Public Health Ontario | Santé publique Ontario

SURVEILLANCE REPORT

Influenza Genomic Surveillance in Ontario: 2025–26 Season

Published: August 2026

Introduction

This report summarizes the results of influenza whole genome sequencing completed by Public Health Ontario (PHO) for the 2025–26 influenza season. The 2025–26 early season report and 2024–25 season report can be found on PHO's website.

Highlights

- A total of 394 specimens were included for the current season (August 24, 2025 to May 23, 2026), representing 3.7% of specimens that tested positive at PHO.
- Of the 379 influenza A specimens sequenced from the current season, 22.7% were H1N1pdm09 and 77.3% were seasonal H3N2.
  - 67 specimens (17.7%) were H1N1pdm09 genetic subclade D.3.1.1 and 17 specimens (4.5%) were genetic subclade D.3.1, both belonging to clade 5a.2a.1. The H1N1pdm09 component of the 2025-2026 Northern Hemisphere influenza vaccine belongs to the genetic subclade C.1.1 (clade 5a.2a.1).
  - 251 specimens (66.2%) were H3N2 genetic subclade K and 41 specimens (10.8%) were genetic subclade J.2.4, both belonging to clade 2a.3a.1. The H3N2 component of the 2025-2026 Northern Hemisphere influenza vaccine belongs to the genetic subclade J.2 (clade 2a.3a.1).
- Of the 15 influenza B specimens sequenced from the current season, eight specimens (53.3%) were Victoria genetic subclade C.5.6.1 and six specimens (40.0%) were Victoria genetic subclade C.5.6 (both belonging to clade 3a.2). The Victoria component of the 2025-2026 Northern Hemisphere influenza vaccine belongs to the genetic subclade C (clade 3a.2).
- Of the H1N1pdm09 specimens sequenced, one specimen (1.2%) had the H275Y amino acid substitution in the neuraminidase (NA) gene known to be associated with resistance to oseltamivir.
- Of the 360 specimens sequenced that met quality control criteria for the polymerase acidic (PA) gene, none had the I38T amino acid substitution in the PA gene known to be associated with resistance to baloxavir.

Background

Two types of influenza virus are responsible for most human cases during the influenza season, influenza A and B. Influenza A can be further classified into subtypes (e.g., H1N1pdm09, seasonal H3N2) and influenza B can be further classified into lineages (i.e., Victoria). As influenza spreads through populations, changes can occur to the virus' genome. The accumulation of these changes or mutations can result in new subdivisions beyond subtypes or lineages called clades and subclades. Although many subclades will have no differences in the ability to cause disease, some may have mutations that affect virulence, transmissibility, antiviral susceptibility, or allow the virus to escape natural or vaccine-induced immunity. Genomic surveillance uses whole genome sequencing to monitor these changes in the genome as a virus evolves over time. This allows public health professionals to provide context to the current season, assess whether antivirals are working against the currently circulating viruses, and advise on vaccine strains for the upcoming seasons.[1] For the 2025–2026 influenza season, publicly funded vaccines available in Ontario are trivalent influenza A H1N1pdm09 subclade C.1.1 (clade 5a.2a.1), influenza A H3N2 subclade J.2 (clade 2a.3a.1), and influenza B Victoria subclade C (clade 3a.2).[2-4]

PHO performs routine testing for seasonal respiratory viruses for eligible population groups, including individuals exhibiting respiratory symptoms that are in a congregate living setting, part of an outbreak, or hospitalized.[5] In addition, PHO tests individuals attending physician offices that are part of the Sentinel Practitioner Surveillance Network (SPSN; see Technical Notes for additional information).[6]

PHO also subtypes influenza A specimens initially tested by other laboratories when requested and for enhanced H5N1 surveillance.[7] As a result, PHO accumulated 26% of all influenza positive specimens in Ontario available for sample selection. For more information on provincial influenza surveillance see the Ontario Respiratory Virus Tool.[8]

To understand the diversity of the viruses circulating during the 2025–26 influenza season, PHO sequenced eligible specimens (cycle threshold [Ct] ≤ 27 and sufficient volume remaining) positive for influenza. This excludes specimens that were positive for more than one virus. Additionally, only the first positive specimen from an outbreak was selected for whole genome sequencing. Specimens that were part of the SPSN were also excluded. Sequences were processed using bioinformatics analyses and were assigned subtypes, lineages, clades, and subclades.

Results

Table 1: Number of Positive Influenza Specimens, Number and Percentage Sequenced, Public Health Ontario, August 24, 2025 to May 23, 2026

Month	Number of Positive Specimens	Number Sequenced	Percentage Sequenced
August 2025*	10	1	10.0%
September 2025	67	4	6.0%
October 2025	154	5	3.2%
November 2025	1,933	73	3.8%
December 2025	6,612	259	3.9%
January 2026	1,172	31	2.6%
February 2026	232	4	1.7%
March 2026	211	4	1.9%
April 2026	162	11	6.8%
May 2026*	66	2	3.0%
Total	**10,619**	**394**	**3.7%**

Note: *August and May are partial months. 'Positive specimens' includes specimens that tested positive for influenza at PHO or influenza A positive specimens referred to PHO for subtype testing. Of the 394 specimens sequenced, 9.9% (39/394) were outbreak-associated.

Table 2a: Number and Percentage of Positive Influenza A Specimens Sequenced, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	2025–26 Season (August 24, 2025 – May 23, 2026)
H1N1pdm09	**86 (22.7%)**
C.1.9.3	2 (0.5%)
D.3.1	17 (4.5%)
D.3.1.1	67 (17.7%)
H3N2	**293 (77.3%)**
J.2.3	1 (0.3%)
J.2.4	41 (10.8%)
K	251 (66.2%)
Total Sequenced	**379 (100%)**

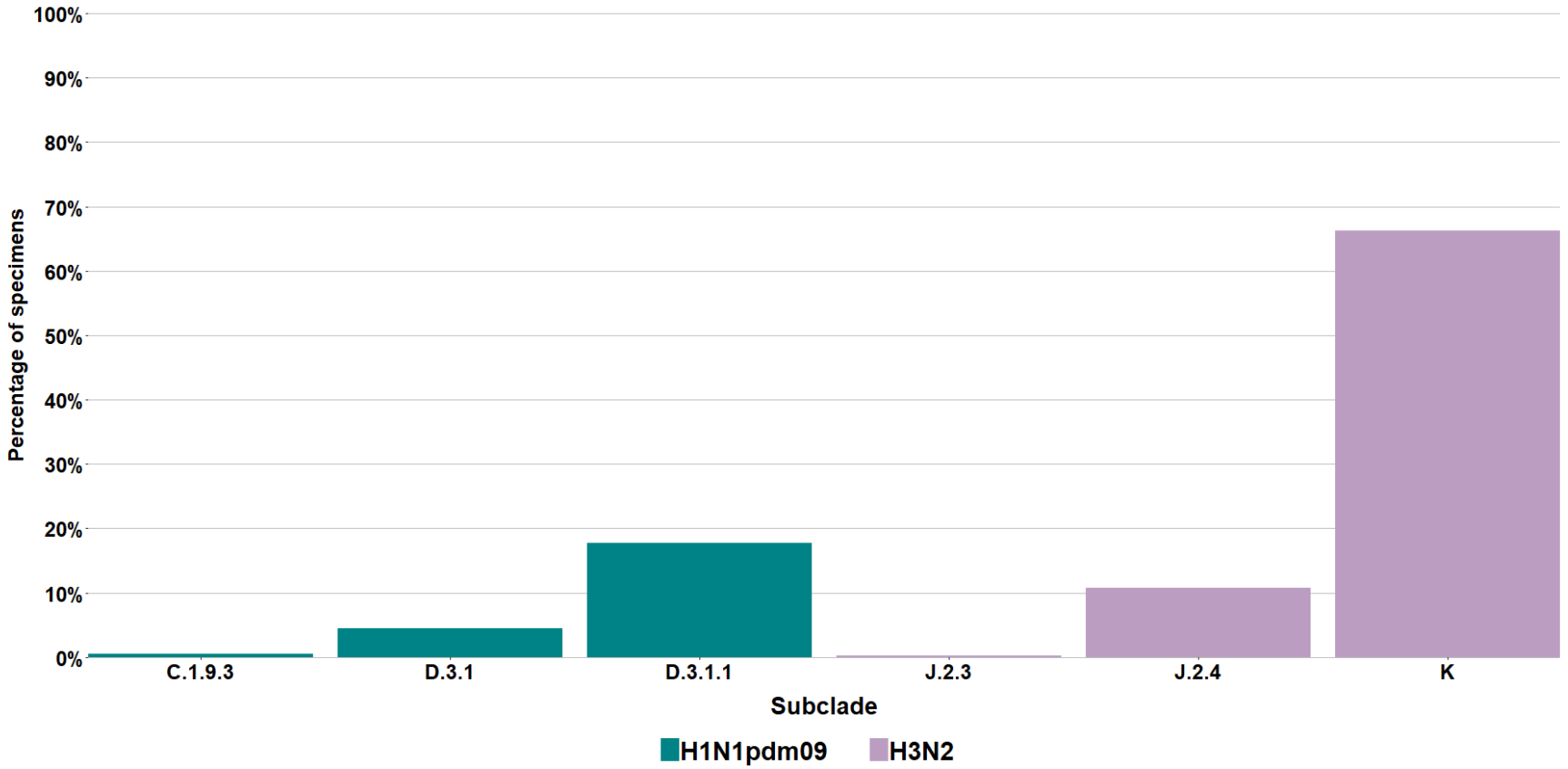
Note: The influenza A genetic subclades included in the 2025–26 season's influenza vaccine are H1N1pdm09 subclade C.1.1 (clade 5a.2a.1) and influenza A H3N2 subclade J.2 (clade 2a.3a.1).[4]

