Public Health Ontario | Santé publique Ontario

SURVEILLANCE REPORT

Influenza Genomic Surveillance in Ontario: 2023-24 Early Season

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Introduction

This report summarizes the results of influenza whole genome sequencing completed by Public Health Ontario (PHO) for the beginning of the 2023-24 season.

Highlights

- A total of 43 specimens were sequenced for the inter-seasonal time period (June 1, 2023 to August 26, 2023) and 72 for the current season (August 27, 2023 to November 17, 2023).
- During the interseasonal time period, the most prevalent influenza A genetic subclades were H1N1pdm09 subclade 6B.1A.5a.2a.1 (73.5%) and H1N1pdm09 subclade 6B.1A.5a.2a (20.6%). All influenza B Victoria lineage genetic subclades were V1A.3a.2 (100%).
- Of the 72 specimens sequenced to date from the current season, two H1N1pdm09 genetic subclades and one H3N2 genetic subclade were identified.
    - 28 specimens (38.9%) were H1N1pdm09 genetic subclade 6B.1A.5a.2a.1 and 20 specimens (27.8%) were genetic subclade 6B.1A.5a.2a. The H1N1 component of the current influenza vaccine belongs to the genetic subclade 6B.1A.5a.2a.1.
    - 24 specimens (33.3%) were H3N2 genetic subclade 3C.2a1b.2a.2a.3a.1. The H3N2 component of the current influenza vaccine belongs to the genetic subclade 3C.2a1b.2a.2a.
    - There were no influenza B specimens sequenced in the current season.
- At the molecular level, 47.9% of influenza A H1N1pdm09 specimens contained an amino acid substitution in the antigenic site Ca or Cb relative to the H1N1pdm09 strain included in the vaccine. All influenza A H3N2 specimens contained at least one amino acid substitution in antigenic sites A to E relative to the H3N2 strain included in the vaccine. However, the effect of the identified antigenic site substitutions on vaccine-induced immunity is unknown.
- Of the H1N1pdm09 specimens sequenced, no amino acid substitutions known to be associated with resistance to oseltamivir were detected.

Background

There are two types of influenza viruses (influenza A and B) that are responsible for most cases during the influenza season. Influenza A can be further classified into subtypes (e.g., H1N1, H3N2) and influenza B can be further classified into lineages (e.g., Yamagata, 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, 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 2023-2024 influenza season, publicly funded vaccines available in Ontario are egg-based trivalent (influenza A H1N1 subclade 6B.1A.5a.2a.1, influenza A H3N2 subclade 3C.2a1b.2a.2a, and influenza B Victoria subclade V1A.3) and quadrivalent (addition of influenza B Yamagata subclade Y3) inactivated vaccines.[2-4]

It is estimated that PHO conducts approximately 31.6% of all influenza virus testing in Ontario that is reported to the Public Health Agency of Canada.[5] PHO performs routine testing for seasonal respiratory viruses for select population groups, including:

- Symptomatic residents (and associated healthcare workers/staff) in congregate living settings (e.g. retirement homes, long-term care homes, correctional facilities, etc.).
- Symptomatic individuals associated with an outbreak investigation.
- Hospitalized individuals, including those in intensive care.
- Symptomatic individuals, <18 years old, who receive care in an emergency department.[6]
- Individuals attending physician offices that are part of the Sentinel Practitioner Surveillance Network (see Technical Notes for additional information).[7]

To understand the diversity of the virus circulating during the influenza season, PHO began sequencing eligible specimens (Ct ≤ 30 and sufficient volume remaining) positive for influenza in the interseasonal time period and the 2023-24 season. This excludes specimens that are positive for more than one virus. Additionally, only the first positive specimen from an outbreak is selected for whole genome sequencing. Sequences are processed using bioinformatics analyses and are assigned subtypes, lineages, clades, and subclades.

