Weekly update on Variants of Concern (VOC)

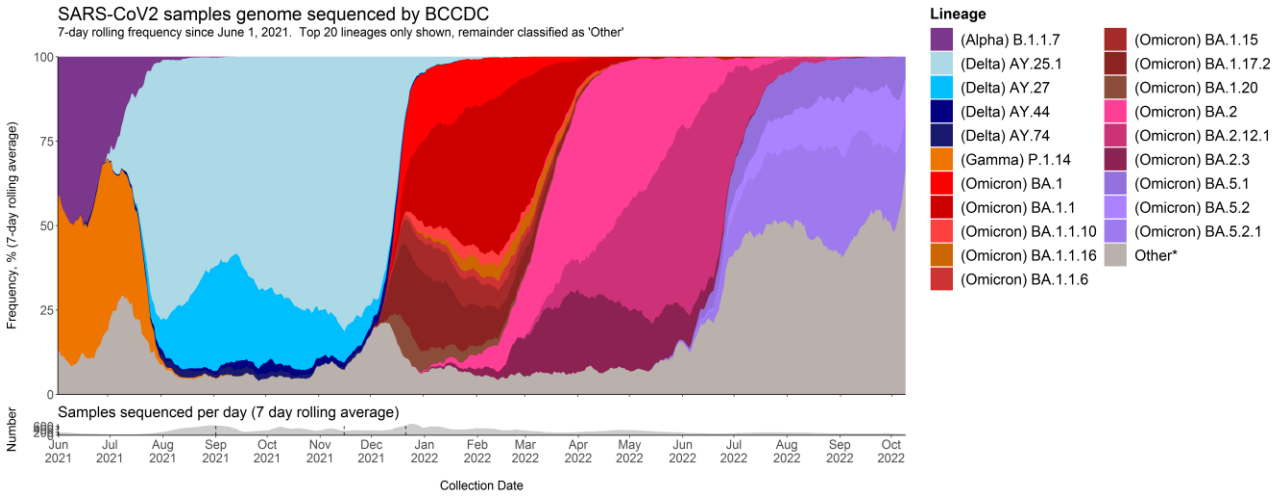
20 October, 2022

Of all positive samples sequenced* in epi week 40 (October 02 - October 08) in BC, ~ 94% were confirmed Variants of Concern (VOCs). Over time, the distribution of variants demonstrate the temporality and changing nature of VOCs circulating as shown in Figure 1. Detection of BA.5, including all descendant sublineages, has plateaued in BC.

Due to the large diversity in BA.5 sublineages (>100 descendants), the total sequenced for each individual descendant strain is low and collapsed in the "Other*" category in Figure 1. This report provides more detail for the breakdown of sequenced samples in the most recent six weeks of data available (Figure 5).

Data from epi week 40 may reflect partial data; estimates are expected to change as more specimens are received and sequenced.

Figure 1. Twenty most prevalent lineages in British Columbia, June 1, 2021 - October 08, 2022**



Other includes: BA.4.6, BA.4.6.1, BA.5.1.1, BA.5.1.18, BA.5.1.2, BA.5.1.20, BA.5.1.22, BA.5.1.23, BA.5.1.24, BA.5.1.25, BA.5.1.27, BA.5.1.3, BA.5.1.5, BA.5.1.7, BA.5.10, BA.5.2.19, BA.5.2.20, BA.5.2.21, BA.5.2.22, BA.5.2.23, BA.5.2.27, BA.5.2.28, BA.5.2.3, BA.5.2.6, BA.5.2.8, BA.5.2.9, BA.5.3, BA.5.5, BA.5.5.1, BA.5.6, BA.5.8, BA.5.9, BE.1, BE.1.1, BE.1.1.2, BE.3, BF.10, BF.11, BF.21, BF.26, BF.27, BF.28, BF.4, BF.5, BF.7, BF.8, BM.1.1, BM.4.1.1, BN.2, BQ.1, BQ.1.1, BQ.1.2, CD.1, other BA.2., XBB in the most recent week of data.
Pangolin version: 4.1.3, Usher version: 1.15.1, Pango version: 1.15.1. Total Pango assignments: 55 459; Total Usher assignments: 74 288