Table 2b: Number and Percentage of Positive Influenza B Specimens Sequenced, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	2025–26 Season (August 24, 2025 – May 23, 2026)
Victoria	**15 (100%)**
C.3.1	1 (6.7%)
C.5.6	6 (40.0%)
C.5.6.1	8 (53.3%)
Total Sequenced	**15 (100%)**

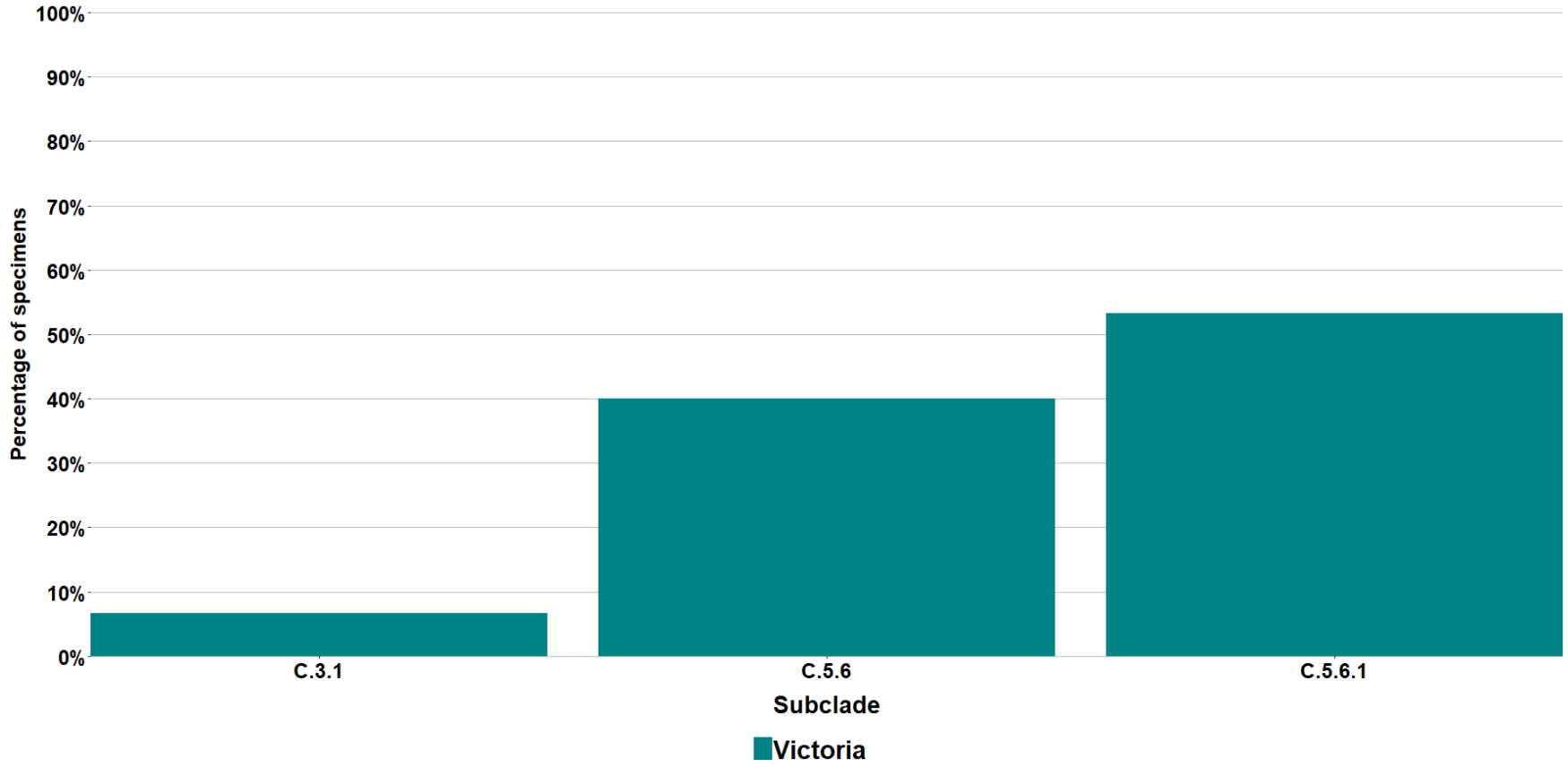
Note: The influenza B genetic subclade included in the 2025–26 season's influenza vaccine is Victoria subclade C (clade 3a.2).[4]

Figure 1a: Percentage of Positive Influenza A Specimens Sequenced, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026



Note: The influenza A genetic subclades included in the 2025–26 season's influenza vaccine are H1N1pdm09 subclade C.1.1 (clade 5a.2a.1) and influenza A H3N2 subclade J.2 (clade 2a.3a.1).[4]

Figure 1b: Percentage of Positive Influenza B Specimens Sequenced, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026



Note: The influenza B genetic subclade included in the 2025–26 season's influenza vaccine is Victoria subclade C (clade 3a.2).[4]

Table 3a: Number and Percentage of Positive Influenza A Specimens Sequenced, by Genetic Characterization and Month, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	August 2025*	September 2025	October 2025	November 2025	December 2025	January 2026	February 2026	March 2026	April 2026	May 2026*	Total
H1N1pdm09	**0 (0.0%)**	**3 (75.0%)**	**3 (60.0%)**	**28 (38.9%)**	**40 (15.4%)**	**7 (22.6%)**	**2 (50.0%)**	**0 (0.0%)**	**3 (100%)**	**0 (0.0%)**	**86 (22.7%)**
C.1.9.3	0 (0.0%)	1 (25.0%)	0 (0.0%)	1 (1.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (0.5%)
D.3.1	0 (0.0%)	2 (50.0%)	0 (0.0%)	7 (9.7%)	8 (3.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	17 (4.5%)
D.3.1.1	0 (0.0%)	0 (0.0%)	3 (60.0%)	20 (27.8%)	32 (12.4%)	7 (22.6%)	2 (50.0%)	0 (0.0%)	3 (100%)	0 (0.0%)	67 (17.7%)
H3N2	**1 (100%)**	**1 (25.0%)**	**2 (40.0%)**	**44 (61.1%)**	**219 (84.6%)**	**24 (77.4%)**	**2 (50.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**293 (77.3%)**
J.2.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.3%)
J.2.4	1 (100%)	0 (0.0%)	1 (20.0%)	8 (11.1%)	28 (10.8%)	3 (9.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	41 (10.8%)
K	0 (0.0%)	1 (25.0%)	1 (20.0%)	35 (48.6%)	191 (73.7%)	21 (67.7%)	2 (50.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	251 (66.2%)
Total Sequenced	**1 (100%)**	**4 (100%)**	**5 (100%)**	**72 (100%)**	**259 (100%)**	**31 (100%)**	**4 (100%)**	**0 (0.0%)**	**3 (100%)**	**0 (0.0%)**	**379 (100%)**

