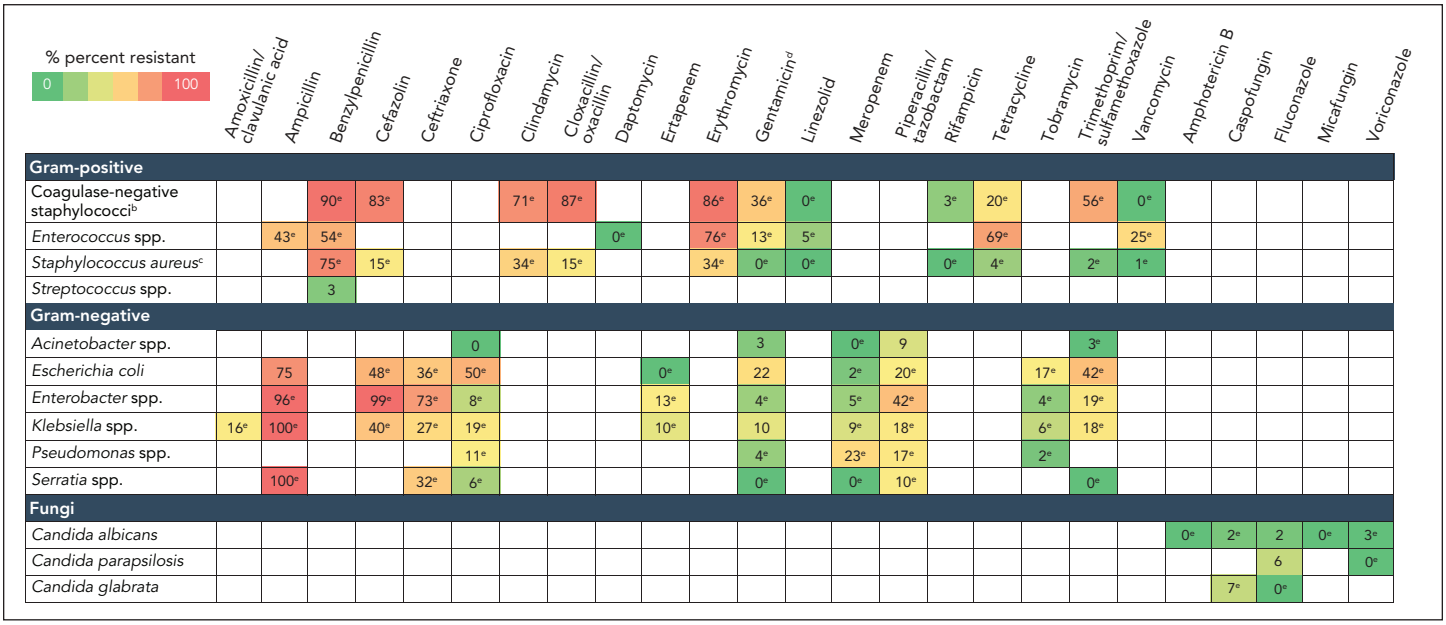
Results of antimicrobial susceptibility testing for the most frequently identified gram-positive, gram-negative and fungal pathogens from device and surgical procedure-related HAIs are listed in **Figure 6** and **Figure 7**. The *S. aureus* isolates were resistant to cloxacillin/oxacillin (MRSA) in 15.1% (n=32/212) of ICU-CLABSIs and 11.1% (n=41/370) of SSIs. Meropenem resistance ranged from 0% to 23% in gram-negative pathogens identified from ICU-CLABSIs. No meropenem resistance was observed among pathogens isolated from SSIs. Ninety-seven vancomycin-resistant *Enterococci* were identified among ICU-CLABSIs (24.8%, n=97/391).

Table 6: Paediatric cardiac surgical site infection rates by year and infection type, 2020–2024

Year	Superficial incisional SSI cases		Organ/space SSI cases		Deep incisional SSI cases		All cases[a]
	n	%	n	%	n	%	n
2020	29	78.4%	6	16.2%	2	5.4%	37
2021	23	65.7%	9	25.7%	3	8.6%	35
2022	16	64.0%	6	24.0%	3	12.0%	25
2023	32	61.5%	12	23.1%	8	15.4%	52
2024	37	74.0%	9	18.0%	4	8.0%	50
Overall	137	68.8%	42	21.1%	20	10.1%	199

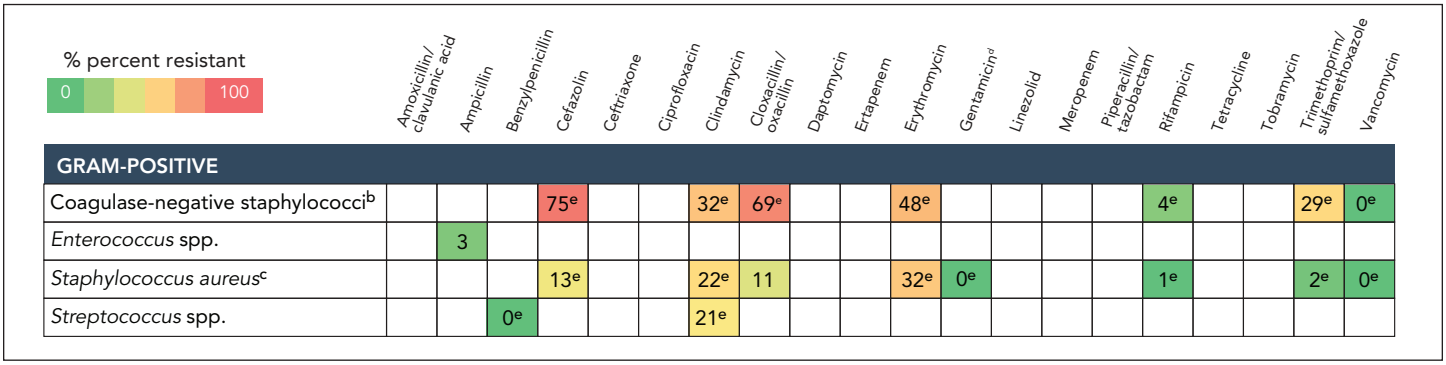
Abbreviation: SSI, surgical site infection
[a] Excludes cases with missing infection type information

Figure 6: Antibiogram results[a] from pathogens identified from intensive care unit central line-associated bloodstream infections, 2020–2024[b,c,d,e]



[a] Antibiotic/organism combinations with fewer than 30 tests were excluded
[b] Coagulase-negative staphylococci included *S. lugdunensis*, *S. haemolyticus*, *S. epidermidis*, *S. capitis*, *S. hominis* and *S. warneri*
[c] *Staphylococcus aureus* included methicillin-susceptible *S. aureus* and methicillin-resistant *S. aureus* (MRSA)
[d] Gentamicin synergy for gram-positive organisms
[e] Less than 90% of isolates were tested

Figure 7: Antibiogram results[a] from pathogens identified from hip and knee, cerebrospinal fluid shunt and paediatric cardiac surgical site infections, 2020–2024[b,c,d,e]



[a] Antibiotic/organism combinations with fewer than 30 tests were excluded
[b] Coagulase-negative staphylococci included *S. lugdunensis*, *S. haemolyticus*, *S. epidermidis*, *S. capitis*, *S. hominis* and *S. warneri*
[c] *Staphylococcus aureus* included methicillin-susceptible *S. aureus* and methicillin-resistant *S. aureus* (MRSA)
[d] Gentamicin synergy for gram-positive organisms
[e] Less than 90% of isolates were tested

Discussion

Between 2020 and 2024, there were up to 67 unique hospitals submitted device (ICU-CLABSI) and surgical procedure-related infection data, including 1,846 ICU-CLABSIs and 1,014 surgical procedure-related infections. A total of 3,111 pathogens were identified from ICU-CLABSIs and 1,072 pathogens from surgical procedure-related cases between 2020 and 2024. Similar to what has been reported in past CNISP surveillance, reports (10–12), the majority of these pathogens were gram-positive and the most commonly reported pathogens were coagulase-negative staphylococci and *S. aureus*.

Intensive care unit central line-associated bloodstream infections

Overall rates of CLABSIs in adult ICUs from 2020 to 2024 (1.89 and 0.97 infections per 1,000 line days in adult mixed ICUs and CVICUs, respectively) were lower than the ICU-CLABSI rates reported from adult ICUs in England during the same period (ranging from 1.8 to 3.6 infections per 1,000 line days) (13). Conversely, CNISP adult ICU CLABSI rates and were higher than quarterly rates reported from 12 adult ICUs in Western Australia (range: 0–0.63 infections per 1,000 line days) (14). Comparisons made between CNISP data and those from other jurisdictions should be interpreted with caution, as data collection is not standardized; therefore, there may be differences in the two populations being compared.