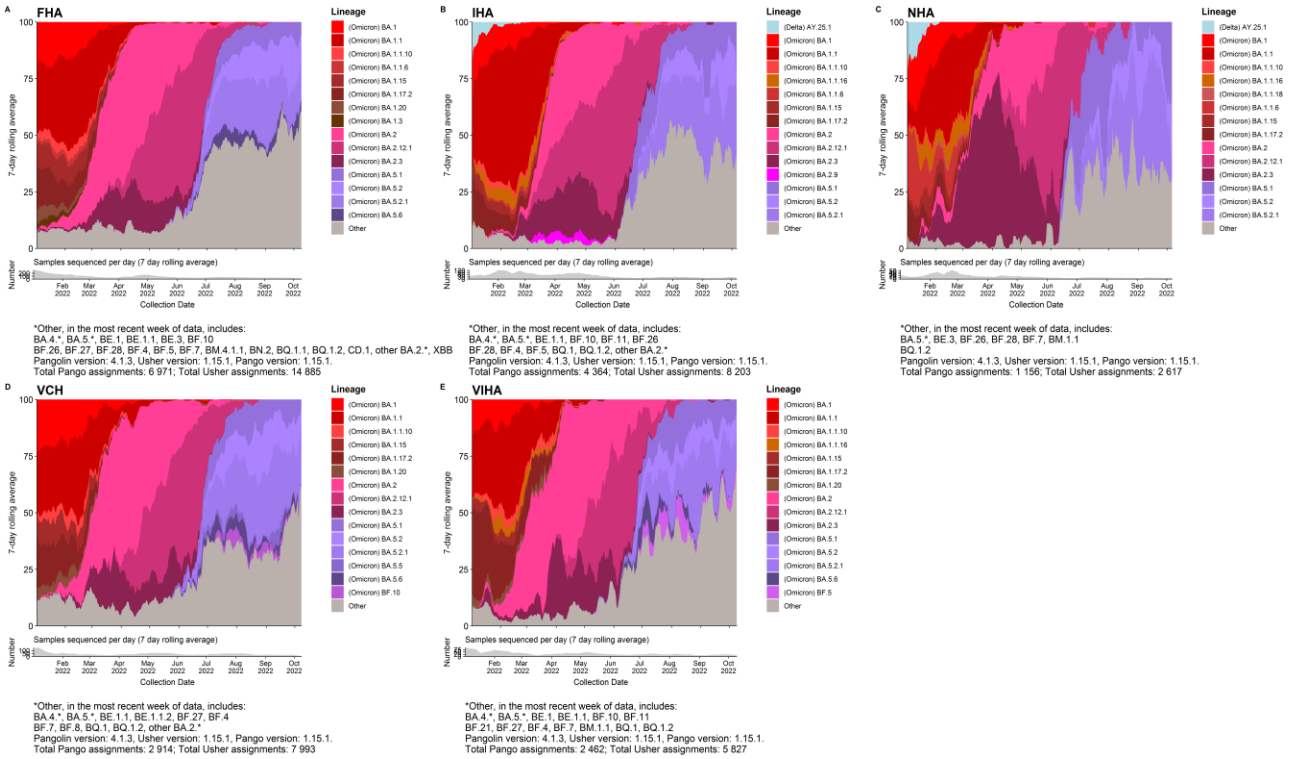
Data from the PLOVER system at the BCCDC Public Health Lab.

***Dashed lines indicate the time of changes in whole genome sequencing (WGS) sampling strategy (epi week 22: all positive samples; epi week 36: transition from full sequencing to sequencing a subset of 10% of representative samples in addition to all targeted samples, while keeping a monthly census of all positive samples on the first week of the month; epi week 46: transition to WGS of all positive samples; epi week 51: transition from full sequencing to sequencing a subset of representative positive samples in addition to priority cases (including outbreaks, long-term care, vaccine escape, travel-related, hospitalization)).*

The main recent circulating variant is Omicron (Figure 1), accounting for about 94% of positive specimens sequenced.