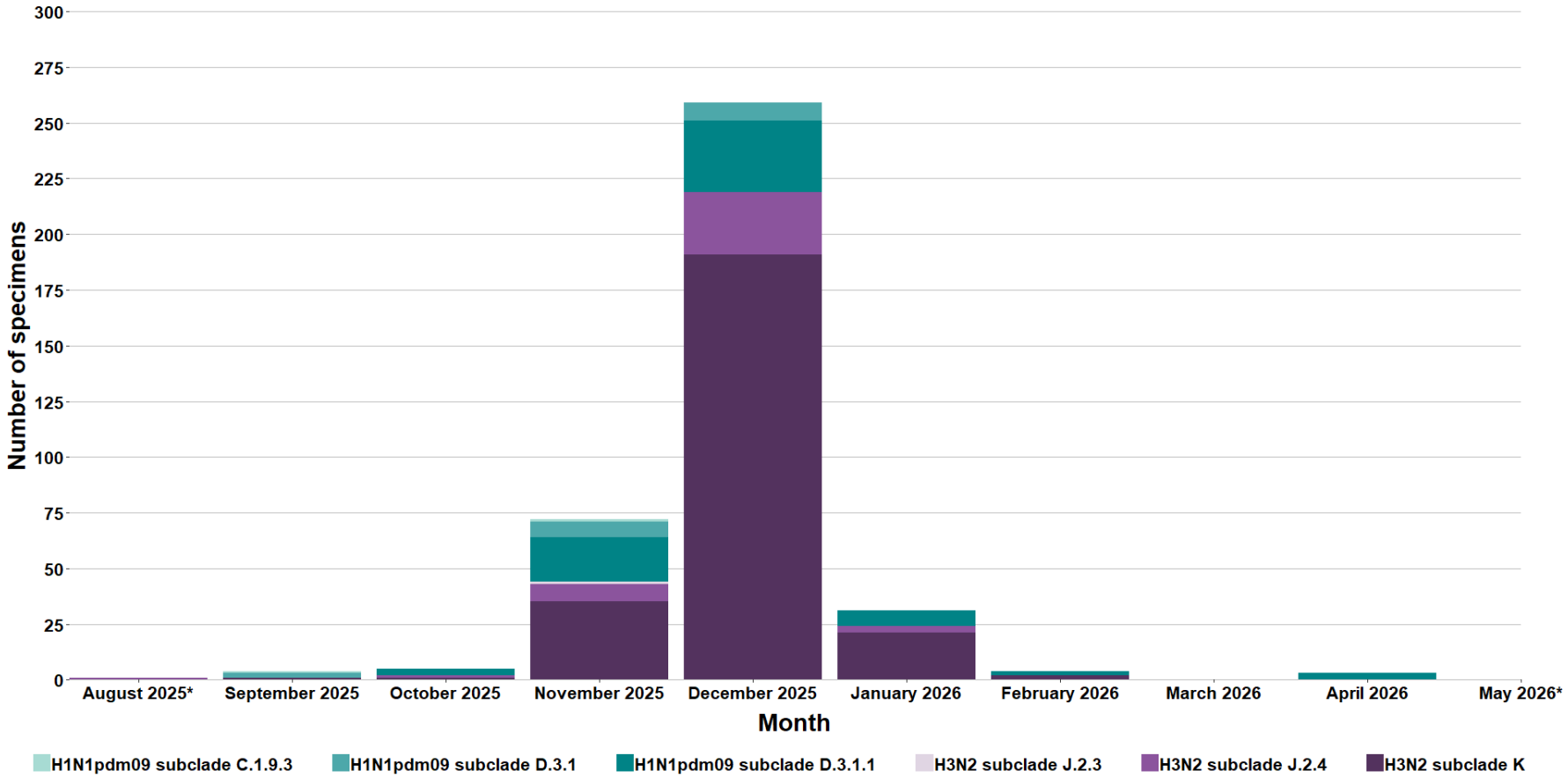
Note: *August and May are partial months. The influenza A genetic subclades included in the 2025–26 season's influenza vaccine are H1N1pdm09 subclade C.1.1 (clade 5a.2a.1) and influenza A H3N2 subclade J.2 (clade 2a.3a.1).[4]

Table 3b: Number and Percentage of Positive Influenza B Specimens Sequenced, by Genetic Characterization and Month, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	August 2025*	September 2025	October 2025	November 2025	December 2025	January 2026	February 2026	March 2026	April 2026	May 2026*	Total
Victoria	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**1 (100%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**4 (100%)**	**8 (100%)**	**2 (100%)**	**15 (100%)**
C.3.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (25.0%)	0 (0.0%)	0 (0.0%)	1 (6.7%)
C.5.6	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (100%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (50.0%)	1 (50.0%)	6 (40.0%)
C.5.6.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (75.0%)	4 (50.0%)	1 (50.0%)	8 (53.3%)
Total Sequenced	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**1 (100%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**4 (100%)**	**8 (100%)**	**2 (100%)**	**15 (100%)**

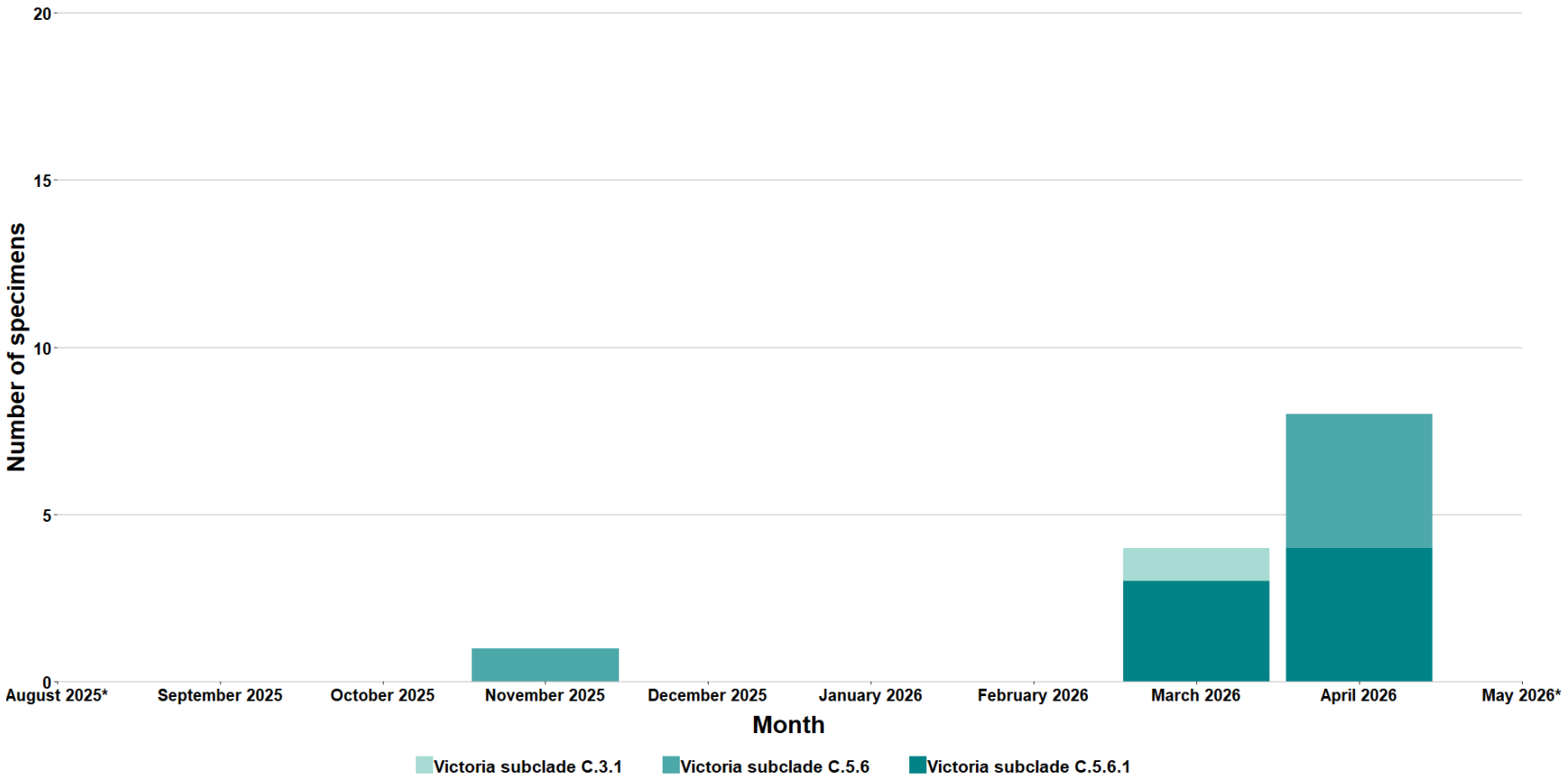
Note: *August and May are partial months. The influenza B genetic subclade included in the 2025–26 season's influenza vaccine is Victoria subclade C (clade 3a.2).[4]