The incidence of CLABSIs in paediatric and neonatal ICUs reported via CNISP was higher compared to England, where rates decreased from fiscal years 2020 to 2024 (1.0 and 0.8 infections per 1,000 line days, respectively) (10). Neonatal ICU-CLABSI rates reported in South Korea from 2020–2022 were 12% lower compared to rates reported by CNISP during the same time period (1.39 vs. 1.58 infections per 1,000 line days) (15).

Differences in catheter utilization ratios likely contributed to the observed variation in CLABSI burden across ICU settings, with higher catheter utilization ratios in adult ICUs (66%–87%) compared to the lowest in the NICU (28%–30%). Thirty-day all-cause mortality was highest in adult ICUs (32%–33%), consistent with greater baseline severity, while paediatric and neonatal mortality remained substantially lower (9.7%–11%), representing different population risk profiles across ICU settings. Thirty-day all-cause mortality was highest in adult ICUs (32%–33%), consistent with greater baseline severity, while paediatric and neonatal mortality remained substantially lower (9.7%–11%). Day-all-cause mortality was highest in adult ICUs (32%–33%), consistent with greater baseline severity, while paediatric and neonatal mortality remained substantially lower (9.7%–11%).

Surgical site infections

Hip and knee surgical site infections: Hip SSI rates fluctuated across reporting years, while knee SSI rates increased non-significantly from 2020 and 2023, before decreasing again in 2024. Hip and knee SSI rates demonstrate ongoing variation across jurisdictions. Long term trends from England's National Health Service hospitals show a continued steady decline in inpatient hip and knee SSI incidence over the past decade from 2015 to 2025 (16). From 2020 to 2024, hip SSI rates in Western Australia were higher than those reported by CNISP (0.75 vs. 0.64 infections per 100 surgeries), while knee SSI rates were lower (0.29 vs. 0.36 per 100 surgeries) (14).

Cerebrospinal fluid shunt surgical site infections: The overall rate of SSIs from CSF shunts was 2.65 per 100 surgeries from 2020 to 2024. The rate is similar to what was previously reported by CNISP from 2019 to 2023 (2.89 per 100 surgeries); however, differences may reflect changes in hospital participation (two fewer hospitals participated in reporting CSF shunt SSIs in 2024 at the time of this study) (10). A national survey conducted in England in 2017 reported a mean brain shunt infection rate of 1.9% (range: 0%–4.4%), which is lower than the overall rate reported by CNISP (17). In contrast, a retrospective single-center study in Sweden reported a higher shunt infection rate of 4.8% in adult hydrocephalus patients who underwent surgery between 2013 and 2019 (18).

Cerebrospinal fluid shunt infection rates vary widely by population (paediatric vs adult), centre and country (18). Combined with a lack of recent literature, comparisons of the data in this report with other regions is limited; therefore, CSF shunt SSIs reported during this time period were compared with previously published CNISP surveillance data (10,11,19). Consistent with earlier findings, CSF shunt SSI rates fluctuated from 2020 to 2024 (10,11,19). The rates observed from 2020 to 2024 were lower than those reported in earlier periods (2000–2002) for both paediatric (3.1% vs 4.9%) and adult patients (2.2% vs 3.2%), similar to the most recent published report (10,19).

Paediatric cardiac surgical site infections: From 2020 to 2024, CNISP hospitals reported an overall paediatric cardiac SSI rate of 3.7 infections per 100 surgeries, with no significant trend observed over the five-year period. Due to a lack of published national reports from other jurisdictions, these data could not be compared directly with other countries. Single-center studies from several jurisdictions have observed varied rates of paediatric cardiac SSIs: from 0.9 infections per 100 surgeries in a California, United States centre (20) to 1.97 in a single centre in Ontario, Canada from 2022 to 2023 (21), to 4.34 in a centre in Chile from 2015 to 2020 (22). However, these studies may not be representative of the entire nation. When compared to previously published CNISP surveillance data, rates of paediatric cardiac SSIs have remained relatively unchanged since data collection began in 2010. From 2011 to 2020, the rate of infection was 3.5 per 100 surgeries (11).

Antibiogram

Meaningful comparisons with other regions are limited by gaps in recent literature and variation in how antibiogram data are reported for device-related and surgical procedure-related infections. To address this, we compared 2020–2024 data with CNISP surveillance data from 2011 to 2020; however, since the time periods overlap, observed changes may not reflect true trends and should be interpreted with caution (11). The percentage of *S. aureus* isolates that were MRSA among ICU-CLABSIs (15%) and SSIs (11%) in the CNISP network remained relatively stable over the 2020–2024 period compared to previous surveillance data from 2011 to 2020, where MRSA accounted for 15% of ICU-CLABSIs and 14% of SSIs. Among *Enterococcus* spp. identified in ICU-CLABSIs, 25% were vancomycin-resistant *Enterococci*, compared to 16% in 2011–2020 (11). During the 2011–2020 time period, results for meropenem resistance in *Pseudomonas* spp. identified in ICU-CLABSIs were not available; however, in later CNISP surveillance reports, a decrease in resistance was observed; from 38% in 2018–2022 to 30% in 2019–2023 to 23% in 2020–2024 (10,12). Meropenem resistance among other gram-negative pathogens identified in ICU-CLABSIs ranged from 0% to 9% in 2020–2024 and from 2% to 7% in 2011–2020 (11).

Strengths and limitations

The main strength of CNISP surveillance is the standardized collection of detailed epidemiological and molecular-linked data from a large representative network of sentinel hospitals from across Canada. From 2020 to 2024, CNISP coverage of Canadian acute care beds has increased from 35% to 49%, including increased representativeness in northern, community, rural and Indigenous populations. To further improve representativeness, CNISP has launched a simplified dataset accessible to all acute care hospitals across Canada to collect and visualize annual HAI rate data. Despite the increased representativeness of CNISP surveillance data, the number of hospitals participating in each HAI surveillance project differed and epidemiologic data collected were limited to the information available in the patient charts. For CLABSI surveillance, data were limited to infections occurring in the ICU settings and, as such, may represent only a subset of CLABSIs occurring in the hospital. Furthermore, when comparing our infection rates with data from other countries, several limitations must be considered, including differences in surveillance methodologies, patient populations and number and types of hospitals under surveillance.

Conclusion

This report summarizes 1,846 device-related infections and 1,014 surgical procedure-related infections as well as antibiogram data identified over five years of surveillance, 2020–2024, from up to 67 hospitals across Canada. During this time, rates of device- and surgical procedure-related HAIs have fluctuated from year to year with no significant trend throughout the study period. The collection and analysis of national surveillance data are important to understanding and reducing the burden of device and surgical procedure-related HAIs. These data provide benchmark rates for national and international comparison and inform antimicrobial stewardship and infection prevention and control programs and policies.

Authors' statement

Canadian Nosocomial Infection Surveillance Program hospitals provided expertise in the development of protocols in addition to the collection and submission of epidemiological and microbiological data. Epidemiologists from Public Health Agency of Canada were responsible for the conception, analysis, interpretation, drafting and revision of the article.

Competing interests

None.

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Appendix

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

Case definitions
Table A1: Rate of central line-associated bloodstream infection per 1,000 line days by intensive care unit type, 2020–2024
Table A2: Rate of hip and knee surgical site infections per 100 surgeries, 2020–2024
Table A3: Cerebrospinal fluid shunt surgical site infection rates per 100 surgeries by hospital type, 2020–2024
Table A4: Paediatric cardiac surgical site infection rates per 100 surgeries, 2020–2024

Healthcare-associated infections and antimicrobial resistance in Canadian acute care hospitals, 2020–2024

Canadian Nosocomial Infection Surveillance Program[1]*

Abstract

Background: Healthcare-associated infections (HAIs) and antimicrobial resistance (AMR) continue to contribute to excess morbidity and mortality among Canadians.

Objective: To describe epidemiologic and laboratory characteristics and trends of HAIs and AMR, 2020–2024, using surveillance and laboratory data submitted by hospitals to the Canadian Nosocomial Infection Surveillance Program (CNISP) and by provincial and territorial laboratories to the National Microbiology Laboratory.

Methods: Data was collected from 109 Canadian sentinel acute care hospitals between January 1, 2020 and December 31, 2024 for *Clostridioides difficile* infections (CDI), methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections (BSIs), vancomycin-resistant *Enterococcus* (VRE) BSIs (specifically *Enterococcus faecalis* and *Enterococcus faecium*), carbapenemase-producing *Enterobacterales* (CPE) and carbapenemase-producing *Acinetobacter baumannii* (CPA) infections and colonizations and *Candidozyma auris* (*C. auris*; formerly *Candida auris*) infections. Trend analysis for case counts, incidence rates (rates), outcomes, molecular characterization and AMR profiles are presented.

Results: From 2020 to 2024, rates remained relatively stable for CDI (range: 5.01–5.38 infections per 10,000 patient days) and MRSA BSI (range: 0.99–1.16 infections per 10,000 patient days) and increased significantly for VRE BSIs (from 0.30 to 0.42 infections per 10,000 patient days; p=0.01). During this time, infection rates for CPE remained low compared to other HAIs but increased significantly (rates: 0.05–0.20; p=0.03), CPA counts continue to remain very low (n=22 infections) and *C. auris* counts remained low compared to other HAIs (n=43 isolates).