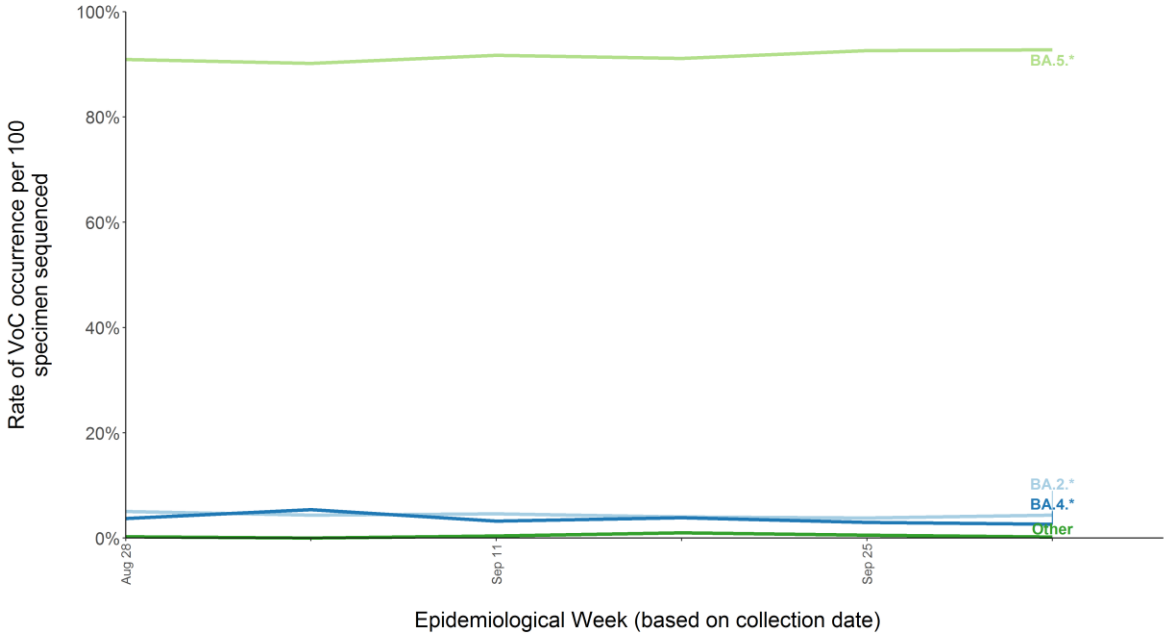
As shown in Figure 2, Omicron sub-lineages have different prevalence distribution in each health authority. In the past week, lineages classified as “Other” include several sub-lineages of BA.4 and BA.5 (refer to Figure 3).

Figure 2. Fifteen most prevalent lineages in British Columbia by Health Authority, January 1, 2022 - October 08, 2022



Pangolin designation beyond three sub-lineages (e.g. BA.5.x.x.x) results in the assignment of a new naming convention whereby a new lineage (e.g. BE) is assigned. These new designations (e.g. BE, BM, etc.) are collapsed in their parental lineage (e.g. BA.5*) in Figure 3. Recombinants (naturally occurring merge of virus variants) are collapsed in the "Other" category

Figure 3. Proportion of lineages # sequenced over the past 6 weeks from 21 August, 2022 to 02 October, 2022

