



## Influenza strain characterization for the 2025/2026 influenza season

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January 28, 2026

### Summary and interpretation of data collected July-December 2025, epidemiological weeks 28-53

#### Genetic Characterization of Influenza A (H1N1, H3N2) from Clinical Cases

- Among subtyped influenza A samples (n=4,824) collected between July 6, 2025 (epi-week 28) and January 3, 2026 (epi-week 53), the proportion of H1 and H3 viruses shifted from H1 predominance in the early season, to H3 predominance in mid-November through December (**Table 1**).
  - In December, the proportion of H3 detections was 86% (**Table 1**).
- A subset of positive samples (n=308/4,824, 6%) were selected for sequencing by the BCCDC Public Health Laboratory.
  - Overall, 303 clinical samples collected between July 11 and December 31, 2025, generated high quality sequence data.
  - Clade assessment based on sequence analysis of the hemagglutinin (HA) gene identified two H1N1 subclades (C.1.9.3 and D.3.1) and five H3N2 subclades (J.2, J.2.2, J.2.3, J.2.4 and K) (**Figure 1**).
  - Since October, 90% of H3 viruses sequenced were subclade K. Most recently in December, this proportion increased to 97% (**Figure 1**).
  - Notably, J.2.4 viruses, in particular subclade K, have vaccine immune escape potential ([Sabaiduc et al., Oct 2025](#)).
- Sequenced samples consisted of non-outbreak (99% of the total samples) and outbreak specimens (1%), the breakdown of which is detailed in **Table 2**.
- For more detailed information on provincial influenza monitoring, please refer to the BCCDC Respiratory Surveillance Viral Pathogen Characterization dashboard ([Viral Pathogen Characterization \(shinyapps.io\)](#)).

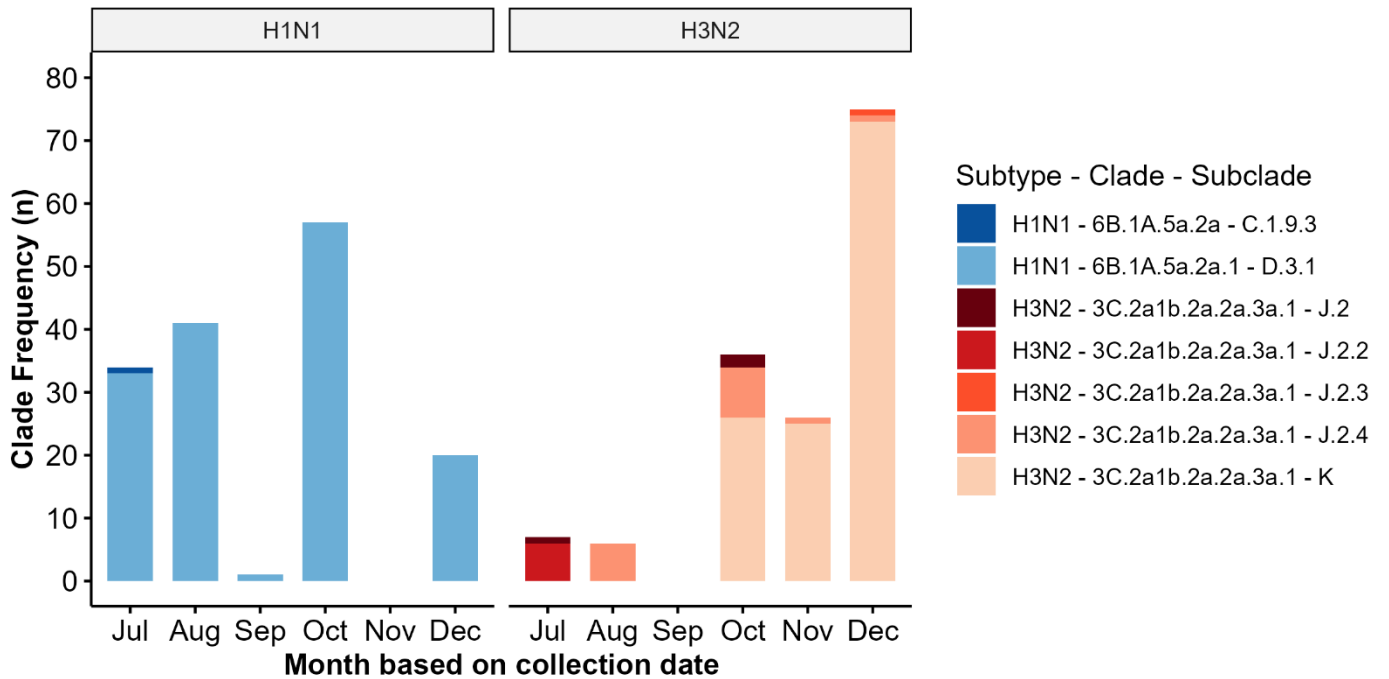
**Table 1.** Provincial influenza A subtyping results by month between July 6, 2025 and January 3, 2026 (based on collection date)