Conclusion: The incidence of MRSA BSIs and CDI remained stable and VRE BSIs and CPE infections increased in the Canadian acute care hospitals participating in CNISP. An increased number of *C. auris* isolates were identified. Reporting standardized surveillance data to inform the application of infection prevention and control practices in acute care hospitals is critical to help decrease the burden of HAIs and AMR in Canada.

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Keywords: healthcare-associated infections, community-associated infections, antimicrobial resistance, surveillance, *Clostridioides difficile* infection, methicillin-resistant *Staphylococcus aureus*, vancomycin-resistant *Enterococcus*, carbapenemase-producing *Enterobacterales*, *Escherichia coli*, *Candidozyma auris*, Canadian Nosocomial Infection Surveillance Program

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Introduction

Though often preventable, healthcare-associated infections (HAIs) represent one of the most common adverse events experienced by patients in acute care settings globally (1). In addition to increasing morbidity and mortality, HAIs are associated with longer lengths of stay in hospitals and higher costs of care (1). In Canada, a point prevalence survey conducted in 2024 estimated that the prevalence of patients with at least one HAI was 8.1% (2). The prevalence of HAIs in 2019–2023 has been estimated to be 7.6% in England, 8.0% in Europe and 9.9% in Australia (3–5).

Many microorganisms responsible for HAIs exhibit high levels of antimicrobial resistance (AMR), and rising resistance rates threaten progress in reducing HAI incidence (6). Infections caused by resistant organisms carry an estimated 85% higher risk of death compared to infections by susceptible organisms, and in 2019, bacterial AMR infections were linked to roughly five million deaths worldwide (7,8). Evidence from Canada and other countries demonstrates that healthcare-associated (HA) methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections (BSIs) lead to substantial morbidity and mortality, longer hospitalizations and increased healthcare costs (9–12). The prevalence of AMR is projected to reach 40% by 2050 (13). Under this scenario, an estimated 13,700 Canadians could die annually from resistant infections, with an associated economic burden of $21 billion per year to Canada's Gross Domestic Product (GDP) (13). In addition, newly emerging resistant organisms, such as *Candidozyma auris* (*C. auris*; formerly *Candida auris*), have prompted the need for strengthened surveillance and revisions to existing infection prevention and control practices (14).

In Canada, the Public Health Agency of Canada (PHAC) collects national data on various HAIs and AMR through the Canadian Nosocomial Infection Surveillance Program (CNISP). In line with the World Health Organization (WHO)'s core components of infection prevention and control (15), CNISP performs consistent, standardized surveillance to reliably estimate HAI burden, establish benchmark rates for national and international comparison, identify potential risk factors and assess and inform specific interventions to improve patient health outcomes. Data provided by CNISP directly support the collaborative goals outlined in the *Pan-Canadian Action Plan on Antimicrobial Resistance* (16) and provides vital information on many of the AMR pathogens included in Canada's 2025 priority antimicrobial-resistant pathogens list (17).

This report describes the most recent HAI and AMR surveillance data collected from CNISP participating hospitals between 2020 and 2024.

Methods

Design

Established in 1994, CNISP is a collaboration between the PHAC, the Association of Medical Microbiology and Infectious Disease Canada and sentinel hospitals from across Canada. The goal of CNISP is to facilitate and inform the prevention, control and reduction of HAIs and AMR organisms in Canadian acute care hospitals through active surveillance and reporting. The CNISP conducts prospective, sentinel surveillance for HAIs (including AMR organisms) (18).

Case definitions

Standardized case definitions for HA and community-associated (CA) infections were used. The 2024 surveillance case definition and eligibility criteria are available upon request from the author.

Data sources

Between January 1, 2020 and December 31, 2024, participating hospitals submitted epidemiologic data and isolates for cases meeting the respective case definitions for *Clostridioides difficile* infections (CDIs), MRSA BSIs, vancomycin-resistant *Enterococcus* (VRE) BSIs (specifically *Enterococcus faecalis* and *Enterococcus faecium*), carbapenemase-producing *Enterobacterales* (CPE) and carbapenemase-producing *Acinetobacter baumannii* (CPA) (infections or colonizations). *Candidozyma auris* isolates (infections or colonizations) were identified by provincial and territorial laboratories and participating hospital laboratories.

In 2024, 109 hospitals in 10 provinces and one territory participated in HAI surveillance and are further described in **Table 1**. Hospital participation varied by surveillance project and year (Supplemental material is available upon request from the author). In 2024, CNISP HAI surveillance, patient admissions were categorized according to hospital bed size; small (1–200 beds, n=56 sites, 51.3%), medium (201–499 beds, n=33 sites, 30.3%) or large (500 or more beds, n=20 sites, 18.3%). Overall, 44 sites (40%) were in Western Canada (British Columbia, Alberta, Saskatchewan and Manitoba), 38 (35%) were in Central Canada (Ontario and Québec), 26 (24%) were in Eastern Canada (Nova Scotia, New Brunswick, Prince Edward Island and Newfoundland and Labrador) and one (0.9%) was in Northern Canada (Yukon, Northwest Territories and Nunavut) (Table 1). In addition to adult, mixed and paediatric hospital types reported in previous years, CNISP added two additional categories of hospital type in 2024. Adult-neonatal intensive care unit (Adult-NICU) and paediatric-obstetric (Paediatric-OB) were added as hospital types to better characterise the patient population served by those facilities.

Table 1: Summary of hospitals participating in the Canadian Nosocomial Infection Surveillance Program, by region, 2024

Hospital characteristics	Region				Total
	Western[a]	Central[b]	Eastern[c]	Northern[d]	
Total number of hospitals	44	38	26	1	109
Hospital type					
Adult[e]	20	15	16	0	51
Adult-NICU	2	6	0	0	8
Mixed[f]	17	11	8	1	37
Paediatric[g]	4	4	1	0	9
Paediatric-OB	1	2	1	0	4
Hospital size					
Small (1–200 beds)	20	13	22	1	56
Medium (201–499 beds)	15	15	3	0	33
Large (500 or more beds)	9	10	1	0	20
Admissions and discharge					
Total number of beds	13,164	13,429	3,207	26	29826
Total number of admissions	634,776	583,028	112,601	1,935	1,332,340
Total number of patient days	5,148,759	4,455,471	1,038,466	6,405	10,649,101

Abbreviations: NICU, neonatal intensive care unit; OB, obstetric
[a] Western refers to British Columbia, Alberta, Saskatchewan and Manitoba
[b] Central refers to Ontario and Québec
[c] Eastern refers to Nova Scotia, New Brunswick, Prince Edward Island and Newfoundland and Labrador
[d] Northern refers to Yukon, Northwest Territories and Nunavut
[e] Adult standalone hospitals excluding adult facilities with a neonatal intensive care unit
[f] Mixed hospitals provide both adult and paediatric care
[g] Paediatric standalone hospitals excluding mixed facilities with women's and obstetric wards

Epidemiologic (demographic, clinical and outcomes) and denominator data (patient days and patient admissions) were collected and submitted by participating hospitals through the Canadian Network for Public Health Intelligence—a secure online data platform.

Reviews of standardized protocols and case definitions are conducted annually by established infectious disease expert working groups; training for data submission is provided to participating CNISP hospital staff as required. Data quality for surveillance projects is periodically evaluated; additional details on the methodology have been published previously (19,20).

Laboratory data

All patient-linked laboratory isolates (stool samples for CDI cases) were sent to the PHAC's National Microbiology Laboratory for molecular characterization and antimicrobial susceptibility testing. Isolates for MRSA BSIs, VRE BSIs, CPE/CPA (infections or colonizations), *C. auris* (infections/colonizations) and paediatric CDIs were submitted year-round. Adult CDI isolates were submitted annually during a targeted two-month period (March 1 to April 30).

Statistical analysis

Rates of HAI were calculated by dividing the total number of cases identified in patients admitted to CNISP participating hospitals by the total number of patient admissions (multiplied by 1,000) or patient days (multiplied by 10,000). Due to low case numbers, rates for *C. auris* and CPA were not calculated. The HAI rates are reported nationally and by region. Due to the low number of CA-VRE BSI cases reported each year, stratified rates as well as mortality rates and laboratory results for CA-VRE BSIs were not included in this report. Sites that were unable to provide case data were excluded from rate calculations and missing denominator data were estimated using their previous years reported data, where applicable. Missing epidemiological and molecular data were excluded from analysis. The Mann-Kendall test was used to assess monotonic trends in rates over time. The chi-square test for trend was used to analyze trends in proportions over time. The chi-square test was used to compare two categorical variables, while the t-test was used to compare differences between groups. Significance testing was two-tailed and differences were considered significant at $p \leq 0.05$. The stability of rates over time indicates that there was no statistically significant trend observed. Where available, all-cause mortality were reported for HAIs. All-cause mortality rate was defined as the number of deaths per 100 HAI cases 30 days following positive culture.

