BC Centre for Disease Control
Provincial Health Services Authority

Seasonal Influenza A virus characterization September 2024 to February 2025 (epi-weeks 36-8)

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This report summarizes influenza virus characterization in British Columbia (BC), Canada from September 1, 2024 to February 22, 2025 (epi-weeks 36-8).

Genetic Characterization of Influenza A (H1N1, H3N2)

- Among influenza A viruses detected during this period (n=12,927) that were successfully subtyped (n= 8,814; 68%), the majority were H1 (n= 6063 69%, **Table 1**).
- A subset of viruses were selected for sequencing at the BCCDC Public Health Laboratory. Overall, 323/352 (92%) viruses from clinical samples collected between September 1, 2024 and February 22, 2025, generated sufficient sequence information for analysis.
- Sequenced samples consisted of some outbreak specimens (e.g., closed setting; 1%) but a large majority were non-outbreak specimens (99%).
- Based upon hemagglutinin (HA) sequence analysis, a single H3N2 clade (2a.3a.1) contributed during this period whereas two major H1N1 (5a.2a and 5a.2a.1) clades contributed, also seen during the 2023/24 season (**Figure 1**).
- The H3N2 clade detected in BC during the September 2024 to February 2025 period is the same clade selected for inclusion in the 2024/25 vaccine. The H1N1 vaccine strain for 2024/25 (unchanged from 2023/24) belongs to clade 5a.2a.1 (**Table 2**).
- Sequenced samples were scanned for neuraminidase (NA) mutations associated with antiviral resistance, and single point mutations were detected in 20/323 samples, all H1N1.
- For more detailed and ongoing 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 (based on collection date)

Date (n= total subtyped*)	Successfully subtyped	
	A/H1N1 N = 6063 (69%); n(row %)	A/H3N2 N = 2310 (26%); n(row%)
September 2024 (n=135)	109 (81%)	17 (13%)
October 2024 (n=99)	82 (83%)	10 (10%)
November 2024 (n=223)	151 (68%)	57 (26%)
December 2024 (n=942)	654 (70%)	237 (25%)
January 2025 (n=3,581)	2407 (67%)	992 (28%)
February 2025 (n=3,834**)	2660 (69%)	997 (26%)

***** *Note:*
1- Numbers (n) by month spanning 4 or 5 epidemiological weeks that best fit the month
2- Proportion of subtyped samples does not sum to 100% because of samples with unknown subtype
*** Data from epi-weeks 6 (start date February 2, 2025) to 8 (start date February 16, 2025)*

Figure 1. Influenza A clade characterization by month and subtype (September 1st, 2024 to February 22, 2025)