Figure 2a: Number of Positive Influenza A Specimens Sequenced, by Genetic Characterization and Month, Public Health Ontario, August 24, 2025 to May 23, 2026



Note: *August and May are partial months. The influenza A genetic subclades included in the 2025–26 season's influenza vaccine are H1N1pdm09 subclade C.1.1 (clade 5a.2a.1) and influenza A H3N2 subclade J.2 (clade 2a.3a.1).[4]

Figure 2b: Number of Positive Influenza B Specimens Sequenced, by Genetic Characterization and Month, Public Health Ontario, August 24, 2025 to May 23, 2026



Note: *August and May are partial months. The influenza B genetic subclade included in the 2025–26 season's influenza vaccine is Victoria subclade C (clade 3a.2).[4]

Table 4a: Number and Percentage of Positive Influenza A Specimens Sequenced, by Genetic Characterization and Age Group, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	0–4 Years	5–19 Years	20–64 Years	65 Years and Over	Total
H1N1pdm09	**11 (23.4%)**	**8 (21.6%)**	**11 (19.3%)**	**56 (23.5%)**	**86 (22.7%)**
C.1.9.3	1 (2.1%)	0 (0.0%)	1 (1.8%)	0 (0.0%)	2 (0.5%)
D.3.1	2 (4.3%)	2 (5.4%)	3 (5.3%)	10 (4.2%)	17 (4.5%)
D.3.1.1	8 (17.0%)	6 (16.2%)	7 (12.3%)	46 (19.3%)	67 (17.7%)
H3N2	**36 (76.6%)**	**29 (78.4%)**	**46 (80.7%)**	**182 (76.5%)**	**293 (77.3%)**
J.2.3	1 (2.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.3%)
J.2.4	5 (10.6%)	6 (16.2%)	5 (8.8%)	25 (10.5%)	41 (10.8%)
K	30 (63.8%)	23 (62.2%)	41 (71.9%)	157 (66.0%)	251 (66.2%)
Total Sequenced	**47 (100%)**	**37 (100%)**	**57 (100%)**	**238 (100%)**	**379 (100%)**

Note: Age was assigned based on the birth date provided on the test requisition; excludes specimens with missing birth dates. The influenza A genetic subclades included in the 2025–26 season's influenza vaccine are H1N1pdm09 subclade C.1.1 (clade 5a.2a.1) and influenza A H3N2 subclade J.2 (clade 2a.3a.1).[4]

Table 4b: Number and Percentage of Positive Influenza B Specimens Sequenced, by Genetic Characterization and Age Group, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	0–4 Years	5–19 Years	20–64 Years	65 Years and Over	Total
Victoria	**4 (100%)**	**3 (100%)**	**6 (100%)**	**2 (100%)**	**15 (100%)**
C.3.1	0 (0.0%)	1 (33.3%)	0 (0.0%)	0 (0.0%)	1 (6.7%)
C.5.6	0 (0.0%)	0 (0.0%)	5 (83.3%)	1 (50.0%)	6 (40.0%)
C.5.6.1	4 (100%)	2 (66.7%)	1 (16.7%)	1 (50.0%)	8 (53.3%)
Total Sequenced	**4 (100%)**	**3 (100%)**	**6 (100%)**	**2 (100%)**	**15 (100%)**

Note: Age was assigned based on the birth date provided on the test requisition; excludes specimens with missing birth dates. The influenza B genetic subclade included in this season's influenza vaccine is Victoria subclade C (clade 3a.2).[4]

Table 5a: Number and Percentage of Positive Influenza A Specimens Sequenced, by Genetic Characterization and Setting, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	Intensive Care Unit	Hospital/ Emergency Department	Congregate Living	Other/ No Setting Reported	Total
H1N1pdm09	**0 (0.0%)**	**35 (25.0%)**	**33 (20.5%)**	**18 (25.0%)**	**86 (22.7%)**
C.1.9.3	0 (0.0%)	1 (0.7%)	0 (0.0%)	1 (1.4%)	2 (0.5%)
D.3.1	0 (0.0%)	8 (5.7%)	4 (2.5%)	5 (6.9%)	17 (4.5%)
D.3.1.1	0 (0.0%)	26 (18.6%)	29 (18.0%)	12 (16.7%)	67 (17.7%)
H3N2	**6 (100%)**	**105 (75.0%)**	**128 (79.5%)**	**54 (75.0%)**	**293 (77.3%)**
J.2.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.4%)	1 (0.3%)
J.2.4	1 (16.7%)	21 (15.0%)	16 (9.9%)	3 (4.2%)	41 (10.8%)
K	5 (83.3%)	84 (60.0%)	112 (69.6%)	50 (69.4%)	251 (66.2%)
Total Sequenced	**6 (100%)**	**140 (100%)**	**161 (100%)**	**72 (100%)**	**379 (100%)**

Note: Setting represents the health care facility at which an individual received care. Congregate living includes long-term care homes, retirement homes, correctional facilities, and undefined institutions (excluding hospitals). The influenza A genetic subclades included in the 2025-26 season's influenza vaccine are H1N1pdm09 subclade C.1.1 (clade 5a.2a.1) and influenza A H3N2 subclade J.2 (clade 2a.3a.1).[4]

Table 5b: Number and Percentage of Positive Influenza B Specimens Sequenced, by Genetic Characterization and Setting, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	Intensive Care Unit	Hospital/ Emergency Department	Congregate Living	Other/ No Setting Reported	Total
Victoria	**0 (0.0%)**	**7 (100%)**	**2 (100%)**	**6 (100%)**	**15 (100%)**
C.3.1	0 (0.0%)	0 (0.0%)	1 (50.0%)	0 (0.0%)	1 (6.7%)
C.5.6	0 (0.0%)	3 (42.9%)	1 (50.0%)	2 (33.3%)	6 (40.0%)
C.5.6.1	0 (0.0%)	4 (57.1%)	0 (0.0%)	4 (66.7%)	8 (53.3%)
Total Sequenced	**0 (0.0%)**	**7 (100%)**	**2 (100%)**	**6 (100%)**	**15 (100%)**

Note: Setting represents the health care facility at which an individual received care. Congregate living includes long-term care homes, retirement homes, correctional facilities, and undefined institutions (excluding hospitals). The influenza B genetic subclade included in this season's influenza vaccine is Victoria subclade C (clade 3a.2).[4]

Table 6a: Number and Percentage of Positive Influenza A Specimens Sequenced, by Genetic Characterization and Region, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	Northern	Eastern	Central East	Toronto	South West	Central West	Total
H1N1pdm09	**1 (12.5%)**	**8 (18.6%)**	**22 (26.5%)**	**13 (24.1%)**	**13 (13.8%)**	**29 (29.9%)**	**86 (22.7%)**
C.1.9.3	0 (0.0%)	0 (0.0%)	1 (1.2%)	1 (1.9%)	0 (0.0%)	0 (0.0%)	2 (0.5%)
D.3.1	1 (12.5%)	0 (0.0%)	5 (6.0%)	0 (0.0%)	5 (5.3%)	6 (6.2%)	17 (4.5%)
D.3.1.1	0 (0.0%)	8 (18.6%)	16 (19.3%)	12 (22.2%)	8 (8.5%)	23 (23.7%)	67 (17.7%)
H3N2	**7 (87.5%)**	**35 (81.4%)**	**61 (73.5%)**	**41 (75.9%)**	**81 (86.2%)**	**68 (70.1%)**	**293 (77.3%)**
J.2.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.0%)	1 (0.3%)
J.2.4	0 (0.0%)	4 (9.3%)	11 (13.3%)	7 (13.0%)	2 (2.1%)	17 (17.5%)	41 (10.8%)
K	7 (87.5%)	31 (72.1%)	50 (60.2%)	34 (63.0%)	79 (84.0%)	50 (51.5%)	251 (66.2%)
Total Sequenced	**8 (100%)**	**43 (100%)**	**83 (100%)**	**54 (100%)**	**94 (100%)**	**97 (100%)**	**379 (100%)**

