



Influenza virus characterization May to September 2024 (epi-weeks 18-39)

Prepared by the BCCDC Public Health Laboratory, BCCDC Data & Analytics Services, and BCCDC Immunization Programs and Vaccine Preventable Diseases Service
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This report summarizes influenza virus characterization in British Columbia (BC), Canada during the inter-seasonal period May-September 2024 (epi-weeks 18-39).
Note that patterns may change as we enter the 2024/25 season.

Genetic Characterization of Influenza A (H1N1, H3N2), epi-weeks 18-39, 2024

- Among influenza A viruses detected during this period (n=639) that were successfully subtyped (n=597; 93%), most were H1 (n= 427; 72%, **Table 1**).
- A subset of viruses was selected for sequencing at the BCCDC Public Health Laboratory. Overall, 220/639 (34%) viruses from clinical samples collected between May 1 and September 28, 2024, generated sufficient sequence information for analysis.
- Sequenced samples consisted of some outbreak specimens (e.g., closed setting; 6%) but the majority were non-outbreak specimens (94%).
- 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 May-September 2024 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**).
- For more detailed and ongoing information on provincial influenza monitoring, please refer to the BCCDC Respiratory Surveillance Viral Pathogen Characterization dashboard ([Viral Pathogen Characterization \(shinyapps.io\)](https://shinyapps.io)).

Table 1. Provincial influenza A subtyping results by month (based on collection date)

Date (n= total detected*)	Successfully subtyped	
	A/H1N1 N = 427 (72%); n (row %)	A/H3N2 N = 170 (28%); n (row%)
May 2024 (n=180)	98 (54%)	67 (37%)
June 2024 (n=192)	130 (68%)	55 (29%)
July 2024 (n=72)	45 (63%)	23 (32%)
August 2024 (n=59)	44 (75%)	8 (14%)
September 2024 (n=136)	110 (81%)	17 (13%)

* 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

Figure 1. Influenza A clade characterization by month and subtype (May 1 to September 28, 2024)

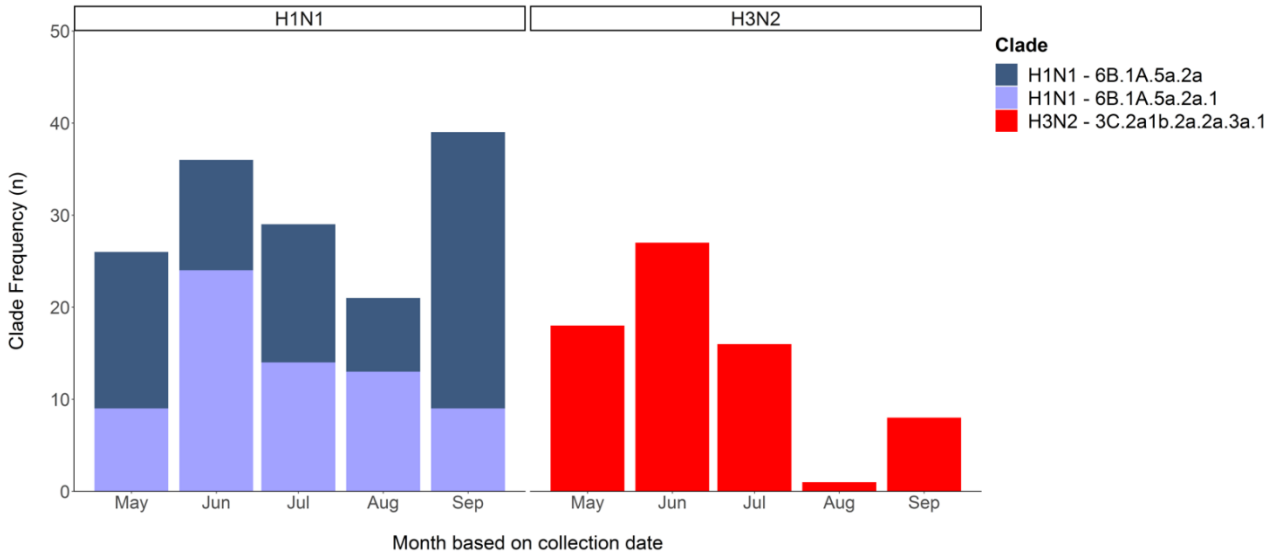


Table 2. Vaccine reference strains included in the 2024-2025 northern hemisphere influenza vaccine*

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)

Antigenic Characterization of Influenza A (H3N2, H1N1)

Thirty-three influenza A viruses from BC collected between September and November 2024 were sent to the National Microbiology Laboratory (NML) for antigenic characterization¹. All 28 H1N1 viruses were considered antigenically like A/Wisconsin/67/2022. Five H3N2 viruses were considered antigenically like A/Massachusetts/18/2022.

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.