Results

Clostridioides difficile infection

Between 2020 and 2024, overall CDI rates remained stable, ranging from 5.01 to 5.38 infections per 10,000 patient days. The rates appeared to decline from 5.38 in 2020 to 5.01 in 2022, followed by a modest increase to 5.19 in 2024; however, no significant trend was observed (p=0.81) (**Table 2**). The median age among CDI patients was 69 years (interquartile range [IQR]: 56–79), with males and females each representing 50.3% of the total cases (Supplemental material).

Source of infection: Stratified by the source of infection, HA-CDI rates decreased from 3.89 per 10,000 patient days in 2020 to 3.60 in 2021, followed by a period of relative stability through 2024 (3.69 per 10,000 patient days), Overall, no significant trend was observed (p=1.00) (Table 2). The CA-CDI rates remained stable over the five-year period. After holding constant at 1.43 per 1,000 patient admissions in 2020 and 2021, the rate was lowest in 2022 (1.40 per 10,000 patient days) before a small increase to 1.47 by 2024 (p=0.61) (Table 2).

Regionally, HA-CDI rates per 10,000 patient days fluctuated across all regions between 2020 and 2024, with no significant trend (Western range: 3.00–3.46, p=1.00; Central range: 3.48–3.82, p=0.09; Eastern range: 3.19–3.56, p=0.22). For CA-CDI, rates per 1,000 patient admissions remain highest in the Central region, with a downward trend from 2020 and 2024 (range: 1.54–1.70, p=0.11), while the Western region showed an upward trend, from 1.11 to 1.45 with a peak of 1.61 in 2023 (p=0.46). The CA-CDI rate in the Eastern region remained relatively stable, with a minor increase from 0.95 to 1.12 per 1,000 patient admissions (p=0.22). This indicates no statistically significant shift over the five-year period (Supplemental material).

Hospital types: The HA-CDI rates per 10,000 patient days were consistently higher in adult (range: 3.63–3.89) and paediatric hospitals (range: 3.34–3.97), with lower rates than observed

Table 2: *Clostridioides difficile* infection data, Canada, 2020–2024[a]

C. difficile infection data	Number of infections and incidence rates (per year)				
	2020	2021	2022	2023	2024
All cases					
Number of *C. difficile* infection cases	3,649	3,639	3,877	4,736	4,818
Rate per 1,000 patient admissions	4.16	3.97	4.18	4.16	4.17
Rate per 10,000 patient days	5.38	5.07	5.01	5.21	5.19
Number of reporting hospitals	81	81	81	99	97
All-cause mortality rate					
Number of deaths	43	66	64	76	76
All-cause mortality rate per 100 cases (%)[b]	9.0	8.8	8.9	8.2	8.0
HA-CDI					
Number of HA-CDI cases	2,624	2,570	2,818	3,310	3,409
Rate per 1,000 patient admissions	3.05	2.85	3.09	2.96	2.99
Rate per 10,000 patient days	3.89	3.60	3.66	3.66	3.69
Number of reporting hospitals	81	81	81	99	97
All-cause mortality rate					
Number of deaths	39	50	54	59	58
All-cause mortality rate per 100 cases (%)[b]	8.7	9.2	9.9	8.6	8.3
CA-CDI					
Number of CA-CDI cases	1,025	1,069	1,059	1,425	1,409
Rate per 1,000 patient admissions	1.43	1.43	1.40	1.51	1.47
Rate per 10,000 patient days	1.86	1.82	1.68	1.87	1.81
Number of reporting hospitals	70	70	70	88	86
All-cause mortality rate					
Number of deaths	15	16	10	16	16
All-cause mortality rate per 100 cases (%)[b]	9.6	7.4	5.8	6.4	6.9

Abbreviations: *C. difficile*, *Clostridioides difficile*; CA, community-associated; CDI, *Clostridioides difficile* infections; HA, healthcare-associated

[a] There was no resistance to tigecycline, vancomycin or metronidazole in *C. difficile* isolates submitted to the National Microbiology Laboratory 2019–2023

[b] Mortality data are collected during the two-month period (March and April of each year) for adults (aged 18 years and older) and year-round for children (aged one year to younger than 18 years old). Among paediatric patients, there was no death attributable to healthcare-associated *C. difficile* infection

in mixed hospitals (range: 2.56–3.09). The CA-CDI rates per 1,000 patient admissions were higher in adult (range: 1.74–1.82) and mixed hospital (range: 1.31–1.67), with lower rates observed in paediatric hospitals (range: 0.35–0.68) between 2020 and 2024 (Supplemental material). Stratified by hospital size, rates of HA-CDI were generally highest among large (range: 3.28–3.82), followed by medium (range: 3.20–3.60) and small size hospitals (range: 2.68–2.98). Rates of CA-CDI per 1,000 patient admissions were similar for large sized hospitals (range: 1.38–1.85) and medium sized hospitals (range: 1.39–1.52) and lower for small sized hospitals (range: 0.82–1.32), which follows a similar trend as HA-CDI (Supplemental material).

30-day all-cause mortality: Overall 30-day all-cause CDI mortality remained stable from 2020 to 2024 (range: 8.0–9.0, *p*=0.09) (Table 2). There was no significant difference in 30-day all-cause mortality between HA-CDI (8.3%) and CA-CDI (6.9%) in 2024 (*p*=0.51).

Antimicrobial resistance: From 2020 to 2024, 24.7% (n=608/2,458) of CDI isolates were resistant to one or more tested antimicrobials. The proportion of *C. difficile* isolates resistant to moxifloxacin fluctuated between 6.1% and 9.0%, with an average of 7.0% and 6.5% in 2024 (**Table 3**). Clindamycin resistance in HA and CA-CDI populations fluctuated from 2020 to 2024, with 2024 exhibiting the highest resistance rates at 34.0% and 30.7%, respectively (Supplemental material). None of 2,458 isolates tested was resistant to metronidazole, vancomycin or tigecycline.

Molecular typing: From 2020 to 2024, the five most prevalent ribotypes of isolates from HA-CDI cases were 106, 014, 020, 002 and 027, with overall prevalences of 15.9%, 8.7%, 7.0%, 5.7% and 4.8%, respectively, while the five most prevalent ribotypes of isolates from CA-CDI were 106, 014, 020, 002 and 015, with overall prevalences of 15.9%, 8.6%, 6.3%, 5.2% and 4.2%. From 2020 to 2024, the prevalence of RT027 associated with NAP1 decreased from 5.9% to 3.4% in HA-CDI but increased from 1.3% to 4.0% in CA-CDI (Supplemental material).

Methicillin-resistant *Staphylococcus aureus* bloodstream infections

Between 2020 and 2024, overall MRSA BSI rates remained stable, ranging from 0.99 to 1.16 infections per 10,000 patient days. The rate was lowest in 2022; however, no significant trend over time was observed (*p*=0.99) (**Table 4**). The median age among MRSA BSI patients was 57 years (IQR: 41–71), with women accounting for 36.6% of cases (Supplemental material).

Source of infection: Rates for CA-MRSA BSI did not change significantly (*p*=0.46) between 2020 (0.65 infections per 10,000 patient days) and 2024 (0.67 per 10,000 patient days). Healthcare-associated-MRSA BSI rates remained stable (range: 0.42–0.47 infections per 10,000 patient days) (Table 4).

Rates for HA-MRSA BSIs have remained stable across all regions (Western range: 0.46–0.58; Central range: 0.36–0.45; Eastern range: 0.36–0.58; Northern range: zero infections per 10,000 patient days) (Supplemental material). The CA-MRSA BSI rates remained stable across all regions except for in the East where there was a significant increase, from 0.34 in 2020 to 0.67 infections per 10,000 patient days in 2024 (*p*=0.03) (Western range: 0.70–0.83; Central range: 0.43–0.63; Eastern range: 0.34–0.67; Northern range: zero infections per 10,000 patient days) (Supplemental material). In 2024, CA-MRSA and HA-MRSA BSI rates were highest in Western Canada (0.71 and 0.57 infections per 10,000 patient days, respectively) (Supplemental material).