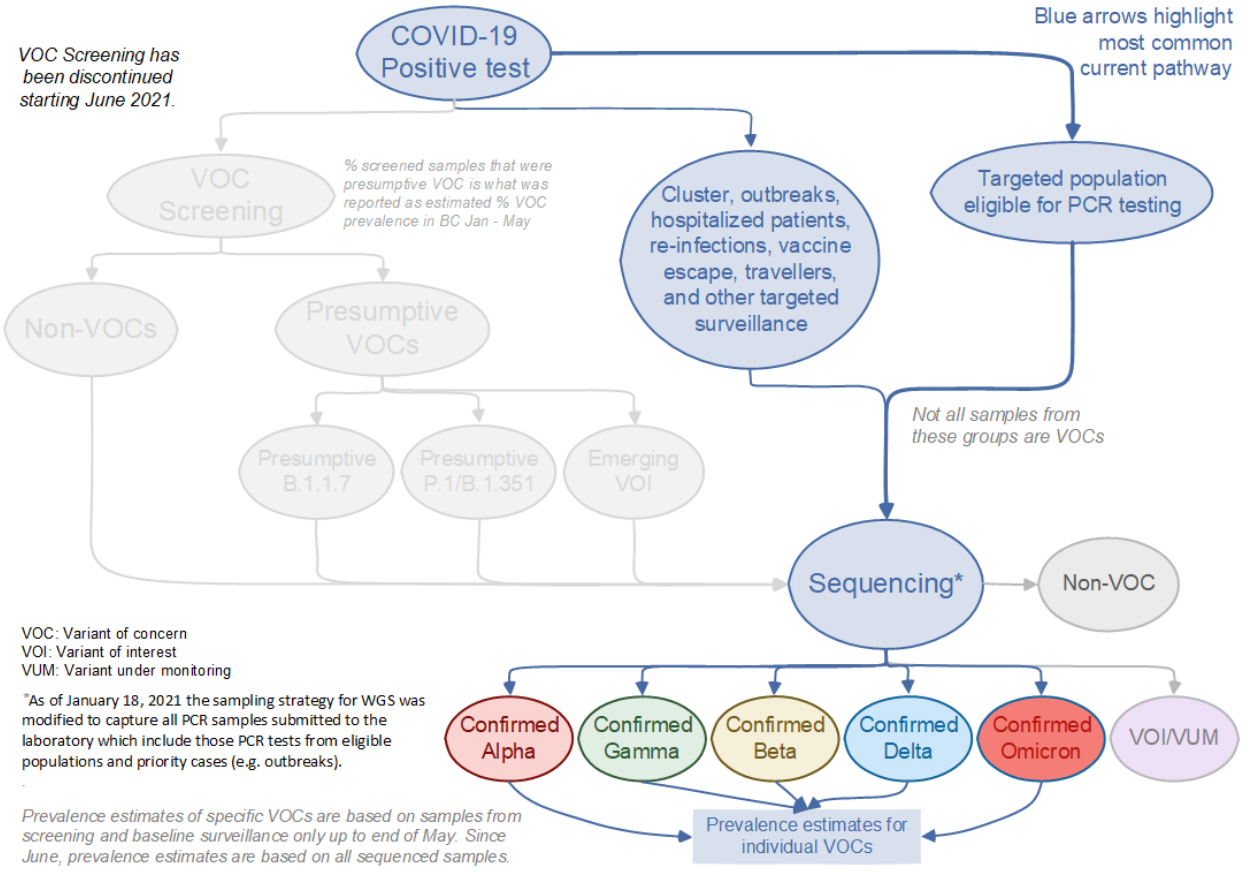


 # See appendix for the definitions of VOC lineages

Monitoring of Variants

BCCDC Public Health Laboratory is continuously monitoring for both VOCs and VOIs and it is tracking a regularly updated Variants Under Monitoring (VUMs) by adapting and optimizing its sampling strategy. To address the latests VOC, Omicron, sequencing of all positives samples was resumed with retrospective specimens collected from November 15th 2021 - December 20th 2021. The sampling strategy for WGS was modified starting December 21st 2021 to capture a subset of representative positive specimens in addition to the priority cases (including outbreaks, long-term care, vaccine escape, travel-related, hospitalization). Reflecting the current testing guidelines, most sequencing is now through positive PCR samples as shown in Figure 4. As of October, 2022 priority cases no longer include travel testing due to the ending of COVID-19 emergency border measures.

