BC Centre for Disease Control
Provincial Health Services Authority

Influenza Strain Characterization: update for the 2023/2024 influenza season

April 18, 2024

Summary and interpretation of data collected September 2023 – January 2024

- Among subtyped influenza A detections (n= 4,565) from September 3, 2023 to January 27, 2024, the majority were H1 (83%, **Table 1**).
- A subset of these positive samples were selected for sequencing, performed at the BCCDC Public Health Laboratory. In total, 300 clinical samples collected between September 3, 2023 and January 22, 2024, generated high quality sequence data.
- Clade assessment based on sequence analysis of the hemagglutinin (HA) gene of these viruses indicated that one H3N2 subclade and two H1N1 subclades were in circulation during this time (**Figure 1**).
- Sequenced samples consisted of non-outbreak (80% of the total samples) and outbreak specimens (20%), 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**),
    - All sequenced influenza A samples were considered a match to the vaccine strains.
    - All sequenced influenza B samples were considered a match to the vaccine strain.
- Although all B.C. influenza viruses tested this season were considered an antigenic match to the strains in the egg-based seasonal flu vaccine, mutations that affect vaccine effectiveness can arise. An in-depth analysis is ongoing, but has not been included in this report.

Genetic Characterization of Influenza A (H3N2, H1N1)

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

	Subtype	
Date (n= total subtyped*)	A/H1N1	A/H3N2
September 2023 (n=138)	115 (83%)	20 (14%)
October 2023 (n=129)	107 (83%)	15 (12%)
November 2023 (n=784)	617 (79%)	132 (17%)
December 2023 (n=2,378)	2,044 (86%)	223 (9%)
January 2024 (n=1,136)	920 (81%)	133 (12%)

***** *Please note:*

1- these numbers(n) are the sum of 4 or 5 epidemiological weeks that best fit the month indicated

2- the proportion of subtyped samples does not sum to 100% because of the small number of samples where the subtype could not be determined

Sequenced samples represent 6.6% (n=300/4565) of the influenza A samples successfully subtyped in the province during this time period. Sequenced samples were selected based on their association with a facility outbreak, or at random as part of background surveillance. For more detailed information on the provincial influenza monitoring, please refer to the BCCDC Respiratory Surveillance Viral Pathogen Characterization dashboard (Viral Pathogen Characterization (shinyapps.io)).

Figure 1. Influenza A clade and subclade characterization by month and by subtype (September 2023 to January 2024)