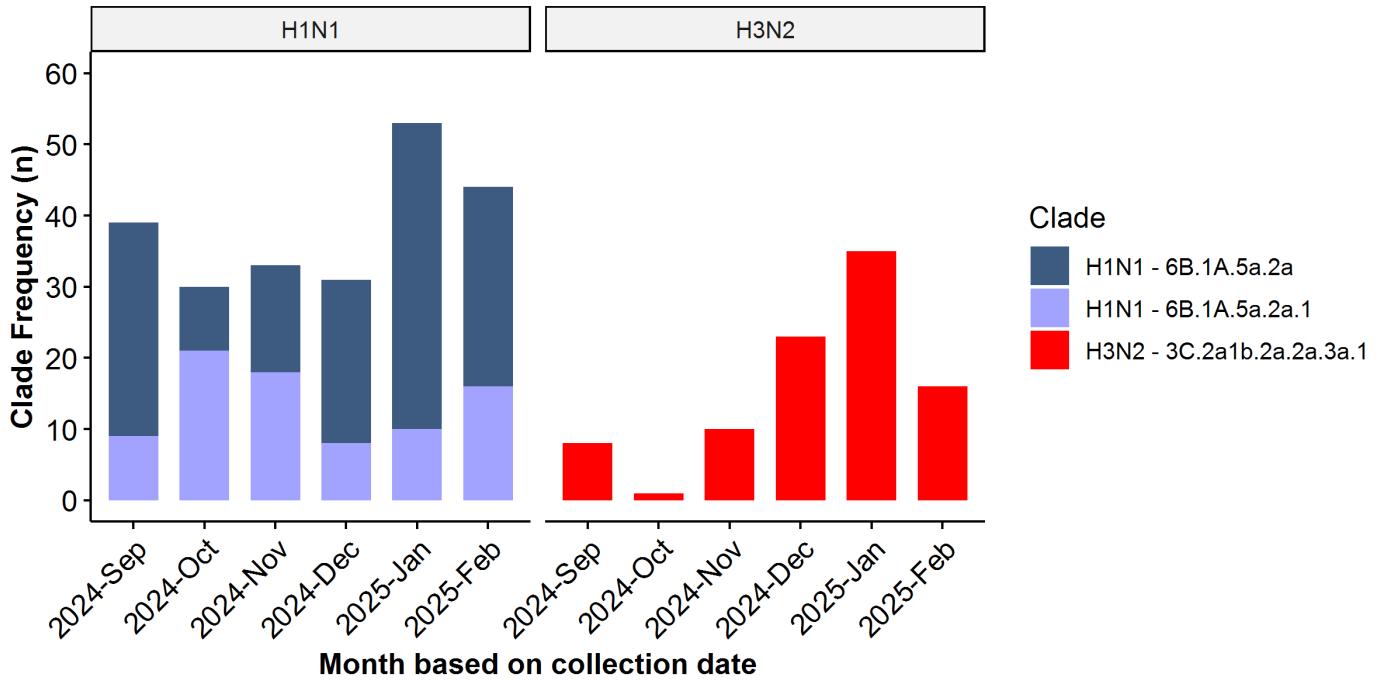

Table 2. Vaccine reference strains included in the 2024-2025 northern hemisphere influenza vaccine*

Vaccine	Strain	Lineage	Clade
Egg-based	A/Victoria/4897/2022	(H1N1)pdm09-like	6B.1A.5a.2a.1
	A/Thailand/8/2022	(H3N2)-like	3C.2a1b.2a.3a.1
	B/Austria/1359417/2021	(B/Victoria lineage)-like	V1A.3a.2
	B/Phuket/3073/2013 (Quadrivalent only)	(B/Yamagata lineage)-like (Quadrivalent only)	Y3
Cell culture- or recombinant-based	A/Wisconsin/67/2022	(H1N1)pdm09-like	6B.1A.5a.2a.1
	A/Massachusetts/18/2022	(H3N2)-like	3C.2a1b.2a.3a.1
	B/Austria/1359417/2021	(B/Victoria lineage)-like	V1A.3a.2
	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 2024-2025 northern hemisphere influenza season (who.int)*

Table 3. Summary of neuraminidase (NA) amino acid substitutions associated with antiviral resistance in samples sequenced September 1st, 2024 to February 22, 2025*

NA Mutation*	Subtype	
	A/H1N1 N= 230 (71%); n(row%)	A/H3N2 N= 93 (29%); n(row%)
D199E	1 (0.4%)	0 (0%)
D199N	1 (0.4%)	0 (0%)
I223K	1 (0.4%)	0 (0%)
I223T	1 (0.4%)	0 (0%)
S247N	14 (6%)	0 (0%)
H275Y	2 (0.8%)	0 (0%)

** As defined by the World Health Organization Guidelines, mutations in A(H1N1)pdm09 and A(H3N2) associated with antiviral resistance described in https://cdn.who.int/human-nai-marker-table. Note: only single mutants were detected.*

Phenotypic Characterization of Influenza A (H3N2, H1N1) – Antigenic Characterization and Antiviral Resistance Testing

Two hundred and twenty-one influenza A viruses collected between September 1, 2024 and February 20, 2025 were sent to the National Microbiology Laboratory (NML) for antigenic characterization[1]. All 153 H1N1 viruses were considered antigenically like A/Wisconsin/67/2022. Sixty-eight H3N2 viruses were considered antigenically like A/Massachusetts/18/2022.

Among the 202 influenza A viruses tested for resistance to antivirals at the NML, one H1N1 strain was resistant to oseltamivir. This strain was sequenced and exhibited a I223K change in the neuraminidase gene, a mutation known to be associated with reduced susceptibility to oseltamivir. All influenza A strains were susceptible to zanamivir.

We acknowledge the following for contributing 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 Authority sites and Northern Health Authority sites.

[1] Antigenic characterization using ferret anti-sera raised against representative 2024/25 northern hemisphere vaccine strains grown in cell culture conducted at the National Microbiology Laboratory (NML) using an approach like the US Centers for Disease Control and Prevention. Per the NML, cell culture and egg-based vaccine components for each influenza A subtype considered antigenically similar.