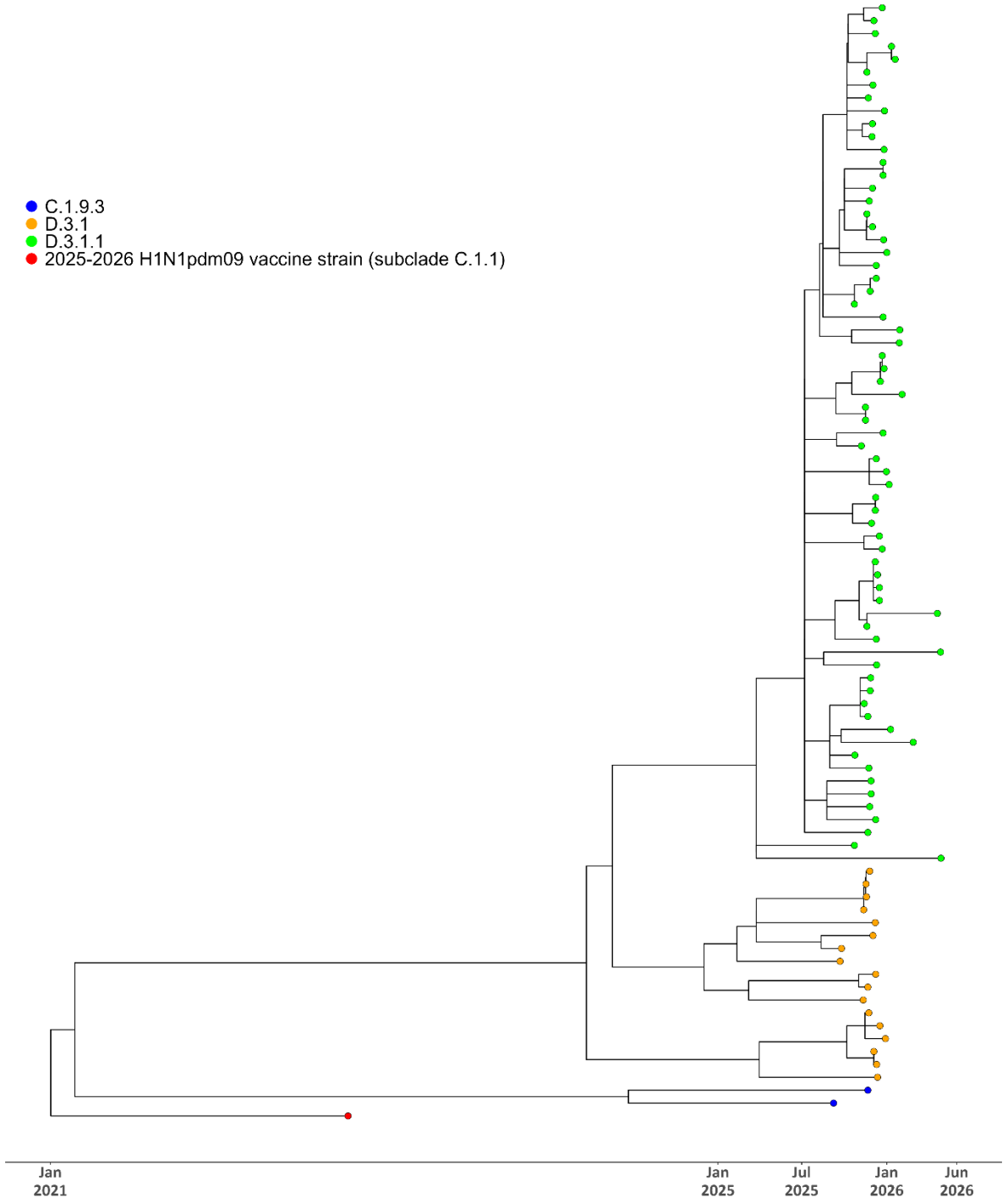
Note: Region was assigned using patient address when available. If missing, region was assigned using submitter address. For additional information on which public health units are included in each region, see Technical Notes. The influenza A genetic subclades included in the 2025–26 season's influenza vaccine are H1N1pdm09 subclade C.1.1 (clade 5a.2a.1) and influenza A H3N2 subclade J.2 (clade 2a.3a.1).[4]

Table 6b: Number and Percentage of Positive Influenza B Specimens Sequenced, by Genetic Characterization and Region, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	Northern	Eastern	Central East	Toronto	South West	Central West	Total
Victoria	**5 (100%)**	**1 (100%)**	**4 (100%)**	**1 (100%)**	**4 (100%)**	**0 (0.0%)**	**15 (100%)**
C.3.1	0 (0.0%)	0 (0.0%)	1 (25.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (6.7%)
C.5.6	0 (0.0%)	1 (100%)	2 (50.0%)	1 (100%)	2 (50.0%)	0 (0.0%)	6 (40.0%)
C.5.6.1	5 (100%)	0 (0.0%)	1 (25.0%)	0 (0.0%)	2 (50.0%)	0 (0.0%)	8 (53.3%)
Total Sequenced	**5 (100%)**	**1 (100%)**	**4 (100%)**	**1 (100%)**	**4 (100%)**	**0 (0.0%)**	**15 (100%)**

Note: Region was assigned using patient address when available. If missing, region was assigned using submitter address. For additional information on which public health units are included in each region, see Technical Notes. The influenza B genetic subclade included in this season's influenza vaccine is Victoria subclade C (clade 3a.2).[4]

Figure 3a: Time-Scaled Phylogenetic Tree of Positive Influenza A H1N1pdm09 Specimens Sequenced, Public Health Ontario, August 24, 2025 to May 23, 2026