Interseasonal and Current Season Results

Table 1a. Number and percentage of positive influenza A specimens by genetic characterization and season, Public Health Ontario, June 1 to November 17, 2023

Genetic characterization	Interseasonal (June 1 - August 26)	2023-24 Season (August 27 – November 17)
H1N1pdm09	**32 (94.1%)**	**48 (66.7%)**
6B.1A.5a.2a	7 (20.6%)	20 (27.8%)
6B.1A.5a.2a.1	25 (73.5%)	28 (38.9%)
H3N2	**2 (5.9%)**	**24 (33.3%)**
3C.2a1b.2a.2a.3a	1 (2.9%)	0 (0.0%)
3C.2a1b.2a.2a.3a.1	1 (2.9%)	24 (33.3%)
Total sequenced	**34 (100%)**	**72 (100%)**

Note: Results may not be representative of Ontario overall. Date was assigned based on the earliest date available for the specimen. In total there were 384 specimens positive for influenza A at PHOL during this time period, of which 27.6% were sequenced.
Data sources: PHO Laboratory Information Management System

Table 1b. Number and percentage of positive influenza B specimens by genetic characterization and season, Public Health Ontario, June 1 to November 17, 2023

Genetic characterization	Interseasonal (June 1 - August 26)	2023-24 Season (August 27 - November 17)
Victoria lineage	**9 (100%)**	**0 (0.0%)**
V1A.3a.2	9 (100%)	0 (0.0%)
Yamagata lineage	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**9 (100%)**	**0 (0.0%)**

Note: Date was assigned based on the earliest date available for the specimen. In total there were 29 specimens positive for influenza B at PHOL (all during the interseasonal time period), of which 31.0% were sequenced.
Data sources: PHO Laboratory Information Management System

Current Season Results

Figure 1. Percentage of influenza specimens by genetic characterization, Public Health Ontario, August 27 to November 17, 2023

Note: The genetic subclades included in this seasons' influenza vaccine are influenza A H1N1 subclade 6B.1A.5a.2a.1, influenza A H3N2 subclade 3C.2a1b.2a.2a, and influenza B Victoria subclade V1A.3, and influenza B Yamagata subclade Y3.[4] Results may not be representative of Ontario overall.
Data sources: PHO Laboratory Information Management System

Table 2. Number of positive influenza specimens, number and percentage sequenced, Public Health Ontario, August 27 to November 17, 2023

Week	Number of positive specimens	Number sequenced	Percentage sequenced
August 27 - September 2	11	0	0.0%
September 3 - September 9	12	0	0.0%
September 10 - September 16	7	0	0.0%
September 17 - September 23	12	0	0.0%
September 24 - September 30	10	0	0.0%
October 1 - October 7	9	0	0.0%
October 8 - October 14	12	1	8.3%
October 15 - October 21	15	1	6.7%
October 22 - October 28	15	4	26.7%
October 29 - November 4	17	6	35.3%
November 5 - November 11	45	25	55.6%
November 12 - November 18*	98	35	35.7%
Total	**263**	**72**	**27.4%**

Note: *The most recent week is a partial week. 'Number of positive specimens' is the number of positive influenza specimens reported by PHO. 'Number sequenced' is the number of specimens sequenced for representative surveillance. Results may not be representative of Ontario overall, and do not include all specimens tested for other reasons including travel, outbreak investigation, coroner's cases, reinfection or possible vaccine escape. 'Percentage sequenced' may be lower than the sampling proportion because not all specimens are eligible to be sequenced (i.e. excludes specimens with cycle threshold >30 or insufficient volume). Week was assigned based on earliest date available for a specimen. The genetic subclades included in this season's influenza vaccine are influenza A H1N1 subclade 6B.1A.5a.2a.1, influenza A H3N2 subclade 3C.2a1b.2a.2a, and influenza B Victoria subclade V1A.3, and influenza B Yamagata subclade Y3.[4]
Data sources: PHO Laboratory Information Management System

