



# Influenza strain characterization in preparation for the 2023/2024 influenza season

November 15, 2023

## Summary and interpretation of data collected May-September 2023, epidemiological weeks 18-39

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

- Among subtyped influenza A detections (n=432) in epidemiological weeks 18-39 in 2023, the majority were H1 (86%, **Table 1**).
- A subset of these positive samples (n=220/432) were selected for sequencing, performed at the BCCDC Public Health Laboratory. In total, 177 clinical samples collected between May 1 and September 30, 2023, generated high quality sequence data.
- Clade assessment based on sequence analysis of the hemagglutinin (HA) gene of these viruses indicated that two H3N2 clades and two H1N1 clades were in circulation during this time (**Figure 1**).
- Sequenced samples consisted of non-outbreak (84% of the total samples) and outbreak specimens (16%), the breakdown of which is detailed in **Table 2**.
- Based on the reference strains included in the 2023-2024 Northern Hemisphere egg-based vaccine (**Table 3**), the circulating clades in B.C., identified in preparation for the respiratory season, indicate a predominant clade match. Note that this is based on a small sample size. Further investigation of mutational profiles is needed to inform complete genomic match to the strains selected in this season’s vaccine.

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

Date (n= total tested*)	Subtype	
	A/H1N1	A/H3N2
May 2023 (n=37)	34 (92%)	2 (5%)
June 2023 (n=83)	78 (94%)	0
July 2023 (n=72)	66 (92%)	6(8%)
August 2023 (n=102)	77 (75%)	17 (17%)
September 2023 (n=138)	115 (83%)	20 (14%)

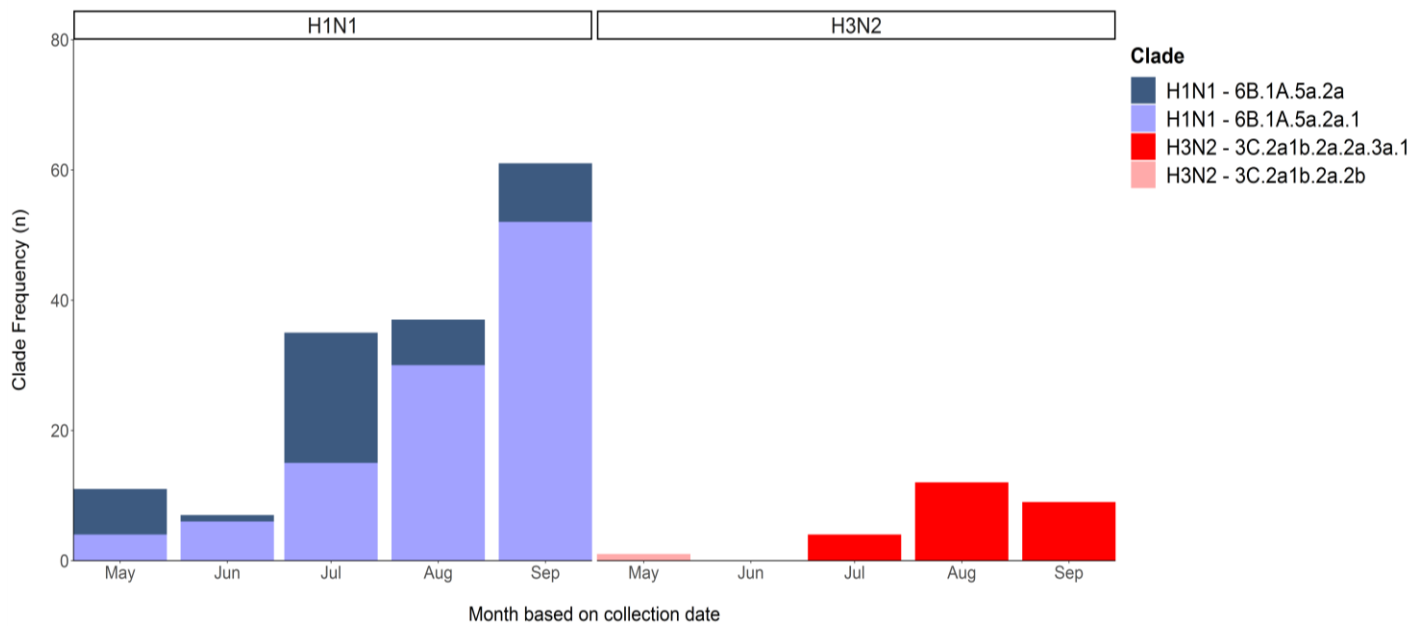
\* Please note:

- 1- these numbers(n) are the total of 4 or 5 epidemiological weeks that best fit the month
- 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 41% (n=177/432) 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 \(shinyapps.io\)](https://shinyapps.io)).

**Figure 1.** Influenza A clade characterization by month and by subtype (May 1 to September 30, 2023)



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

Subtype-Clade-Subclade	Sample Type		
	Outbreak	Non-Outbreak	Total
H1 - 6B.1A.5a.2a	12	32	44
H1 - 6B.1A.5a.2a.1	10	97	107
H3 - 3C.2a1b.2a.2a.3a.1	7	18	25
H3 - 3C.2a1b.2a.2b	0	1	1
All Clades	29	148	177

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

Antigenic characterization for the cell-culture based 2023-2024 Northern Hemisphere vaccine components (i.e. A/Wisconsin/67/2022 (H1N1)pdm09-like and A/Darwin/6/2021 (H3N2)-like viruses) was performed by the National Microbiology Laboratory (NML). This approach is similar to the US Centers for Disease Control and Prevention’s (CDC) approach for influenza surveillance. Note that all influenza vaccine products available in Canada are egg-based products. Per the NML, the cell culture and egg-based vaccine components (Table 3) for each subtype are part of the same antigenic group and are antigenically similar.



- 39 influenza A samples with collection dates in August and September were sent to the NML for antigenic characterization.
- 31/31 influenza A (H1N1) viruses were antigenically similar to A/Wisconsin/67/2022.
  - Of those that were sequenced, 20/23 (87%) were Clade 6B.1A.5a.2a.1, and 3/23 (13%) were Clade 6B.1A.5a.2a.
- 8/8 influenza A (H3N2) viruses were antigenically similar to A/Darwin/6/2021.
  - Of those that were sequenced, 7/7 (100%) of these were Clade 3C.2a1b.2a.2a.3a.1.

### Vaccine Reference Strains and Sequences

**Table 3.** Vaccine-based virus components in the 2023-2024 Northern Hemisphere Influenza Season\*

Vaccine	Strain	Lineage	Clade
Egg-based	A/Victoria/4897/2022	(H1N1)pdm09-like	6B.1A.5a.2a.1
	A/Darwin/9/2021	(H3N2)-like	3C.2a1b.2a.2
	B/Austria/1359417/2022	(B/Victoria lineage)-like	V1A.3a.2
Cell culture-based	A/Wisconsin/67/2022	(H1N1)pdm09-like	6B.1A.5a.2a.1
	A/Darwin/6/2021	(H3N2)-like	3C.2a1b.2a.2
	B/Austria/1359417/2021	(B/Victoria lineage)-like	V1A.3a.2

\* As defined by the World Health Organization Guidelines, [Recommended composition of influenza virus vaccines for use in the 2023-2024 northern hemisphere influenza season \(who.int\)](https://www.who.int/publications/m/item/recommended-composition-of-influenza-virus-vaccines-for-use-in-the-2023-2024-northern-hemisphere-influenza-season)

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