Hospital types: Both HA- and CA-MRSA BSI rates remained higher over time in adult and mixed hospitals from 2020 to 2024 (HA-MRSA: adult range: 0.50–0.65; mixed range: 0.36–0.47; CA-MRSA: adult range: 0.70–0.86; mixed range: 0.55–0.79, with lower rates observed in adult hospitals with a NICU (HA-MRSA range: 0.30–0.46; CA-MRSA range: 0.24–0.47 infections per 10,000 patient days), paediatric (HA-MRSA range: 0.30–0.43; CA-MRSA range: 0.32–0.43 infections per 10,000 patient days)

Table 3: *Clostridioides difficile* antimicrobial resistance data, Canada, 2020–2024[a,b]

Antibiotic	Number of isolates and % resistance (per year)									
	2020		2021		2022		2023		2024	
	n	%	n	%	n	%	n	%	n	%
Clindamycin	62	17.0	67	12.4	101	22.7	69	13.1	192	33.0
Moxifloxacin	24	6.6	49	9.0	31	7.0	32	6.1	38	6.5
Rifampin	3	0.8	9	1.7	4	0.9	4	0.8	6	1.0
Total number of isolates tested[c]	365	N/A	542	N/A	444	N/A	525	N/A	582	N/A

Abbreviation: N/A, not applicable
[a] *Clostridioides difficile* infection isolates are collected for resistance testing during the two-month period (March and April of each year) for adults (aged 18 years and older) and year-round for children (aged one year to younger than 18 years old) from admitted patients only
[b] There was no resistance to tigecycline, vancomycin, or metronidazole in *C. difficile* isolates submitted to the National Microbiology Laboratory 2019–2023
[c] Total reflects the number of isolates tested for each of the antibiotics listed above

Table 4: Methicillin-resistant *Staphylococcus aureus* bloodstream infections data, Canada, 2020–2024

MRSA BSI data	Year				
	2020	2021	2022	2023	2024
All cases					
Number of MRSA BSIs	868	872	835	914	993
Rate per 1,000 patient admissions	0.88	0.84	0.80	0.87	0.91
Rate per 10,000 patient days	1.16	1.11	0.99	1.11	1.16
Number of reporting hospitals	81	81	81	82	77
All-cause mortality rate[a]					
Number of deaths	145	164	164	175	187
All-cause mortality rate per 100 cases	16.7	18.8	20.2	19.1	19.0
HA-MRSA BSI					
Number of HA-MRSA BSIs	323	348	347	378	415
Rate per 1,000 patient admissions	0.33	0.34	0.33	0.36	0.38
Rate per 10,000 patient days	0.43	0.44	0.41	0.46	0.49
Number of reporting hospitals	81	81	81	82	77
All-cause mortality rate[a]					
Number of deaths	62	86	81	94	94
All-cause mortality rate per 100 cases	19.2	24.7	23.7	24.9	22.8
CA-MRSA BSI					
Number of CA-MRSA BSIs	480	471	453	528	560
Rate per 1,000 patient admissions	0.49	0.46	0.44	0.51	0.52
Rate per 10,000 patient days	0.65	0.61	0.55	0.66	0.67
Number of reporting hospitals	80	80	80	81	76
All-cause mortality rate[a]					
Number of deaths	72	71	79	80	91
All-cause mortality rate per 100 cases	15.0	15.1	17.8	15.2	16.4

Abbreviations: CA, community-associated; HA, healthcare-associated; MRSA BSI, methicillin-resistant *Staphylococcus aureus* bloodstream infection
[a] Based on the number of cases with associated 30-day outcome data

and paediatric-OB hospitals (HA-MRSA and CA-MRSA range: 0.04–0.22 infections per 10,000 patient days) (Supplemental material). Stratified by hospital size, both HA-and CA-MRSA BSI rates were generally highest among medium (201–499 beds; HA-MRSA range: 0.38–0.47; CA-MRSA range: 0.64–0.81) and large size hospitals (500 or more beds; HA-MRSA range: 0.41–0.60; CA-MRSA range: 0.52–0.73) (Supplemental material). There were no significant trends over time observed by hospital type or size during this reporting period ($p>0.05$).

30-day all-cause mortality: Thirty-day all-cause mortality remained stable from 2020 to 2024 (range: 16.7–20.2) (Table 4). In 2024, 30-day all-cause mortality was significantly higher for HA-MRSA (22.8%) compared to CA-MRSA (16.4%) ($p=0.02$).

Antimicrobial resistance: Clindamycin resistance among MRSA isolates decreased significantly from 33.4% to 27.6% between 2020 and 2024 ($p<0.01$) (**Table 5**). Since 2020, the proportion of MRSA isolates resistant to erythromycin has stayed relatively stable and high at around 68% in relation to other antibiotics tested. Resistance to tetracycline significantly increased from 6.6% in 2020 to 10.1% in 2024 ($p=0.02$). All tested MRSA BSI isolates from 2020 to 2024 were susceptible to linezolid, daptomycin and vancomycin.

Comparing isolates from HA-MRSA with CA-MRSA cases, clindamycin resistance was consistently higher among isolates from HA-MRSA each year from 2020 (35.0%, n=89/254 vs. 31.1%, n=117/376) to 2024 (32.2%, n=125/388 vs. 24.3%, n=117/481) (Supplemental material). There were no other notable differences in antibiotic resistance patterns by MRSA BSI case type.

Molecular typing: Between 2020 and 2024, the proportion of spa types identified as t002, most commonly associated with HA-MRSA, continued to decrease from 15.7% of all isolates in HA-MRSA cases in 2020 to 8.2% in 2024 ($p<0.01$) (Supplemental material). Spa type t008, most commonly associated with CA-MRSA, accounted for the largest proportion of isolates identified in both CA-MRSA (33.7%) and HA-MRSA (47.4%) cases (Supplemental material). Among CA-MRSA, the proportion of t008 increased from 45.4% in 2020 to 47.2% in 2024 ($p=0.59$).

Table 5: Methicillin-resistant *Staphylococcus aureus* bloodstream antimicrobial resistance data, Canada, 2020–2024[a]

Antibiotic	Year									
	2020		2021		2022		2023		2024	
	n	%	n	%	n	%	n	%	n	%
Ciprofloxacin	460	65.6	490	65.8	415	66.5	512	63.4	566	61.6
Clindamycin	234	33.4	220	29.5	157	25.2	186	23.0	254	27.6
Daptomycin	0	0	0	0	0	0	0	0	0	0
Erythromycin	507	72.3	510	68.5	428	68.6	543	67.2	629	68.4
Gentamicin	22	3.1	35	4.7	20	3.2	33	4.1	44	4.8
Linezolid	0	0	0	0	0	0	0	0	0	0
Rifampin	6	0.9	10	1.3	5	0.8	9	1.1	12	1.3
Trimethoprim/sulfamethoxazole	16	2.3	32	4.3	36	5.8	20	2.5	20	2.2
Tetracycline	46	6.6	63	8.5	52	8.3	71	8.8	93	10.1
Tigecycline	1	0.1	6	0.8	5	0.8	5	0.6	13	1.4
Vancomycin	0	0	0	0	0	0	0	0	0	0
Total number of isolates tested[b,c]	701	N/A	745	N/A	624	N/A	808	N/A	919	N/A

Abbreviation: N/A, not applicable
[a] All methicillin-resistant *Staphylococcus aureus* bloodstream infection (MRSA) isolates from 2020 to 2024 submitted to the National Microbiology Laboratory were susceptible to nitrofurantoin
[b] In some years, the number of isolates tested for resistance varied by antibiotic
[c] Total reflects the number of isolates tested for each of the antibiotics listed above

In contrast, spa type t008 among HA-MRSA significantly increased from 28.0% in 2020 to 35.4% in 2024 ($p<0.01$).

Vancomycin-resistant *Enterococcus* bloodstream infections

From 2020 to 2024, VRE BSI rates significantly increased from 0.30 to 0.42 infections per 10,000 patient days ($p=0.01$) (**Table 6**). The median age among patients with VRE BSI was 63 years (IQR: 51–71) and women accounted for 38.8% of VRE BSI cases (Supplemental material).

Source of infection: Vancomycin-resistant *Enterococcus* BSIs were predominantly HA, as 90.3% (n=1,325/1,468) of VRE BSIs reported from 2020 to 2024 were acquired in a healthcare facility. Stratified by source of infection, HA-VRE BSI rates significantly increased from 2020 to 2024 from 0.28 to 0.39 infections per 10,000 patient days ($p=0.03$) (Supplemental material). Community-acquired-VRE BSI rates remained low and stable over time (range: 0.02–0.04 infections per 10,000 patient days).

Regionally, VRE BSI rates in Western and Central Canada significantly increased between 2020 and 2024 from 0.39 to 0.54 infections per 10,000 patient days ($p=0.04$) and 0.29 to 0.38 infections per 10,000 patient days ($p=0.04$), respectively. No significant increasing trend was observed in Eastern Canada (range: 0.00–0.12 infections per 10,000 patient days, $p=0.11$) (Supplemental material).