Table 3a. Number and percentage of influenza A H1N1 specimens with any antigenic site amino acid substitutions by genetic characterization, Public Health Ontario, August 27 to November 17, 2023

Genetic characterization	HA antigenic site Ca	HA antigenic site Cb	Total
H1N1pdm09	**43.8% (21/48)**	**4.2% (2/48)**	**47.9% (23/48)**
6B.1A.5a.2a	100% (20/20)	0.0% (0/20)	100% (20/20)
6B.1A.5a.2a.1	3.6% (1/28)	7.1% (2/28)	10.7% (3/28)
Total sequenced	**43.8% (21/48)**	**4.2% (2/48)**	**47.9% (23/48)**

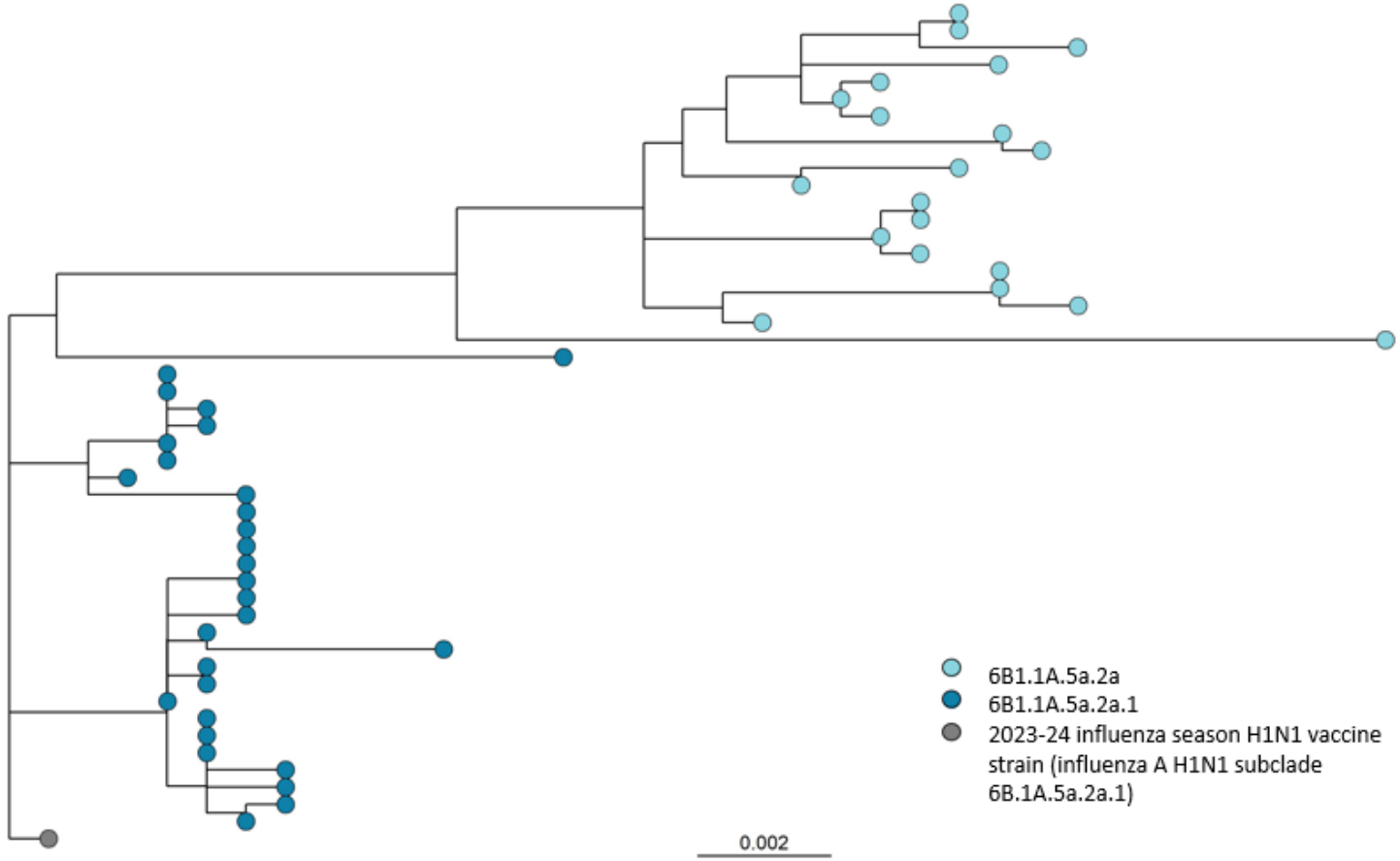
Note: The effect of the identified antigenic site substitutions on vaccine-induced immunity is unknown. This data is exploratory in nature and should be interpreted with caution. This data should not be used to directly inform clinical decisions or infer impacts on vaccine-induced immunity. See technical notes for details. Antigenic site amino acid substitutions were identified relative to the strain included in the 2023-24 influenza vaccine (influenza A H1N1 subclade 6B.1A.5a.2a.1). Specimens may have substitutions at more than one position within the antigenic site. Antigenic site Ca includes substitutions at positions 137, 138, 139, 142, 169, 204 of the HA protein. Antigenic site Cb includes substitutions at position 74 of the HA protein.
Data sources: PHO Laboratory Information Management System