Figure 4. Overview of the screening and sequencing process applied to positive COVID-19 tests in BC, Oct 2022.



Please note the turnaround time sequencing which takes approximately 7-11 days, but it could also take longer if there are lab backlogs or if there are delays in receiving current positive samples from frontline laboratories.

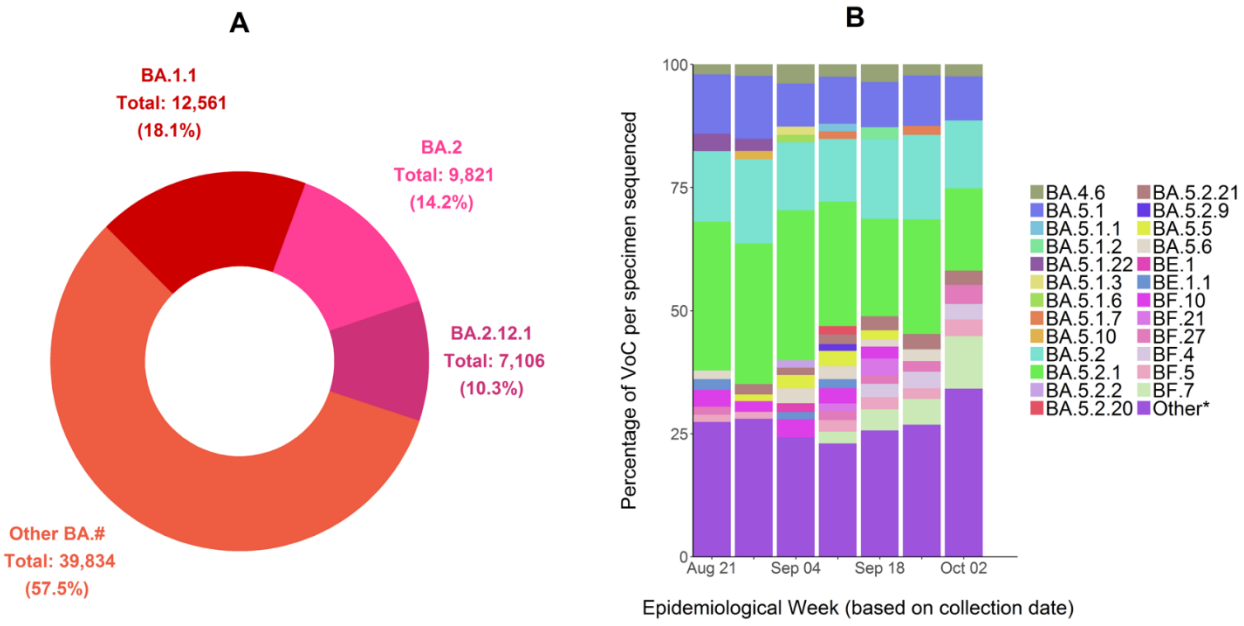
Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 178,298 specimens up to epi week 40 (October 02 - October 08) in BC, of which 156,337 came back as variants under closer observation. Figure 4 above illustrates BC's whole genome sequencing strategy of COVID cases.

The VOCs represent a cumulative 98.4% of all the variants that were detected in the province since the start of the pandemic (see WGS frequency of lineages table on BCCDC website). The Delta (n = 57,836) and Omicron (n = 69,322) variants account for largest proportion of the VOCs. Omicron includes B.1.1.529, the parent lineage, and BA sub-lineages (Figure 5 and appendix Table).