Hospital types: Stratified by hospital type, VRE BSI rates remained highest in adult hospitals from 2020 to 2024 (range: 0.43–0.57 infections per 10,000 patient days). From 2020 to 2024, VRE BSI rates in paediatric hospitals were low (range: 0.00–0.11 infections per 10,000 patient days) and there were no VRE BSIs in paediatric-OB hospitals. In 2024, VRE BSI rates were

Table 6: Vancomycin-resistant *Enterococcus* bloodstream infections data, Canada, 2020–2024[a]

VRE BSI data	Year				
	2020	2021	2022	2023	2024
Number of VRE BSIs	224	251	305	318	370
Rate per 1,000 patient admissions	0.23	0.24	0.29	0.29	0.33
Rate per 10,000 patient days	0.30	0.32	0.36	0.37	0.42
Number of reporting hospitals	81	80	80	85	85
All-cause mortality rate[b]					
Number of deaths	82	84	117	118	142
All-cause mortality rate per 100 cases	36.6	33.5	38.5	37.1	38.4

Abbreviation: VRE BSI, vancomycin-resistant *Enterococcus* bloodstream infection
[a] Due to the low number of community-associated VRE BSI cases reported each year, this table presents data for all cases combined (healthcare-associated and community-associated)
[b] Based on the number of cases with associated 30-day outcome data
Note: Aggregate mortality data reported in-text due to fluctuations in the small numbers of VRE BSI deaths reported each year

highest in large hospitals (500 or more beds) at 0.56 infections per 10,000 patient days, followed by medium hospitals (201–499 beds) at 0.31 infections per 10,000 patient days and small hospitals (1–200 beds) at 0.20 infections per 10,000 patient days. A significant increasing trend in VRE BSI rates was observed over time in large hospitals (500 or more beds, p=0.01), but not in medium hospitals (201–499 beds, p=0.50) and small hospitals (1–200 beds, p=0.07). The incidence rates for HA-VRE BSI by region, hospital type and hospital size are presented in Supplemental material.

30-day all-cause mortality: All-cause mortality remained high and stable over time from 2020 to 2024 (range: 33.5–38.5) (p=0.23) (Table 6).

Antimicrobial resistance: Resistance to last resort antimicrobials such as daptomycin and linezolid has remained low from 2020 to 2024. Daptomycin resistance rates were relatively stable at 4.5% (n=6/134) in 2020 to 4.0% (n=13/328) in 2024, while linezolid resistance rates were 0.7% (n=1/134) in 2020 and 1.2% (n=4/328) in 2024 (**Table 7**).

Molecular typing: From 2020 to 2024, most VRE BSI isolates were identified as *E. faecium*. *Enterococcus faecalis* was detected infrequently, with one isolate identified in 2020 (0.7%), 2021 (0.6%) and 2022 (0.5%); three isolates in 2023 (1.3%); and seven isolates in 2024 (2.1%) (Supplemental material).

Although VanA remained predominant, an increasing proportion of *E. faecium* isolates harboured VanB, rising from 3.0% (n=4) in 2020 to 6.7% (n=22) in 2024 (p=0.60) (Supplemental material).

Four predominant sequence types were identified among *E. faecium* isolates from 2020 to 2024, with a notable shift in their distribution observed over time (Supplemental material). A significant decrease in ST1478 was observed, declining from 19.5% (n=26/133) in 2020 to 2.2% (n=7/320) in 2024 (p<0.01). The proportion of ST17 isolates also decreased; from 33.8% (n=45/133) in 2020 to 25.0%, (n=80/320) in 2024 (p=0.16). In contrast, ST117 increased from 10.5% (n=14/133) in 2020 to 22.2% (n=71/320) in 2024 (p=0.02), while ST80 increased from 16.5% (n=22/133) to 30.6% (n=98/320) over the same period (p=0.02). A statistically significant increasing trend in ST80 was observed from 2020 to 2024, and by 2024, ST80 had become the predominant sequence type among all tested isolates (p=0.04).

Carbapenemase-producing *Enterobacterales* and *Acinetobacter baumannii*

From 2020 to 2024, CPE infection rates have remained low compared to other HAIs in Canada, although there has been a significant increase in the rates over this period (0.05–0.20 infections per 10,000 patient days, p=0.03) (**Table 8**). The number of CPA infections were very low with eight or fewer

Table 7: Antimicrobial resistance of *Enterococcus faecium* isolates, Canada, 2020–2024[a]

Antimicrobial	Year									
	2020		2021		2022		2023		2024	
	n	%	n	%	n	%	n	%	n	%
Ampicillin	132	98.5	166	98.8	199	97.5	223	97.8	320	97.6
Chloramphenicol	28	20.9	51	30.4	34	16.7	38	16.7	59	18.0
Ciprofloxacin	132	98.5	166	98.8	203	99.5	226	99.1	322	98.2
Daptomycin	6	4.5	5	3.0	4	2.0	4	1.8	13	4.0
Erythromycin	128	95.5	159	94.6	199	97.5	221	96.9	304	92.7
High-level gentamicin	36	26.9	34	20.2	39	19.1	42	18.4	85	25.9
Levofloxacin	131	97.8	166	98.8	202	99.0	226	99.1	323	98.5
Linezolid	1	0.7	3	1.8	6	2.9	1	0.4	4	1.2
Nitrofurantoin	56	41.8	131	78.0	143	70.1	141	61.8	187	57.0
Penicillin	133	99.3	166	98.8	200	98.0	223	97.8	320	97.6
Quinupristin/dalfopristin	9	6.7	8	4.8	16	7.8	34	14.9	41	12.5
Rifampicin	115	85.8	155	92.3	188	92.2	211	92.5	311	94.8
High-level streptomycin	29	21.6	48	28.6	51	25.0	63	27.6	106	32.3
Tetracycline	89	66.4	134	79.8	180	88.2	186	81.6	258	78.7
Tigecycline	0	0	0	0	0	0	0	0	2	0.6
Vancomycin	130	97.0	163	97.0	203	99.5	228	100	322	98.2
Total number of isolates[b]	134	-	168	-	204	-	228	-	328	-

[a] Due to the low number of community-associated vancomycin-resistant *Enterococcus* bloodstream infection cases reported each year, this table presents data for all cases combined (healthcare-associated and community-associated)
[b] Total reflects the number of isolates tested for each of the antibiotics listed above
Note: Antimicrobials presented are for surveillance purposes. Please refer to Clinical & Laboratory Standards Institute (CLSI) for appropriate treatment of bloodstream infection *Enterococcus* infections (CLSI M100 ED34:2024)

Table 8: Carbapenemase-producing *Enterobacterales* data, Canada, 2020–2024

CPE data	Year				
	2020	2021	2022	2023	2024
Number of CPE infections	39	67	101	169	218
Infection rate per 1,000 patient admissions	0.04	0.07	0.09	0.13	0.16
Infection rate per 10,000 patient days	0.05	0.09	0.12	0.17	0.20
Number of reporting hospitals	81	81	85	102	105
All-cause mortality rate					
Number of CPE infection deaths	7	13	17	25	33
All-cause mortality rate per 100 cases	18	19.4	16.8	14.8	15.1

Abbreviation: CPE, Carbapenemase-producing *Enterobacterales*
Note: All-cause mortality only includes CPE infections that have a 30-day outcome available

cases per year between 2020 and 2024 (total n=22). The median age for CPE infections was 65 years and 42.6% of cases were female (Supplemental material).

From 2020 to 2024, the majority (51.7%; n=307/594) of CPE infections of the were identified in Western Canada, followed by 44.3% (n=263/594) in Central Canada and 4.0% (n=307/594) in Eastern Canada (Supplemental material). From 2020 to 2024, large hospitals (500 or more beds) generally reported the highest rates of CPE infections (0.06–0.28 infections per 10,000 patient days) compared to small hospitals (fewer than 200 beds) (0.03–0.09 infections per 10,000 patient days). During this period, 26.7% (n=119/445) of CPE-infected patients reported travel outside of Canada and of those, 79.1% (n=83/105) received medical care while abroad. The majority of CPE infections were acquired domestically, with 86.8% (n=446/514) of CPE infections acquired in Canada and 80% (n=357/446) acquired within a Canadian acute care hospital between 2020 and 2024. The number of CPE infections acquired in the community has also increased from 12.9% (n=4/31) in 2020 to 20.6% (n=37/180) in 2024.

Organisms: Of all isolates submitted (infections and colonizations), the top four carbapenemase producing organisms during 2024 were *Escherichia coli* (42.1%), *Klebsiella pneumoniae* (16.3%), *Enterobacter cloacae* (15.8%) and *Citrobacter freundii* (14.6%). From 2020 to 2024, there has been an increase in the proportion of *E. coli*-producing carbapenemases (39.3%–42.1%) and a decrease in the proportion of *K. pneumoniae* (19.9%–16.34%) and *E. cloacae* (18.1%–15.8%) producing carbapenemases (Supplemental material). The predominant carbapenemases, in order identified in Canada have not changed over the study period and were *K. pneumoniae* carbapenemase (KPC), New Delhi metallo-β-lactamase (NDM) and oxacillinase-48 (OXA-48), accounting for over 90% of identified carbapenemases from 2020 to 2024 (**Table 9**). Historically, KPC has been the most commonly identified carbapenemase in Canada; however, the proportion of KPC and NDM have been continually trending closer and were almost equal in 2024. Over time a significant decrease in KPC and an increase in NDM, OXA-48, and NDM+OXA-48 was observed ($p \leq 0.002$).

