BC Centre for Disease Control
Provincial Health Services Authority

Influenza strain characterization in preparation for the 2025/2026 influenza season

November 6, 2025

Summary and interpretation of data collected July-October 2025, epidemiological weeks 28-43

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

- Among subtyped influenza A viruses (n=416) between July 11 (epi-week 28) to October 19 (epi-week 43), 2025, most were H1 (76%, **Table 1**).
    - Since the start of the 2025-2026 respiratory season that began in epi-week 35 (Aug 24 – 30, 2025), most subtyped influenza A samples have also been H1 (75%).
    - During the two most recent epi-weeks 42 and 43, H3 represented a greater proportion of subtyped viruses at 33% and 36%, respectively.
- A subset of positive samples (n=97/416, 23%) were selected for sequencing by the BCCDC Public Health Laboratory.
    - Overall, 93 clinical samples collected between July 11 and October 19, 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 four H3N2 subclades (J.2, J.2.2, J.2.4 and J.2.4.1, the latter recently renamed subclade K) (**Figure 1**).
    - A detailed analysis of the recent diversification among influenza A(H3N2) viruses across the northern and southern hemispheres has recently been published, suggesting that subclade K is likely to predominate among A(H3N2) variants for the coming season (Sabaiduc *et al.*, Oct 2025).
- Sequenced samples consisted of non-outbreak (98% of the total samples) and outbreak specimens (2%), the breakdown of which is detailed in **Table 2**.

Table 1. Provincial influenza A subtyping results by month between July 11 and October 19th (based on collection date)

	Subtype	
Date (n= total tested*)	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%)	18 (14%)
October 2025 (n=139)	94 (68%)	36 (26%)

***** *Please note:*

1- *these numbers(n) are for the dates of July 11 and October 19, 2025. As such, July and October are incomplete months.*
2- *the proportion of subtyped samples does not sum to 100% because of the small number of samples that are of unknown subtype*

Sequenced samples represent 23% of the samples submitted for subtyping. For more detailed information on provincial influenza monitoring, please refer to the BCCDC Respiratory Surveillance Viral Pathogen Characterization dashboard (Viral Pathogen Characterization (shinyapps.io)).

Figure 1. Influenza A clade characterization by month, subtype and subclade (July 11 to October 19, 2025)

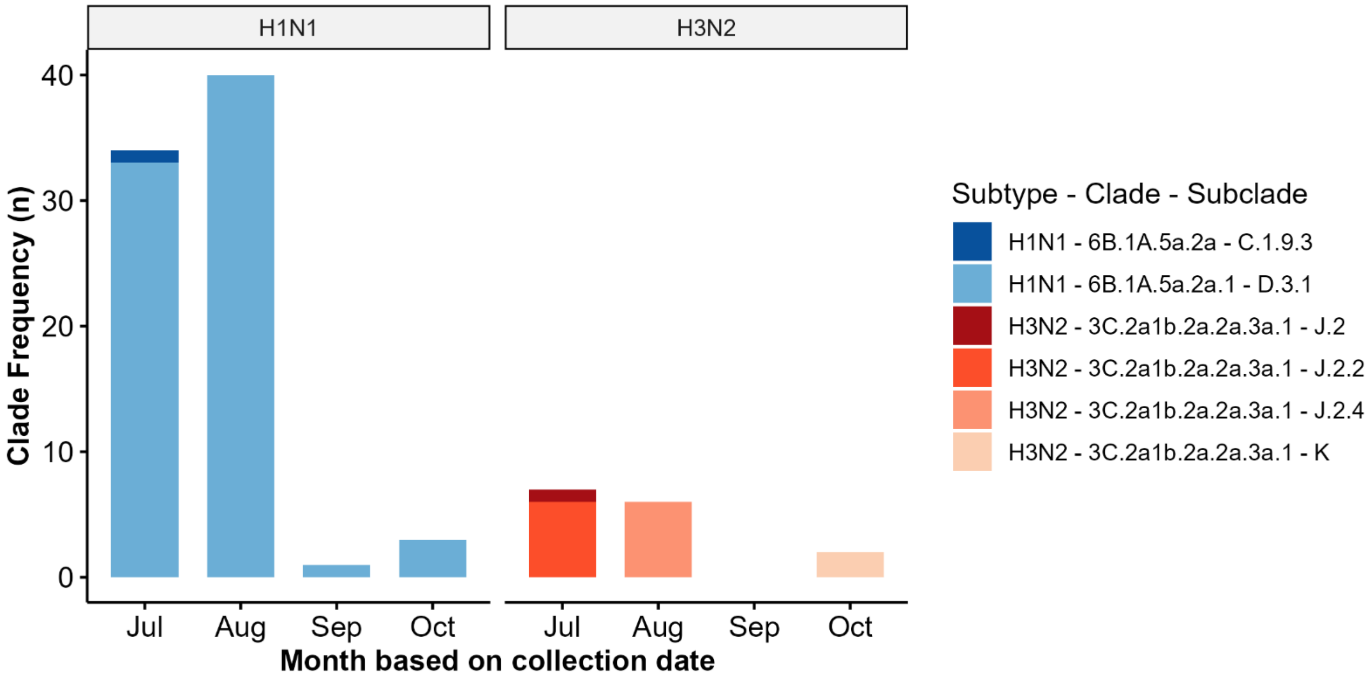

Table 2. Sequenced influenza samples based on collection type (surveillance vs. outbreak)

	Sample Type		
Subtype-Clade-Subclade	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	75	75
H3 - 3C.2a1b.2a.2a.3a.1 - J.2	0	1	1
H3 - 3C.2a1b.2a.2a.3a.1 - J.2.2	0	6	6
H3 - 3C.2a1b.2a.2a.3a.1 - J.2.4	0	6	8
H3 - 3C.2a1b.2a.2a.3a.1 - K	2	0	0
All Clades	2	91	93

**Outbreak samples were from one distinct outbreak that occurred in October 2025.*

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 A detections are still sporadic in wastewater, consistent with early season patterns.
- For samples that are positive for influenza A, increasing incidence of H3 and N2 sequences was observed in October, consistent with clinical data.
- Earlier sequences (June-September) showed a higher proportion of H1 and N1 sequences.

Antigenic Characterization of Influenza A (H3N2, H1N1)

Antigenic characterization of BC influenza A isolates is performed by the National Microbiology Laboratory (NML). Since September 1, 2025, NML has antigenically characterized 23 influenza A viruses (27 H1N1, 24 H3N2). The results are summarized below.

Regarding H1N1 viruses:

- All 27 subclade D.3.1 viruses were shown to be antigenically similar to an A/Wisconsin/67/2022 (H1N1)pdm09-like virus.

Regarding H3N2 viruses:

- Of the 24 influenza A (H3N2) viruses characterized, 6 were antigenically similar to an A/District of Columbia/27/2023 (H3N2)-like virus and 18 showed reduced titers.
- Specifically, viruses representing subclade K showed reduced titres, indicating they were antigenically distinct from the A/District of Columbia/27/2023 (H3N2)-like virus.

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:

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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.