Figure 5. Distribution of Omicron**

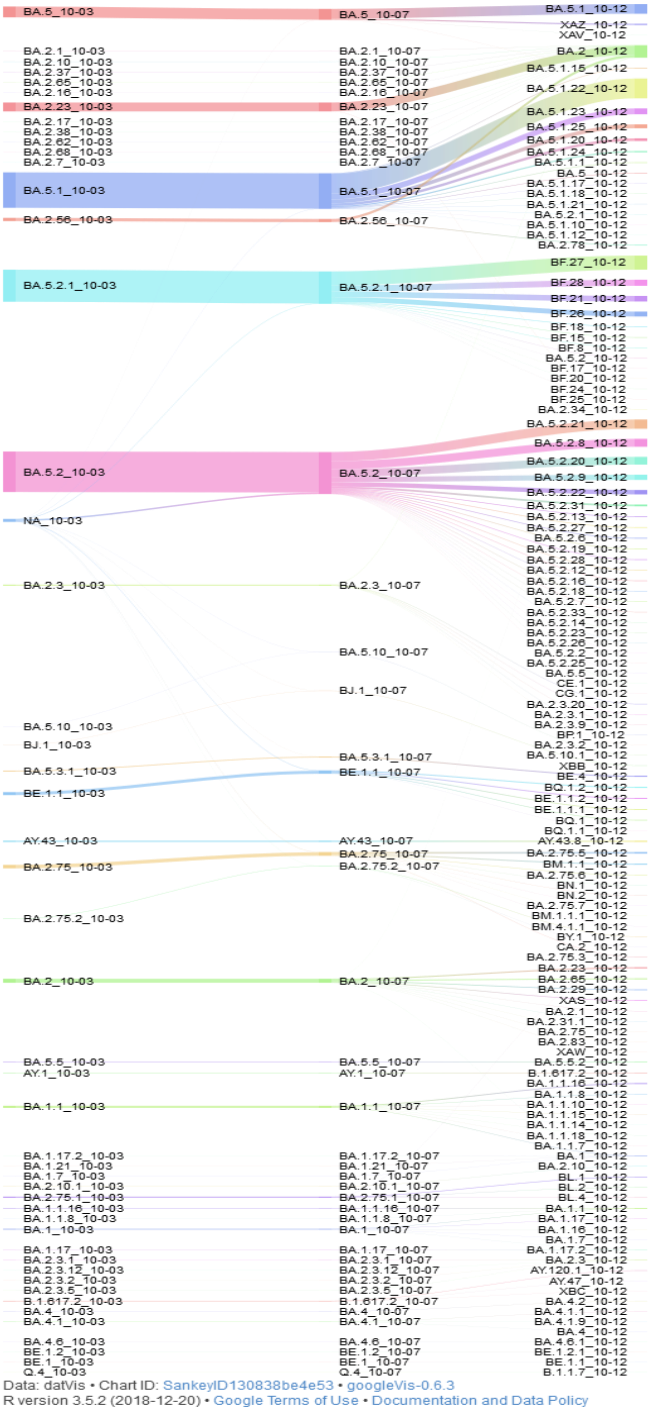
Panel A: three most prevalent lineages cumulatively; Panel B: sublineages in the past 6 weeks



*** These counts represent the total number of samples (not cases) sequenced.*

BCCDC Public Health Laboratory updates the lineage assignment tool (Pangolin), on an at least weekly basis, to reflect current lineage classification changes. Figure 6 below demonstrates how these updates affect changes in the Delta and Omicron variants from one sub-lineage to another over time.

Figure 6. Lineage assignment changes* in Pangolin



Appendix – VOC Lineages*** Table

VOC	Associated Lineages
Alpha	B.1.1.7, Q.*
Beta	B.1.351, B.1.351.*
Gamma	P.1, P.1.*
Delta	B.1.617.2, AY.*
Omicron**	B.1.1.529, BA.*, BC, BD, BE, BF, BG, BH, BJ, BK, BL, BM, BN, BQ, BR, XAA, XAB, XAC, XAD, XAE, XAF, XAG, XAH, XBB, XE, XG, XH, XJ, XK, XL, XM, XN, XP, XQ, XR, XT, XU, XV, XW, XY, XZ

** Indicates an additional numerical value (e.g. Q.1).*

*** Lineages starting with X indicate a recombination of Omicron variants.*

**** Lineage assignments are based on the use of Pangolin, an epidemiological lineage assignment tool (github.com/cov-lineages/pangolin); these may change with time as new SARS-CoV-2 genomic data becomes available.*