Table 3b. Number and percentage of influenza A H3N2 specimens with any antigenic site amino acid substitutions by genetic characterization, Public Health Ontario, August 27 to November 17, 2023

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% (24/24)**	**100% (24/24)**	**100% (24/24)**	**100% (24/24)**	**25.0% (6/24)**	**100% (24/24)**
3C.2a1b.2a.2a.3a.1	100% (24/24)	100% (24/24)	100% (24/24)	100% (24/24)	25.0% (6/24)	100% (24/24)
Total sequenced	**100% (24/24)**	**100% (24/24)**	**100% (24/24)**	**100% (24/24)**	**25.0% (6/24)**	**100% (24/24)**

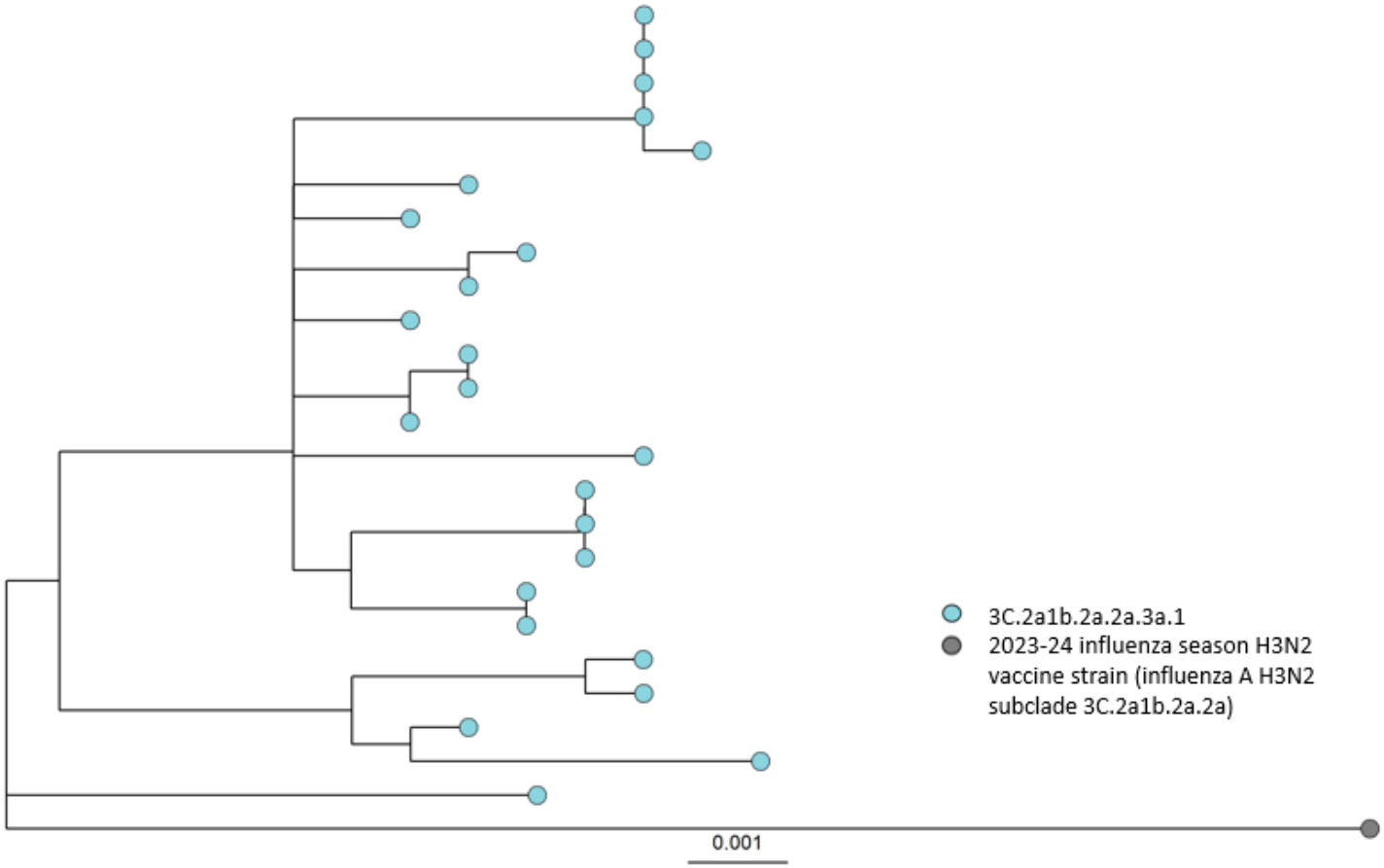
Note: The effect of the identified antigenic site substitutions on vaccine-induced immunity is unknown. This data is exploratory in nature and should be interpreted with caution. This data should not be used to directly inform clinical decisions. See technical notes for details. Antigenic site amino acid substitutions were identified relative to the strain included in the 2023-24 influenza vaccine (influenza A H3N2 subclade 3C.2a1b.2a.2a). Specimens may have substitutions at more than one position within the antigenic site. Antigenic site A includes substitutions at positions 122, and 140 of the HA protein. Antigenic site B includes substitutions at position 157, 186, and 192 of the HA protein. Antigenic site C includes substitutions at positions 50, 53, 54, 276, and 309 of the HA protein. Antigenic site D includes substitutions at position 96 and 182 of the HA protein. Antigenic site E includes substitutions at positions 63 and 78 of the HA protein.
Data sources: PHO Laboratory Information Management System

Figure 2a. Phylogenetic tree of influenza A H1N1 positive specimens, Public Health Ontario, August 27 to November 17, 2023



Note: Each circle represents a separate specimen. Results may not be representative of Ontario overall. The maximum likelihood phylogenetic tree was generated using the IQ-TREE GTR model with 100 bootstrap replicates. Identical sequences are retained in the tree. The tree is rooted with the vaccine reference strain A/Victoria/4897/2022_H1N1_pdm09-like-virus (EPI_ISL_16714268).
Data sources: PHO Laboratory Information Management System

Figure 2b. Phylogenetic tree of influenza A H3N2 positive specimens, Public Health Ontario, August 27 to November 17, 2023



Note: Each circle represents a separate specimen. Results may not be representative of Ontario overall. The maximum likelihood phylogenetic tree was generated using the IQ-TREE GTR model with 100 bootstrap replicates. Identical sequences are retained in the tree. The tree is rooted with the vaccine reference strain A/Darwin/9/2021_H3N2-like-virus (EPI_ISL_2233240).
Data sources: PHO Laboratory Information Management System