30-day all-cause mortality: All-cause mortality for CPE infections fluctuated between 2020 and 2024, with a mean of 16.8% (Table 8).

Table 9: Carbapenemases identified in carbapenemase-producing *Enterobacterales* isolates, Canada, 2020–2024

Carbapenemases identified[a]	Year									
	2020		2021		2022		2023		2024	
	n	%	n	%	n	%	n	%	n	%
KPC	98	40	178	50.1	214	45.3	397	38.4	525	38.4
NDM	80	32.7	85	23.9	131	27.8	350	33.8	458	33.5
OXA-48	48	19.6	57	16.1	94	19.9	194	18.7	277	20.3
SME[b]	2	0.8	1	0.3	0	0	2	0.2	3	0.2
NDM/OXA-48	9	3.7	12	3.4	14	3	57	5.5	69	5.0
GES	0	0	1	0.3	0	0	0	0	0	0
IMP	1	0.4	2	0.6	2	0.4	1	0.1	7	0.5
IMI/NMC	7	2.9	15	4.2	3	0.6	13	1.3	7	0.5
VIM	0	0	1	0.3	6	1.3	4	0.4	3	0.2
Other	0	0	3	0.8	8	1.7	17	1.6	18	1.3
Total number of isolates tested[c]	245	N/A	355	N/A	427	N/A	1,035	N/A	1,367	N/A

Abbreviations: CPE, carbapenemase-producing *Enterobacterales*; GES, Guiana extended-spectrum β-lactamase; IMI, imipenem-hydrolyzing β-lactamase; IMP, active-on-imipenem; KPC, *Klebsiella pneumoniae*; carbapenemase; NDM, New Delhi metallo-β-lactamase; NMC, not metalloenzyme carbapenemase; N/A, not applicable; OXA-48, oxacillinase-48; SME, *Serratia marcescens* enzymes; VIM, Verona integron-encoded metallo-β-lactamase
[a] Includes data for all CPE isolates submitted (infections and colonisations)
[b] Only found in *Serratia marcescens*
[c] Some isolates contain multiple carbapenemases, therefore the total number of isolates tested and the number of carbapenemases indicated may not match. *Acinetobacter baumanii* were not included in this table

Antibiotic resistance: In all years, NDM producing isolates were predominantly extensively drug-resistant (XDR) (range: 83.8%–91.8%). Conversely, in 2020, 37.5% of OXA-48-like producers were XDR compared to 2024 where 16.7% are XDR, showing an overall downward trend in resistance. *Klebsiella pneumoniae* carbapenemase has been more equally distributed throughout 2020–2024 for either XDR (range: 40.8–56.3) or multidrug-resistant (MDR) (range: 31.1–52.2). When examining resistance among the top three carbapenemases, we noted that there was an increase in resistance to all aminoglycosides from 2021 to 2024 in KPC producers (Supplemental material). New Delhi metallo-β-lactamase producers showed increasing trends in Tobramycin. Conversely, among OXA-48-like producers, there was a decline in resistance to aztreonam, doxycycline, minocycline, trimethoprim/sulfamethoxazole, carbapenems, tobramycin and gentamicin. This agrees with observations that fewer OXA-48-like producers were XDR or MDR over time. From 2020 to 2024, the overall resistance in KPC, NDM and OXA-48-like producers to ertapenem was 75.1%, 97.8% and 63.3%, respectively, and for meropenem was 54.5%, 92.1% and 14.5%, respectively. Resistance to newer combination drugs, such as meropenem/vaborbactam, imipenem/relebactam and ceftazidime/avibactam among KPC producers (0.5%, 1.4% and 1.3%) and OXA-48-like producers (10.2%, 11.5% and 0.3%), was low. Meropenem/vaborbactam and imipenem/relebactam resistance in NDM producers ranged from 61.3% to 69.5% and 86.3% to 93.0%, respectively, over five years.

Candidozyma auris (Candida auris)

Ninety-six percent (n=105/109) of CNISP hospitals participate in *C. auris* surveillance. Between CNISP and the National Microbiology Laboratory surveillance, a total of 43 isolates (colonizations and infections) has been reported from 2020 to 2024: 19 (44%) from CNISP hospitals and 24 (56%) from other hospital laboratories. The number of *C. auris* cases detected per year was four in 2020, three in 2021, 12 in 2022, 10 in 2023 and 14 in 2024. Twelve (27.9%) of the total cases were from Western Canada, 29 (67.4%) cases were from Central Canada and two (4.7%) cases were from Eastern Canada. Of the 43 *C. auris* isolates, 19.5% were resistant to amphotericin B and 90.2% were resistant to fluconazole (**Table 10**). The first identification of echinocandin-resistant *C. auris* in Canada occurred in 2024; this isolate was to fluconazole and micafungin. Between 2020 to 2024, 22% of isolates were MDR (resistant to two classes of antifungals). Based on available travel information (n=24), 33.3% reported no travel while 66.7% either received health care or travelled abroad (Table 8). Of the 15 *C. auris* patients who received health care abroad, 10 (66.7%) had known carbapenemase-producing organism status and four (40%) were carbapenemase-producing organism positive.

Table 10: Antifungal resistance of *Candidozyma auris* isolates, Canada, 2020–2024

Isolate or patient characteristics[a]	Number of cases	
	n	%
Antifungal resistance of *Candidozyma auris* isolates (n=41)		
Fluconazole	37	90.2
Amphotericin B	8	19.5
Multidrug resistant	9	22.0
Micafungin	1	2.4
Travel history (n=24)		
Receipt of health care abroad	15	62.5
Travel abroad (receipt of health care unknown)	1	4.2
No travel reported	8	33.3

[a] 2/43 isolates did not have antifungal susceptibility results and 19/43 cases had unknown travel history

Discussion

Between 2020 and 2024, CNISP surveillance data indicate HAI infection rates in Canada have remained relatively stable for CDI (−3.5% change) and MRSA BSI (no change); however, rates have increased for VRE BSI and CPE infections (40% and 300%, respectively). A total of 43 *C. auris* isolates were identified from 2020 to 2024 with the number of cases increasing each year.

Clostridioides difficile infections between 2020 to 2024, overall CDI rates in the CNISP network were stable, with HA-CDI rates ranging from 3.60 to 3.89 per 10,000 patient days and CA-CDI rates ranging from 1.40 to 1.51 per 1,000 patient admissions. When compared to pooled WHO regional rates from 2016 to 2024, overall CNISP CDI rates were lower than the pooled North America rate (6.23 per 10,000 patient days), higher than Latin America rate (3.09 per 10,000 patient days) and similar to Western Pacific (3.90 per 10,000 patient days) and European (3.57 per 10,000 patient days) rates (21). At the country level, in contrast to the stable CDI rates observed in the CNISP network, the United Kingdom has recently reported an approximate 33% increase in rate in 2023/2024 compared to 2020/2021, following a previously stable trend (22).

While CDI results remained stable, the 30-day all-cause mortality rates among CDI patients decreased during the reporting period. These declining mortality rates occurred in both CA-CDI and HA-CDI and are likely, in part, associated with the decreased prevalence of the hypervirulent NAP1 (23). Improved diagnosis and management may also have reduced case fatality rates.

Clostridioides difficile infection AMR is less common in Canada than in the United States or globally (24). In a representative

sample of Canadian acute care hospitals, from 2020 to 2024, we saw a stabilization in moxifloxacin resistance in both HA- and CA-CDI populations with an average resistance of 7.0%. The decrease in moxifloxacin resistance from 24.8% in 2015 is concordant with an overall decrease in the prevalence of RT027 (NAP1). Furthermore, moxifloxacin resistance remained lower (6.5% in 2024) than previously published weighted pooled resistance data for North America (44.0%) and Asia (33.0%) (25,26). The decline in the prevalence of RT027 has been replaced with a concomitant increase in the prevalence of RT106, RT014 and RT020, consistent with trends observed in the United States (23,27). Additionally, the emergence of RT106 now found worldwide, presents additional challenges as this strain has been shown to produce more spores, have higher rates of recurrence, and be highly resistant to erythromycin, clindamycin, fluoroquinolones and third-generation cephalosporins. The potential emergence of resistant ribotypes warrants further surveillance, monitoring and investigation (27,28).

Methicillin-resistant *Staphylococcus aureus* remains a high priority pathogen due to its estimated burden of disease and mortality rate (29,30). Between 2020 and 2024, MRSA BSI rates in the CNISP network remained stable (0.99–1.16 infections per 10,000 patient days). Similarly, surveillance data measuring population based estimated incidence from the European Union/ European Economic area showed no significant trends among MRSA BSIs during this period (31).

From 2020 to 2024, HA-MRSA BSI rates in CNISP (0.41–0.49 infections per 10,000 patient days), were considerably higher than rates reported in Australian public hospitals between 2020 and 2024 (0.09–0.13 infections per 10,000 patient days); however, broader CNISP case definitions likely capture more cases with indirect healthcare exposures not included in the Australian case definition (32,33).