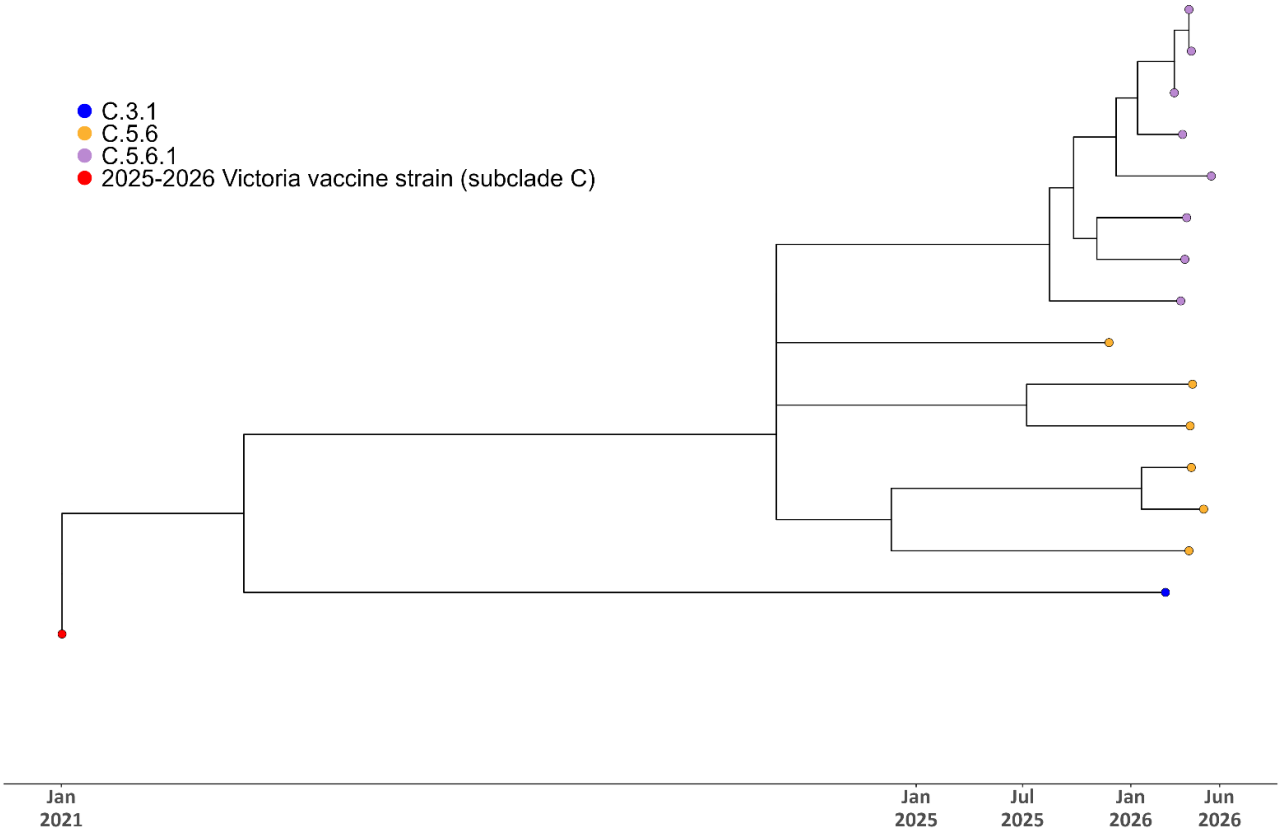


Note: Sequences of the influenza HA gene (which encodes the virus' surface protein) were analyzed and shown in the time-scaled phylogenetic tree. Each circle (tip) represents one specimen, and the colour indicates its influenza A H1N1pdm09 subclade. The branches (horizontal lines) are proportional to time and represent the inferred evolutionary relationships among viruses, with internal nodes showing the estimated time to a common ancestor, with the tips representing descendants. The x-axis represents time and approximates the specimen collection date. The 2025–2026 vaccine reference strain, A/Wisconsin/67/2022 (H1N1)pdm09-like virus (EPI_ISL_15928563), is shown in red.

Figure 3b: Time-Scaled Phylogenetic Tree of Positive Influenza A H3N2 Specimens Sequenced, Public Health Ontario, August 24, 2025 to May 23, 2026

Note: Sequences of the Influenza HA gene (which encodes the virus' surface protein) were analyzed and shown in the phylogenetic tree. Each circle (tip) represents one specimen, and the colour indicates its influenza A H3N2 subclade. The branches (horizontal lines) are proportional to time and represent the inferred evolutionary relationships among viruses, with internal nodes showing the estimated time to a common ancestor, with the tips representing descendants. The 2025–2026 vaccine reference strain**,** A/District_Of_Columbia/27/2023 (H3N2)-like virus (EPI_ISL_18937823), is shown in red.

Figure 3c: Time-Scaled Phylogenetic Tree of Positive Influenza B Specimens Sequenced, Public Health Ontario, August 24, 2025 to May 23, 2026



Note: Sequences of the Influenza HA gene (which encodes the virus' surface protein) were analyzed and shown in the phylogenetic tree. Each circle (tip) represents one specimen, and the colour indicates its influenza B subclade. The branches (horizontal lines) are proportional to time and represent the inferred evolutionary relationships among viruses, with internal nodes showing the estimated time to a common ancestor, with the tips representing descendants. The 2025–2026 vaccine reference strain**,** B/Austria/1359417/2021 (B/Victoria lineage)-like virus (EPI_ISL_1519459), is shown in red.

Table 7a: Number and Percentage of Positive Influenza A H1N1pdm09 Specimens Sequenced with Any Antigenic Site Amino Acid Substitutions, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	HA Antigenic Site Ca	HA Antigenic Site Cb	HA Antigenic Site Sa	HA Antigenic Site Sb	Total
H1N1pdm09	**80.2% (69/86)**	**1.2% (1/86)**	**3.5% (3/86)**	**0.0% (0/86)**	**81.4% (70/86)**
C.1.9.3	100% (2/2)	50.0% (1/2)	50.0% (1/2)	0.0% (0/2)	100% (2/2)
D.3.1	0.0% (0/17)	0.0% (0/17)	5.9% (1/17)	0.0% (0/17)	5.9% (1/17)
D.3.1.1	100% (67/67)	0.0% (0/67)	1.5% (1/67)	0.0% (0/67)	100% (67/67)
Total Sequenced	**80.2% (69/86)**	**1.2% (1/86)**	**3.5% (3/86)**	**0.0% (0/86)**	**81.4% (70/86)**

Note: The effect of the identified antigenic site substitutions on vaccine-induced immunity is unknown. This data is exploratory in nature and should be interpreted with caution. This data should not be used to directly inform clinical decisions or infer impacts on vaccine-induced immunity. See Technical Notes for details. Antigenic site amino acid substitutions were identified relative to the strain included in the 2025–26 season's influenza vaccine (influenza A H1N1pdm09 subclade C.1.1 (clade 5a.2a.1)).[4] Sequenced viruses may have substitutions at more than one position within the antigenic site. Antigenic site Ca includes substitutions at positions 139, 142, 166, 169, and 205 of the hemagglutinin (HA) protein. Antigenic site Cb includes substitutions at position 69 of the hemagglutinin (HA) protein. Antigenic site Sa includes substitutions at positions 121 and 155 of the HA protein. No substitution was observed at antigenic site Sb.

Table 7b: Number and Percentage of Positive Influenza A H3N2 Specimens Sequenced with Any Antigenic Site Amino Acid Substitutions, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	HA Antigenic Site A	HA Antigenic Site B	HA Antigenic Site C	HA Antigenic Site D	HA Antigenic Site E	Total
H3N2	**100% (293/293)**	**100% (293/293)**	**1.4% (4/293)**	**86.7% (254/293)**	**3.4% (10/293)**	**100% (293/293)**
J.2.3	100% (1/1)	100% (1/1)	0.0% (0/1)	0.0% (0/1)	0.0% (0/1)	100% (1/1)
J.2.4	100% (41/41)	100% (41/41)	0.0% (0/41)	7.3% (3/41)	4.9% (2/41)	100% (41/41)
K	100% (251/251)	100% (251/251)	1.6% (4/251)	100% (251/251)	3.2% (8/251)	100% (251/251)
Total Sequenced	**100% (293/293)**	**100% (293/293)**	**1.4% (4/293)**	**86.7% (254/293)**	**3.4% (10/293)**	**100% (293/293)**

Note: The effect of the identified antigenic site substitutions on vaccine-induced immunity is unknown. This data is exploratory in nature and should be interpreted with caution. This data should not be used to directly inform clinical decisions. See Technical Notes for details. Antigenic site amino acid substitutions were identified relative to the strain included in the 2025–26 season's influenza vaccine (influenza A H3N2 subclade J.2 (clade 2a.3a.1)).[4] Sequenced viruses may have substitutions at more than one position within the antigenic site. Antigenic site A includes substitutions at positions 133, 135, 144, and 145 of the HA protein. Antigenic site B includes substitutions at positions 128, 156, 158, 160, 189, 198, 222, 227, and 229 of the HA protein. Antigenic site C includes substitutions at position 45, 51, 53, and 54 of the HA protein. Antigenic site D includes substitutions at positions 96, 121, 171, 173, 182, 208, 212, 214, 218, and 242 of the HA protein. Antigenic site E includes substitutions at positions 57, 62, 82, 83, 88, 92, 94, and 260 of the HA protein.

Table 7c: Number and Percentage of Positive Influenza B Victoria Specimens Sequenced with Any Antigenic Site Amino Acid Substitutions, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	120-loop	150-loop	160-loop	190-helix	Total
Victoria	**100% (15/15)**	**0.0% (0/15)**	**0.0% (0/15)**	**100% (15/15)**	**100% (15/15)**
C.3.1	100% (1/1)	0.0% (0/1)	0.0% (0/1)	100% (1/1)	100% (1/1)
C.5.6	100% (6/6)	0.0% (0/6)	0.0% (0/6)	100% (6/6)	100% (6/6)
C.5.6.1	100% (8/8)	0.0% (0/8)	0.0% (0/8)	100% (8/8)	100% (8/8)
Total Sequenced	**100% (15/15)**	**0.0% (0/15)**	**0.0% (0/15)**	**100% (15/15)**	**100% (15/15)**

Note: The effect of the identified antigenic site substitutions on vaccine-induced immunity is unknown. This data is exploratory in nature and should be interpreted with caution. This data should not be used to directly inform clinical decisions. See Technical Notes for details. Antigenic site amino acid substitutions were identified relative to the strain included in the 2025–26 season's influenza vaccine (influenza B Victoria subclade C (clade 3a.2).[4] Sequenced viruses may have substitutions at more than one position within the antigenic site. Antigenic site 120-loop includes substitutions at positions 128 and 129 of the HA protein. Antigenic site 190-helix includes substitutions at positions 194, 195, and 196 of the HA protein. No substitution was observed at antigenic site 150-loop and 160-loop.