Table 4. Number and percentage of positive influenza A specimens by genetic characterization and age group, Public Health Ontario, August 27 to November 17, 2023

Genetic characterization	Ages: 0-4	Ages: 5-19	Ages: 20-64	Ages: 65 and over	Total
H1N1pdm09	**11 (91.7%)**	**13 (86.7%)**	**15 (55.6%)**	**9 (50.0%)**	**48 (66.7%)**
6B.1A.5a.2a	4 (33.3%)	6 (40.0%)	7 (25.9%)	3 (16.7%)	20 (27.8%)
6B.1A.5a.2a.1	7 (58.3%)	7 (46.7%)	8 (29.6%)	6 (33.3%)	28 (38.9%)
H3N2	**1 (8.3%)**	**2 (13.3%)**	**12 (44.4%)**	**9 (50.0%)**	**24 (33.3%)**
3C.2a1b.2a.2a.3a.1	1 (8.3%)	2 (13.3%)	12 (44.4%)	9 (50.0%)	24 (33.3%)
Total sequenced	**12 (100%)**	**15 (100%)**	**27 (100%)**	**18 (100%)**	**72 (100%)**

Note: Results may not be representative of Ontario overall. Age was assigned based on the birth date provided; excludes specimens with missing birth dates. The genetic subclades included in this season's influenza vaccine are influenza A H1N1 subclade 6B.1A.5a.2a.1, influenza A H3N2 subclade 3C.2a1b.2a.2a, and influenza B Victoria subclade V1A.3, and influenza B Yamagata subclade Y3.[4]
Data sources: PHO Laboratory Information Management System

Table 5. Number and percentage of positive influenza A specimens by genetic characterization and setting, Public Health Ontario, August 27 to November 17, 2023

Genetic characterization	Intensive Care Unit	Hospital/Emergency Department	Congregate Living	Ambulatory or no setting reported	Total
H1N1pdm09	**1 (100%)**	**34 (79.1%)**	**3 (42.9%)**	**10 (47.6%)**	**48 (66.7%)**
6B.1A.5a.2a	1 (100%)	17 (39.5%)	1 (14.3%)	1 (4.8%)	20 (27.8%)
6B.1A.5a.2a.1	0 (0.0%)	17 (39.5%)	2 (28.6%)	9 (42.9%)	28 (38.9%)
H3N2	**0 (0.0%)**	**9 (20.9%)**	**4 (57.1%)**	**11 (52.4%)**	**24 (33.3%)**
3C.2a1b.2a.2a.3a.1	0 (0.0%)	9 (20.9%)	4 (57.1%)	11 (52.4%)	24 (33.3%)
Total sequenced	**1 (100%)**	**43 (100%)**	**7 (100%)**	**21 (100%)**	**72 (100%)**

Note: Results may not be representative of Ontario overall. 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). Only one specimen per outbreak was selected for sequencing. Approximately 26.4% of specimens are missing information on setting and are grouped into 'Ambulatory or no setting reported' category. The genetic subclades included in this season's influenza vaccine are influenza A H1N1 subclade 6B.1A.5a.2a.1, influenza A H3N2 subclade 3C.2a1b.2a.2a, and influenza B Victoria subclade V1A.3, and influenza B Yamagata subclade Y3.[4]
Data sources: PHO Laboratory Information Management System

Table 6. Number and percentage of positive influenza A specimens by genetic characterization and region, Public Health Ontario, August 27 to November 17, 2023