During this reporting period, CA-MRSA BSI rates have slightly increased; however, this trend was not significant. Increases in CA-MRSA BSI have been reported in other jurisdictions, suggesting an expanding community reservoir of MRSA in Canada and globally (34).

The CNISP 30-day all-cause mortality rates for MRSA BSI (HA: 19.2%–24.90%; CA: 15.0%–17.8%) were lower than those previously reported in the United States (HA: 29%; CA: 18%) (35). Differences may stem from CNISP's strict 30-day mortality cut-off versus undefined United States time frames or from variances in healthcare systems, infection prevention strategies and population characteristics (35,36).

A significant decrease in clindamycin resistance among MRSA BSI isolates between 2020 and 2024 coincided with shifts in MRSA spa types. The proportion of spa type t002 (commonly HA-MRSA) declined, while spa type t008 (historically CA-MRSA) increased. Notably, t008 rose among CA-MRSA isolates (45.4%–47.2%) and HA-MRSA isolates (28%–35.4%). The growing prevalence of traditionally CA clones in hospitals emphasizes the need for ongoing surveillance and tailored infection prevention strategies, as well as continued monitoring of antimicrobial resistance to guide treatment and mitigate MRSA burden in both healthcare and community settings. Populations at increased risk for CA-MRSA infection include children, athletes, incarcerated individuals, older adults with comorbidities, people who inject drugs and people experiencing homelessness that use public facilities including shelters (37–40). Injection drug use may represent an emerging risk factor for CA-MRSA (38–40). Targeted strategies such as MRSA screening and decolonization in high-risk populations may contribute to reducing the burden of MRSA BSIs (37–40).

Vancomycin resistance related to VRE BSI has been shown to be associated with higher mortality rates and longer hospital stays, making it a significant public health concern (41–43). The rate of VRE BSIs has increased year-over-year among CNISP-participating hospitals and reached an all-time high in 2024 (0.42 infections per 10,000 patient days). The highest VRE BSI rates were observed among Western and Central Canadian adult hospitals with 500 or more beds. The success of certain sequence types likely contributed to the increasing burden of VRE BSIs in CNISP-participating hospitals. In 2024, the prevalence of the previously dominant clone ST17 decreased to 25.0%, while ST80 emerged as the predominant clone, accounting for 30.6% of isolates. Compared to other sequence types, a distinct association has been identified between ST80 and the VanB gene. This association of VanB genes harboured predominantly among ST80 isolates has also been documented in recent studies related to VanB outbreaks in Sweden and Denmark (44,45). Increasing trends have been noted in other jurisdictions, such as Germany and India, which may be associated, in part, with the introduction and spread of new clones, differences in antibiotic prescription practices, and gaps in infection prevention practices (46–50). Because all-cause 30-day mortality remains high and most VRE BSI cases reported by CNISP-participating hospitals were HA, continued surveillance and targeted infection prevention measures in hospital are of utmost importance. Furthermore, treatment options for VRE BSIs are limited and require the use of daptomycin and linezolid, which are classified as last-resort reserve antibiotics under WHO's AWaRe classification (51). Antibiotic susceptibility data up to 2024 show that the great majority of VRE BSI isolates remain susceptible to daptomycin and linezolid (more than 95%); however, continued monitoring is needed to capture any changes in AMR trends over time.

Carbapenemase-producing *Enterobacterales* infections are a significant threat to public health as they are becoming increasingly prevalent in healthcare environments worldwide and are associated with high mortality and limited treatment options (52–55). The Centers for Disease Control and Prevention and WHO have classified CPE as one of the most urgent

AMR threats (56,57). Among CNISP-participating hospitals, the number of CPE infections increased more than five-fold from 2020 to 2024 and the increased infection rate was significant (p=0.03). Data on the incidence of CPE infections in other countries, such as Denmark, Italy, Switzerland and the United Kingdom, have also shown an increasing incidence of CPE infections (30,58–61). From 2020 to 2024, 86.8% of CPE infections were domestically acquired and 80% were acquired in a Canadian acute care hospital, emphasizing the importance of continued surveillance and rigorous, multi-layered infection control measure strategies, including screening patients with a previous hospitalization (domestic or abroad). Data from new antimicrobial drugs such as ceftazidime/avibactam show low resistance to carbapenemases such as KPC and OXA-48. In agreement with several other studies drugs such as imipenem/relebactam, meropenem/vaborbactam and ceftazidime/avibactam are not affective on NDM producers where high resistance is often observed. As increasing trends in NDM prevalence is observed testing of newer agents affective to this carbapenemase are needed.

Candidozyma auris

Candidozyma auris is an emerging MDR fungus that can cause invasive infections and outbreaks, in which invasive infections have a very high mortality rate (15%–60%) (62–64). *Candidozyma auris* has also been detected in dozens of countries (62–68). Although still relatively rare in Canada, the number of cases increased from four cases in 2020 to 14 cases in 2024. The United States reported over 7,000 clinical cases in 2025 (69). Identifying *C. auris* in routine microbiology laboratories requires identification of *Candida* to the species level, which, even in CNISP hospitals, was performed for all isolates of *Candida* in 45% of laboratories in 2018 and 81% in 2024 (70). Treatment options are limited, as over 20% of identified *C. auris* isolates in Canada were MDR and additional resistance can develop during antifungal therapy (71,72). Rapid identification, screening for colonization in at-risk patients' adherence to routine practices and additional precautions, and investigation of potential transmission are all required to reduce the transmission of *C. auris* in Canadian healthcare settings. With increasing detection of *C. auris* in Canada, continued reporting is critical to monitor the risk and identify epidemiological and microbiological trends.

Strengths and limitations

The strengths of CNISP lie in its network size, collaborative nature, detailed data collection (epidemiological and laboratory), standardized procedures and frequent and routine data quality evaluation. Epidemiological data collected through CNISP include information available in patient medical charts related to clinical care as well as data collected by infection prevention and control programs. Although staff turnover in hospitals might have influenced the consistent application of CNISP case definitions during chart reviews, data collection was carried out by trained and experienced infection prevention and control professionals who receive regular refresher training on CNISP methodology and definitions. In addition, routine data quality assessments were conducted to support data accuracy and consistency. These data may also be affected by selection bias due to the exclusion of sites with missing or incomplete information during the study period. A further limitation of *C. auris* surveillance is that detailed epidemiologic information is only available for patients identified at CNISP participating hospitals.

Efforts to improve the quality and representativeness of Canadian HAI surveillance data are ongoing. Additionally, the enhanced hospital screening practices survey is conducted annually to contextualize changes in HAI rates in the CNISP network. Canadian Nosocomial Infection Surveillance Program also conducts point prevalence surveys to assess the burden and incidence of HAIs and antimicrobial use; the fourth point prevalence survey was conducted from February to March 2024 (2). To further improve representativeness and generalizability of national HAI benchmark rates, CNISP has launched a simplified dataset accessible to all acute care hospitals across Canada to collect and visualize annual HAI rate data and has 109 hospitals participating in the project. With the launch of the simplified dataset, CNISP's coverage of acute care beds in Canada increased from 35% in 2020 to 49% in 2024, thereby improving representativeness across northern, community, rural and Indigenous populations (73). These and other detailed CNISP data, data exploration tools and analytics are available on the CNISP Health Infobase website (73).

Conclusion

Surveillance findings from a national sentinel network of Canadian acute care hospitals indicate that rates of MRSA BSI and CDI have remained stable from 2020 to 2024, while rates of VRE BSI and CPE infections have increased. Few cases of *C. auris* were detected in Canada, but the numbers have increased. Continued monitoring of HAIs in Canada is vital to understanding trends in the data, to provide benchmark rates for national and international comparisons and to evaluate and create interventions and policy to improve the quality of healthcare in Canada. These data also continue to form one of the key evidence bases for monitoring rates of AMR in Canada, as we work towards meeting commitments outlined in the *Pan-Canadian Action Plan on Antimicrobial Resistance* (16).

Authors' statement

Canadian Nosocomial Infection Surveillance Program hospitals provided expertise in the development of protocols in addition to the collection and submission of epidemiological data and lab isolates. The National Microbiology Laboratory completed the laboratory analyses and contributed to the interpretation and revision of the paper. Epidemiologists from PHAC were responsible for the conception, analysis, interpretation, drafting and revision of the article.

Competing interests

None.

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Appendix

Supplemental material and tables are available upon request to the author: cnisp-pcsin@phac-aspc.gc.ca

Surveillance case definitions and eligibility criteria, 2024
Table S1.0: Summary of patient characteristics for *Clostridioides difficile* infections (CDIs), carbapenemase-producing *Enterobacterales* (CPE) infections, methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections (BSIs), and vancomycin-resistant *Enterococcus* (VRE) BSIs, 2020–2024
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