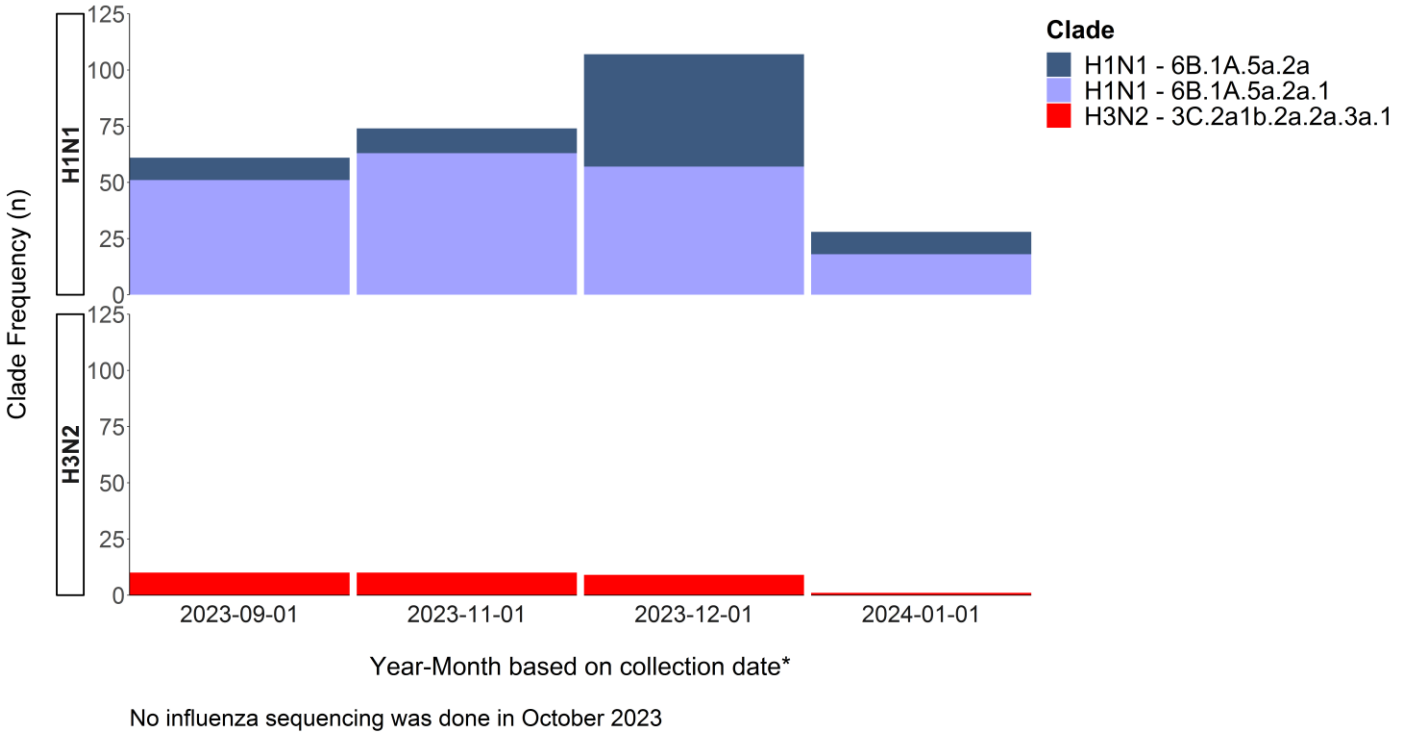

Table 2. Sequenced influenza samples based on collection type (non-outbreak vs. outbreak) between September 2023 and January 2024

	Sample Type		
Subtype-Clade	Outbreak	Non-Outbreak	Total
H1 - 6B.1A.5a.2a	15	66	81
H1 - 6B.1A.5a.2a.1	42	147	189
H3 - 3C.2a1b.2a.2a.3a.1	4	26	30
All Clades	61	239	300

Antigenic Characterization:

From September 1, 2023 to March 14, 2024, the National Microbiology Laboratory (NML) Branch antigenically characterized a total of 334 influenza viruses submitted by the BCCDC Public Health Laboratory.

Influenza A (H3N2, H1N1)

Antigenic characterization for A/Wisconsin/67/2022 (H1N1) and A/Darwin/6/2021-like (H3N2) viruses was performed by the NML from culture, similar to the US CDC's approach for influenza surveillance. These viruses represent the cell culture-based 2023-2024 Northern Hemisphere vaccine components. Antigenic match does not in and of itself predict vaccine effectiveness. Further investigation is required to understand vaccine effectiveness.

- 282 influenza A samples with collection dates from September to March were analyzed by the National Microbiology Laboratory for antigenic characterization.
    - 189 influenza A(H1N1) viruses were antigenically similar to A/Wisconsin/67/2022
        - Of those that were sequenced, 111/154 (72%) were Clade 6B.1A.5a.2a.1, and 43/154 (28%) were Clade 6B.1A.5a.2a.
    - 93 influenza A(H3N2) viruses were antigenically similar to A/Darwin/6/2021
        - Of those that were sequenced, 70/70 (100%) were Clade 3C.2a1b.2a.2a.3a.1.

Influenza B

Influenza B viruses can be divided into two antigenically distinct lineages represented by B/Yamagata/16/88 and B/Victoria/2/87 viruses. The recommended influenza B components for the 2023-24 Northern Hemisphere influenza vaccine were based on the B/Austria/1359417/2021-like virus.

- 52 influenza B samples with collection dates from September to March were analyzed by the National Microbiology Laboratory for antigenic characterization.
    - All samples were antigenically similar to B/Austria/1359417/2021-like
    - Of those that were sequenced, 20/20 samples (100%) were clade V1A.3a.2

Vaccine Reference Strains

Table 3. Virus strains 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)