Genetic characterization	Northern	Eastern	Central East	Toronto	South West	Central West	Total
H1N1pdm09	**0 (0.0%)**	**6 (54.5%)**	**24 (88.9%)**	**9 (42.9%)**	**2 (100%)**	**7 (63.6%)**	**48 (66.7%)**
6B.1A.5a.2a	0 (0.0%)	2 (18.2%)	13 (48.1%)	1 (4.8%)	1 (50.0%)	3 (27.3%)	20 (27.8%)
6B.1A.5a.2a.1	0 (0.0%)	4 (36.4%)	11 (40.7%)	8 (38.1%)	1 (50.0%)	4 (36.4%)	28 (38.9%)
H3N2	**0 (0.0%)**	**5 (45.5%)**	**3 (11.1%)**	**12 (57.1%)**	**0 (0.0%)**	**4 (36.4%)**	**24 (33.3%)**
3C.2a1b.2a.2a.3a.1	0 (0.0%)	5 (45.5%)	3 (11.1%)	12 (57.1%)	0 (0.0%)	4 (36.4%)	24 (33.3%)
Total sequenced	**0 (0.0%)**	**11 (100%)**	**27 (100%)**	**21 (100%)**	**2 (100%)**	**11 (100%)**	**72 (100%)**

Note: Results may not be representative of Ontario overall. 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 genetic subclades included in this season's influenza vaccine are influenza A H1N1 subclade 6B.1A.5a.2a.1, influenza A H3N2 subclade 3C.2a1b.2a.2a, and influenza B Victoria subclade V1A.3, and influenza B Yamagata subclade Y3.[4]
Data sources: PHO Laboratory Information Management System

Table 7. Number and percentage of H1N1pdm09 specimens with amino acid substitution H275Y associated with oseltamivir resistance, among influenza A specimens by genetic characterization, Public Health Ontario, August 27 to November 17, 2023

Genetic characterization	Amino acid substitution H275Y
H1N1pdm09	**0.0% (0/48)**
6B.1A.5a.2a	0.0% (0/20)
6B.1A.5a.2a.1	0.0% (0/28)
Total sequenced	**0.0% (0/48)**

Note: H275Y substitution has been associated with oseltamivir resistance in influenza A H1N1 viruses.[8] See technical notes for details. 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.
Data sources: PHO Laboratory Information Management System

Technical Notes

Data Sources

PUBLIC HEALTH ONTARIO (PHO)

- Data were extracted from the PHO Laboratory Information Management System on December 22, 2023 at approximately 12:00 p.m.
- Bioinformatics processing of data by the Biocomputing Centre were completed on December 21, 2023 at approximately 4:00pm.

Public Health Ontario's influenza Whole Genome Sequencing Strategy

- Due to low case counts in the beginning of the season, Public Health Ontario has used a convenience sampling to select all eligible specimens (Ct ≤ 30 and sufficient volume remaining) for whole genome sequencing. This excludes specimens that are positive for more than one virus.
- Only the first specimen from an outbreak is selected for whole genome sequencing. Multiple specimens from the same outbreak are not selected.

Public Health Ontario Respiratory Testing Algorithm

- PHO's laboratory respiratory testing algorithm is based on patient setting.
- PHO laboratory performs multiplex respiratory virus PCR (MRVP) on symptomatic children (<18 years) seen in the emergency department (ED), symptomatic hospitalized patients (ward and ICU/CCU), symptomatic residents in institutional settings (non-outbreak), specimens from the first four symptomatic individuals (including healthcare workers/staff) in an outbreak that requests respiratory virus testing.
- PHO laboratory performs FLUVID, which detects influenza A, influenza B, respiratory syncytial virus, and SARS-CoV-2, on symptomatic residents and healthcare workers/staff in the institutional settings in an outbreak beyond the first four that has been tested for SARS-CoV-2 and MRVP.
- Individuals attending physician offices that are part of the Sentinel Practitioner Surveillance Network (SPSN) [7] are tested by MRVP and are exempt from laboratory testing restrictions.

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 H3N2, influenza A H1N1pdm09, and influenza B.
  - A FLUVID assay includes influenza A and B, as well as respiratory syncytial virus (RSV A/B), and SARS-CoV-2 (COVID-19). This assay may be used as an initial test prior to MRVP to provide earlier results during influenza and RSV seasons.