Date (n= total tested*)	Subtype	
	A/H1N1	A/H3N2
July 2025 (n=59)	48 (81%)	8 (14%)
August 2025 (n=91)	75 (82%)	12 (13%)
September 2025 (n=127)	100 (79%)	20 (16%)
October 2025 (n=260)	159 (61%)	78 (30%)
November 2025 (n=935)	314 (34%)	570 (61%)
December 2025 (n=3352)	447 (13%)	2870 (86%)

\* Please note:

- 1- these numbers(n) are for the epi weeks spanning from of July 6, 2025 to Jan 3, 2026. As such, July is an incomplete month, and December includes Jan 1-3, 2026
- 2- some epi weeks span over two months – these are added to the month that matches the first date of the epi week (e.g. epi week 44, Oct 26 – Nov 1, 2025 will be added to the month of October)
- 3- the proportion of subtyped samples does not sum to 100% because of the small number of samples that are of unknown subtype

**Figure 1.** Influenza A clade characterization by month, subtype and subclade (July 11 to December 31, 2025)



**Table 2.** Summary of sequenced influenza samples based on subtype, subclade and collection type (surveillance vs. outbreak)

Subtype-Clade-Subclade	Sample Type		
	Outbreak	Non-Outbreak	Total
H1 - 6B.1A.5a.2a - C.1.9.3	0	1	1
H1 - 6B.1A.5a.2a.1 - D.3.1	0	152	152
H3 - 3C.2a1b.2a.2a.3a.1 - J.2	0	3	3
H3 - 3C.2a1b.2a.2a.3a.1 - J.2.2	0	6	6
H3 - 3C.2a1b.2a.2a.3a.1 - J.2.3	0	1	1
H3 - 3C.2a1b.2a.2a.3a.1 - J.2.4	0	16	16
H3 - 3C.2a1b.2a.2a.3a.1 - K	2	122	124
All Clades	2	301	303

### Genetic Characterization of Influenza A (H1N1, H3N2) from Wastewater

Sequencing of influenza A in wastewater is being performed as part of a research project.

- Influenza sequence abundance shows a significant upward trend at most sites in the latter half of December and early January, with H3N2 now completely dominating over H1N1. This is consistent with observed clinical trends.
- Earlier sequences (June-September) showed a higher proportion of H1 and N1 sequences.

### Antigenic Characterization of Influenza A (H3N2, H1N1)

Antigenic characterization of influenza A isolates from across Canada, including BC, is performed by the National Microbiology Laboratory (NML) by hemagglutination inhibition. Since September 1, 2025, NML has antigenically characterized 950 influenza A viruses in total (223 H1N1, 727 H3N2). The results are summarized below.

Regarding H1N1 viruses:

- Of the 223 viruses characterized, 220 were shown to be antigenically similar to an A/Wisconsin/67/2022 (H1N1)pdm09-like virus. Three viruses showed reduced titres, suggesting they are antigenically distinct.

Regarding H3N2 viruses:

- Of the 727 influenza A (H3N2) viruses characterized, 42 were antigenically similar to an A/District of Columbia/27/2023 (H3N2)-like virus and 685 showed reduced titres.
- Specifically, viruses belonging to subclades J.2.3 (n=3), J.2.4 (n=18) and K (n=557), as well as 106 viruses pending genetic characterization, exhibited reduced titres, suggesting they are antigenically distinct from the A/District of Columbia/27/2023 (H3N2)-like strain.



## Vaccine Reference Strains and Sequences

The reference strains included in the 2025-2026 Northern Hemisphere egg-based vaccine are shown below (**Table 3**). A substantial proportion of J.2.4 viruses, including the recently emerged subclade K, show immune escape potential from the 2025-2026 J.2 vaccine strain ([Sabaiduc et al., Oct 2025](#)).

**Table 3.** Vaccine-based virus components in the 2025-2026 Northern Hemisphere Influenza Season\*

Vaccine	Strain	Lineage	Clade (Subclade)
Egg-based	A/Victoria/4897/2022	(H1N1)pdm09-like	5a.2a.1 (D)
	A/Croatia/10136RV/2023	(H3N2)-like	2a.3a.1 (J.2)
	B/Austria/1359417/2021	(B/Victoria lineage)-like	3a.2 (C)
Cell culture- or recombinant-based	A/Wisconsin/67/2022	(H1N1)pdm09-like	5a.2a.1 (C.1.1)
	A/District of Columbia/27/2023	(H3N2)-like	2a.3a.1 (J.2)
	B/Austria/1359417/2021	(B/Victoria lineage)-like	3a.2 (C)
	B/Phuket/3073/2013 (Quadrivalent only)	(B/Yamagata lineage)-like (Quadrivalent only)	Y3

\* As defined by the World Health Organization Guidelines, *Recommended composition of influenza virus vaccines for use in the 2025-2026 northern hemisphere influenza season (who.int)*

We would like to acknowledge the following laboratories for their contribution to provincial surveillance by providing testing data and samples for further characterization:

Children's and Women's Hospital Laboratory, Fraser Health Medical Microbiology Laboratory, Victoria General Hospital, Providence Health Care, Vancouver Coastal Health sites, Interior Health sites and Northern Health sites.

Prepared by the BCCDC Public Health Laboratory and BCCDC Data & Analytics Services with input from the Public Health Response and Immunization Programs and Vaccine Preventable Disease Services teams.