Table 8: Number and Percentage of Positive H1N1pdm09 Specimens Sequenced with Amino Acid Substitution H275Y Associated with Oseltamivir Resistance, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	Amino Acid Substitution H275Y
H1N1pdm09	**1.2% (1/86)**
C.1.9.3	0.0% (0/2)
D.3.1	0.0% (0/17)
D.3.1.1	1.5% (1/67)
Total Sequenced	**1.2% (1/86)**

Note: H275Y substitution in the NA gene of the influenza genome has been associated with oseltamivir resistance in influenza A H1N1pdm09 viruses.[9] This data is exploratory in nature and should be interpreted with caution. Antiviral resistance is determined by investigation at specific sites previously identified to confer resistance and does not account for all potential mechanisms of resistance. This data should not be used to directly inform clinical decisions. See Technical Notes for details.

Table 9a: Number and Percentage of Positive Influenza A Specimens Sequenced with Amino Acid Substitution I38T Associated with Baloxavir Resistance, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	Amino Acid Substitution I38T
H1N1pdm09	**0.0% (0/69)**
C.1.9.3	0.0% (0/2)
D.3.1	0.0% (0/13)
D.3.1.1	0.0% (0/54)
H3N2	**0.0% (0/278)**
J.2.3	0.0% (0/1)
J.2.4	0.0% (0/39)
K	0.0% (0/238)
Total Sequenced	**0.0% (0/347)**

Note: I38T substitution in the PA gene of the influenza A or B genome has been associated with baloxavir resistance.[10] Not all influenza sequences within this report had sufficient sequence quality at the PA gene to be included within the I38T analysis. As such, the total number of sequences included differs from other tables and figures based on the NA gene. This data is exploratory in nature and should be interpreted with caution. Antiviral resistance is determined by investigation at specific sites previously identified to confer resistance and does not account for all potential mechanisms of resistance. This data should not be used to directly inform clinical decisions. See Technical Notes for details.

Table 9b: Number and Percentage of Positive Influenza B Specimens Sequenced with Amino Acid Substitution I38T Associated with Baloxavir Resistance, by Genetic Characterization, Public Health Ontario, August 24, 2025 to May 23, 2026

Genetic Characterization	Amino Acid Substitution I38T
Victoria	**0.0% (0/13)**
C.3.1	0.0% (0/1)
C.5.6	0.0% (0/6)
C.5.6.1	0.0% (0/6)
Total Sequenced	**0.0% (0/13)**

Note: I38T substitution in the PA gene of the influenza A or B genome has been associated with baloxavir resistance.[10] Not all influenza sequences within this report had sufficient sequence quality at the PA segment to be included within the I38T analysis. As such, the total number of sequences included differs from other tables and figures based on the NA gene. This data is exploratory in nature and should be interpreted with caution. Antiviral resistance is determined by investigation at specific sites previously identified to confer resistance and does not account for all potential mechanisms of resistance. This data should not be used to directly inform clinical decisions. See Technical Notes for details.

Technical Notes

Data Sources

Public Health Ontario (PHO)

- Data were extracted from the PHO Laboratory Information Management System on May 26, 2026 at approximately 5:00 p.m.
- Bioinformatics processing of data by the Biocomputing Centre were completed on June 23, 2026 at approximately 12:00 pm.

Influenza Whole Genome Sequencing Strategy

- The 2025-2026 influenza season began on August 24, 2025.
- A random sample of 399 eligible specimens from November 16, 2025 to May 23, 2026 were selected for whole genome sequencing. Of those, 373 were successfully sequenced, this represented 3.7% of influenza positive specimens at PHO. The early season (August 24, 2025 to November 15, 2025) was subsampled to include a random sample of 3.7% of specimens as well. In total, 394 specimens were included in this report.
- Specimens were eligible for WGS if they had Ct value ≤ 27 for influenza, sufficient volume remaining, and were PCR positive only for influenza A or influenza B (no co-infection). Additionally, only the first specimen from an outbreak was eligible for WGS and specimens that were submitted on behalf of the Sentinel Practitioner Surveillance Network (SPSN) were excluded.
- Only upper respiratory specimens (e.g. nasopharyngeal or throat swabs) were included.
- Genetic characterization of specimens was completed using whole genome sequencing and analyzed by a bioinformatics pipeline using Fastp (0.23.2), CFIA-NCFAD/nf-flu (3.10.1), bwa (0.7.17), bedtools (2.31.1), bcftools (1.22), ivar (1.4.3), emboss (6.6.0), and BLAST (2.17.0).[11-19] Clade and subclade were assigned with Nextclade (3.18.0) and Nextclade dataset (2026-04-14—11-55-23Z).[20-21] Time-scaled phylogenetic tree was created using IQ-TREE 3 and TreeTime.[22-23] The maximum likelihood phylogenetic tree was generated based on influenza HA-gene sequences using IQ-TREE 3 with the GTR model (General time reversible model with unequal rates and unequal base freq), and 100 bootstrap replicates.[24] The tree was rooted on the vaccine strain and time-scaled using a clock rate of 3×10^{-3} substitutions/site/year for influenza A(H1N1pdm09) and influenza B, and 5.88×10^{-3} substitutions/site/year for influenza A(H3N2), with clock filtering disabled.

Respiratory Testing Algorithm

- PHO's laboratory respiratory testing algorithm is based on patient setting.
- MRVP testing is offered to individuals exhibiting respiratory symptoms that meet at least one of the following eligibility criteria:
  - Hospitalized patients requiring intensive care
  - Hospitalized admitted patients that are
    - Children < 18 years who are at risk of complications, in the presence of community-acquired pneumonia, or
    - immunocompromised or immunosuppressed, or
    - pregnant

- Patients/residents who are part of a hospital or PHU-declared respiratory outbreak. Only the first four symptomatic patients in a respiratory outbreak are eligible, subsequent patients will be tested by FLUVID.

- FLUVID testing is offered to individuals exhibiting respiratory symptoms that meet at least one of the following eligibility criteria:
  - Residents in congregate living setting (long-term care, retirement home, and correctional facilities) that are not in an outbreak
  - Residents of a congregate living setting that is in an outbreak beyond the first four specimens tested by MRVP
  - Adults admitted to the hospital
  - Staff from congregate living settings that are part of an outbreak.
- Individuals attending physician offices that are part of the Sentinel Practitioner Surveillance Network (SPSN)[19] are tested by MRVP and are exempt from laboratory testing restrictions.

Respiratory Testing Methods

- Testing for influenza at PHO is performed using:
  - A laboratory-developed multiplex respiratory virus PCR panel assay (MRVP). The assay includes 11 targets including influenza A, influenza A H1N1pdm09, influenza Aseasonal H3N2, and influenza B.
  - FLUVID assay includes influenza A and B, as well as respiratory syncytial virus (RSV A/B), and SARS-CoV-2 (COVID-19).
  - A separate influenza A subtype real-time PCR assay. This assay is mainly used for influenza A positive specimens referred to PHO for subtype testing.

Antigenic Characterization

- Antigenic characterization of influenza viruses involves an investigation of key proteins present on the outer surface of the influenza virus that can stimulate an immune response in the infected host. The main antigenic sites are contained within proteins which are involved in the entry and release of viral particles in host cells (the hemagglutinin (HA) and neuraminidase (NA) proteins). Antibodies that bind to specific regions of these proteins can initiate recognition of the virus by the infected host cells.[25]
- Within a respiratory season, antigenic characterization (typing/matching) of circulating influenza viruses can be assessed by in vitro laboratory experiments that measure the strength of antibody responses and by sequence-based analysis of the viral genome. The similarity in genetic sequence can be used to determine the degree of relatedness between currently circulating influenza strains and those included in the recommended annual influenza vaccine.
- The data presented provides a summary of the mutations identified in the main antigenic sites relative to the influenza viruses in circulation at the time of this report. This data is exploratory in nature and should be interpreted with caution. The potential outcomes of the identified mutations on vaccine-induced immunity or antiviral response are unknown. This data should not be used to directly inform clinical decisions.