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.[8]

- 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 is 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 has been well-documented to be a clinically relevant amino acid substitution associated with oseltamivir resistance in influenza A H1N1 viruses.[9] The effect of other substitutions (including those in H3N2 viruses) on antiviral resistance are not well described.

Data Caveats

This report is based on specimens tested at PHO and may not be representative of Ontario, 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.

- PHO conducts approximately 31.6% of influenza testing in Ontario. Further, only 27.4% of positive specimens were sequenced during the current season. Biases may introduced due 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, the results may not represent Ontario overall.
- Counts based on specimens do not represent unique individuals, as some individuals may have more than one specimen tested.
- Region was assigned based on patient address when available and submitter address when missing. As such, individuals with missing patient address on the requisition may be misclassified.
- Northern region includes Northwestern Health Unit, Thunder Bay District Health Unit, Porcupine Health Unit, Algoma Public Health, Public Health Sudbury & Districts, Timiskaming Health Unit, and North Bay Parry Sound District Health Unit; Eastern includes Renfrew County and District Health Unit,

Ottawa Public Health, Eastern Ontario Health Unit, Leeds, Grenville & Lanark District Health Unit, Kingston, Frontenac and Lennox & Addington Public Health (KFLA), and Hastings Prince Edward Public Health; Central East includes Haliburton, Kawartha, Pine Ridge District Health Unit (HKPR), Peterborough Public Health , Durham Region Health Department , Simcoe Muskoka District Health Unit, York Region Public Health, Peel Public Health; Toronto includes Toronto Public Health; Central West includes Niagara Region Public Health, Halton Region Public Health , Hamilton Public Health Services, Brant County Health Unit, Wellington-Dufferin-Guelph Public Health, Region of Waterloo Public Health and Emergency Services, City of Haldimand-Norfolk Health Unit; South West: Grey Bruce Health Unit, Huron Perth Public Health, Southwestern Public Health, Middlesex-London Health Unit , Lambton Public Health, Chatham-Kent Public Health, Windsor-Essex County Health Unit.

- Age was assigned based on the birth date provided and the specimen collection or login date.
- Patient setting is missing for almost 26.4% of specimens. Therefore, results by patient setting should be interpreted with caution.

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Appendix A: Jurisdictional Comparison

Supplementary table 1. Number and percentage of positive influenza A specimens by genetic characterization and jurisdiction, August 20 to November 18, 2023

Genetic characterization	Ontario (August 27 - November 17)	Canada (September 1 - November 18)	United States of America (October 1 - November 18)	United Kingdom (August 20 - November 18)
H1N1pdm09	**48 (66.7%)**	**63 (87.5%)**	**440 (84.6%)**	**20 (47.6%)**
6B.1A.5a.2a	20 (27.8%)	14 (19.4%)	141 (27.1%)	14 (33.3%)
6B.1A.5a.2a.1	28 (38.9%)	49 (68.1%)	299 (57.5%)	6 (14.3%)
H3N2	**24 (33.3%)**	**9 (12.5%)**	**80 (15.4%)**	**22 (52.4%)**
3C.2a1b.2a.2a.1b	0 (0.0%)	0 (0.0%)	1 (0.2%)	0 (0.0%)
3C.2a1b.2a.2a.3a	0 (0.0%)	0 (0.0%)	4 (0.8%)	0 (0.0%)
3C.2a1b.2a.2a.3a.1	24 (33.3%)	9 (12.5%)	74 (14.2%)	22 (52.4%)
3C.2a1b.2a.2a.2b	0 (0.0%)	0 (0.0%)	1 (0.2%)	0 (0.0%)
Total sequenced	**72 (100%)**	**72 (100%)**	**520 (100%)**	**42 (100%)**

Notes: Prevalence may not be directly comparable across jurisdictions due to varying time periods and sampling strategies.
Data Sources: Public Health Ontario, Public Health Agency of Canada , UK Health Security Agency , Centres for Disease Control and Prevention

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