Antiviral Resistance

- Antiviral resistance was based on screening of genomic data for molecular markers of resistance as opposed to susceptibility testing.
- H275Y in the neuraminidase gene is considered a clinically relevant amino acid substitution associated with oseltamivir resistance in influenza A H1N1pdm09 viruses.[9] The effect of other substitutions (including those in H3N2 viruses) within this gene on oseltamivir resistance are not well described.
- I38T in the polymerase acidic (PA) gene is considered a clinically relevant amino acid substitution associated with baloxavir resistance in influenza A and influenza B viruses.[10] The effect of other substitutions within this gene on baloxavir resistance are not well described.

Data Caveats

This report is based on specimens tested at PHO and may not be representative of Ontario overall, as other hospitals and private laboratories also provide respiratory pathogen testing services. In addition, specimen selection for genetic characterization may not fully represent all patient settings across Ontario.

- Specimens available for this report represented 26% of all influenza positive specimens in Ontario during this time period.
- PHO tests more individuals over 65 years of age and that reside in congregate living settings. For this reason, results may overrepresent older individuals and those residing in congregate living settings.
- Additional biases may be introduced due to eligibility criteria for diagnostic testing, catchment area of PHO testing, the volume of specimen available, whole genome sequencing specimen selection criteria, and whether a specimen can be successfully sequenced. As a result, H1N1pdm09 and H3N2 subtype proportions sequenced may not align with the Ontario Respiratory Virus Tool.
- Counts based on specimens do not represent unique individuals, as some individuals may have more than one specimen tested.
- The specimen date was assigned using the sample collection date when available, or the date of entry into PHO's laboratory information system if the collection date was missing.
- Age was assigned based on the birth date provided and the specimen date (sample collection date when available, or the date of entry into PHO's laboratory information system if the collection date was missing).
- Patient setting is missing for approximately 17% of influenza specimens.
- Region was assigned based on patient address when available and submitter address when missing. As such, a small proportion of individuals with missing patient address on the requisition may be misclassified.

  The regional groupings include the following public health units:

  - Northern region includes Algoma Public Health, Northeastern Public Health (formerly Porcupine Health Unit and Timiskaming Health Unit), Northwestern Health Unit, North Bay Parry Sound District Health Unit, Public Health Sudbury & Districts, and Thunder Bay District Health Unit.
  - Eastern includes Eastern Ontario Health Unit, Ottawa Public Health, Renfrew County and District Health Unit, and Southeast Public Health (formerly Hastings and Prince Edward Counties Health Unit, Kingston, Frontenac and Lennox and Addington Health Unit, and Leeds, Grenville and Lanark District Health Unit).

- Central East includes Durham Region Health Department, Lakelands Public Health (formerly Haliburton, Kawartha, Pine Ridge District Health Unit and Peterborough County-City Health Unit), Peel Public Health, Simcoe Muskoka District Health Unit, and York Region Public Health.
- Toronto includes Toronto Public Health.
- South West includes Chatham-Kent Public Health, Grey Bruce Health Unit, Huron Perth Public Health, Lambton Public Health, Middlesex-London Health Unit, Southwestern Public Health, and Windsor-Essex County Health Unit.
- Central West includes City of Hamilton Public Health Services, Grand Erie Public Health (formerly Brant County Health Unit and Haldimand-Norfolk Health Unit), Halton Region Public Health, Niagara Region Public Health, Region of Waterloo Public Health and Emergency Services, and Wellington-Dufferin-Guelph Public Health.

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Appendix A: Number of Positive Influenza A and B Specimens Tested at Public Health Ontario by Subtype

Table A1: Number and Percentage of Positive Influenza A and B Specimens, Number and Percentage Sequenced, by Subtype, Public Health Ontario, August 24, 2025 to May 23, 2026

Subtype	Number of Positive Specimens (Percentage)	Number Sequenced (Percentage)
Influenza A	**6,810 (93.4%)**	**379 (96.2%)**
H1N1pdm09	1,142 (15.7%)	86 (21.8%)
Seasonal H3N2	5,668 (77.8%)	293 (74.4%)
Influenza B	**478 (6.6%)**	**15 (3.8%)**
Total Positives	**7,288 (100%)***	**394 (100%)**

Notes: *Includes specimens that tested positive for both H1N1pdm09 and seasonal H3N2 (n=2). Excludes 3,333 positive specimens with unknown subtype (specimens that were unable to be assigned to a subtype or not subtyped). 'Number of Positive Specimens' includes positive specimens initially tested at PHO or positive specimens initially tested by other laboratories and sent to PHO for subtyping by PCR. 'Number Sequenced' includes positive specimens randomly selected for whole genome sequencing and included in this report.

Appendix B: Jurisdictional Comparison of Influenza Specimens by Genetic Characterization

Table B1: Number and Percentage of Positive Influenza A Specimens Sequenced, by Genetic Characterization and Jurisdiction, August 24, 2025 to May 23, 2026

Genetic Characterization	Ontario (August 24 – May 23)	Canada (September 1 – May 23)	United States of America (September 28 – May 23)	United Kingdom (September 29 – May 17)
H1N1pdm09	**86 (22.7%)**	**380 (22.0%)**	**945 (27.3%)**	**277 (14.6%)**
C.1.9.3	2 (0.5%)	5 (0.3%)	3 (0.9%)	3 (0.2%)
D.3.1	17 (4.5%)	138 (8.0%)	256 (7.4%)	6 (0.3%)
D.3.1.1	67 (17.7%)	237 (13.7%)	686 (19.8%)	268 (14.2%)
H3N2	**293 (77.3%)**	**1,351 (78.0%)**	**2,513 (72.7%)**	**1,616 (85.4%)**
J.2	0 (0.0%)	7 (0.4%)	6 (0.2%)	12 (0.6%)
J.2.2	0 (0.0%)	32 (1.8%)	5 (0.1%)	3 (0.2%)
J.2.3	1 (0.3%)	14 (0.8%)	77 (2.2%)	6 (0.3%)
J.2.4	41 (10.8%)	79 (4.6%)	91 (2.6%)	16 (0.8%)
J.2.5	0 (0.0%)	0 (0.0%)	0 (0.0%)	6 (0.3%)
K	251 (66.2%)	1,219 (70.4%)	2,334 (67.5%)	1,573 (83.1%)
Total sequenced	**379 (100%)**	**1,731 (100%)**	**3,458 (100%)**	**1,893 (100%)**

Note: Prevalence may not be directly comparable across jurisdictions due to varying time periods and sampling strategies.

Data Sources: Public Health Ontario (Table 2a), Public Health Agency of Canada[4], Centres for Disease Control and Prevention[26], UK Health Security Agency[27]

Table B2: Number and Percentage of Positive Influenza B Specimens Sequenced, by Genetic Characterization and Jurisdiction, August 24, 2025 to May 23, 2026

Genetic Characterization	Ontario (August 24 – May 23)	Canada (September 1 – May 23)	United States of America (September 28 – May 23)	United Kingdom (September 29 – May 17)
Victoria	**15 (100%)**	**598 (100%)**	**1,162 (100%)**	**53 (100%)**
C.3	0 (0.0%)	9 (1.5%)	5 (0.4%)	1 (1.9%)
C.3.1	1 (6.7%)	67 (11.2%)	804 (69.2%)	14 (26.4%)
C.3.3	0 (0.0%)	9 (1.5%)	18 (1.5%)	0 (0.0%)
C.5	0 (0.0%)	1 (0.2%)	0 (0.0%)	0 (0.0%)
C.5.1	0 (0.0%)	154 (25.8%)	44 (3.8%)	6 (11.3%)
C.5.6	6 (40.0%)	93 (15.6%)	36 (3.1%)	18 (34.0%)
C.5.6.1	8 (53.3%)	256 (42.8%)	209 (18.0%)	13 (24.5%)
C.5.7	0 (0.0%)	9 (1.5%)	46 (4.0%)	1 (1.9%)
Total sequenced	**15 (100%)**	**598 (100%)**	**1,162 (100%)**	**53 (100%)**

Note: Prevalence may not be directly comparable across jurisdictions due to varying time periods and sampling strategies.

Data Sources: Public Health Ontario(Table 2b), Public Health Agency of Canada[4], Centres for Disease Control and Prevention[26], UK Health Security Agency[27]

Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Influenza genomic surveillance in Ontario: 2025–26 season. Toronto, ON: King's Printer for Ontario; 2026.

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