

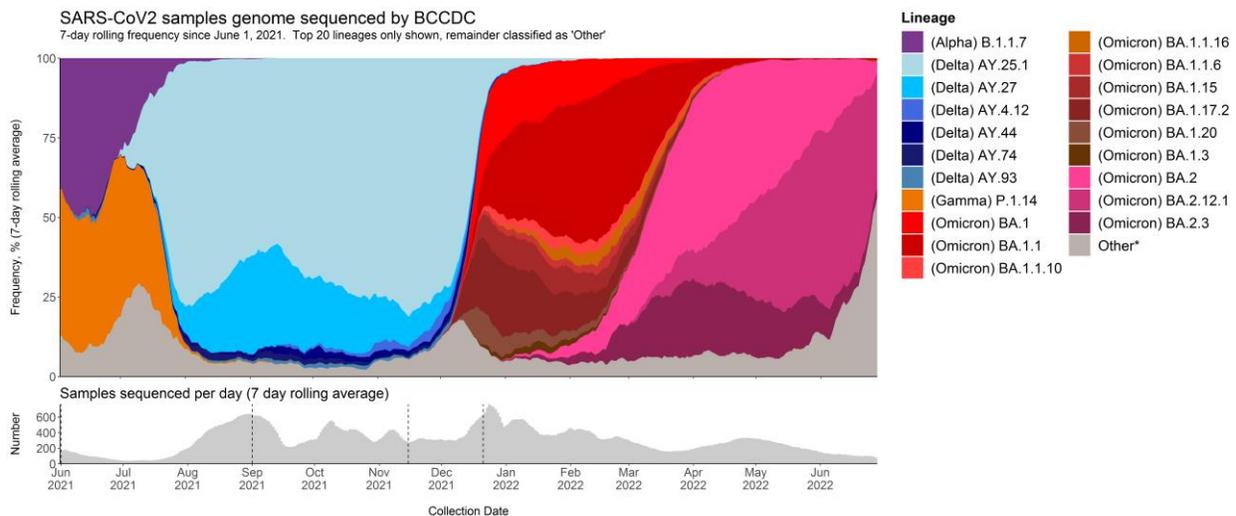
## Weekly update on Variants of Concern (VOC)

07 July, 2022

Of all positive samples sequenced\* in epi week 25 (Jun 19 - Jun 25) in BC, ~ 97% 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. BA.5.\* sub-variants detection is increasing the fastest in BC with a 7-day rolling average of 40% of all sequenced samples in epi week 25.

Data from epi week 25 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 - Jun 25, 2022\*\*



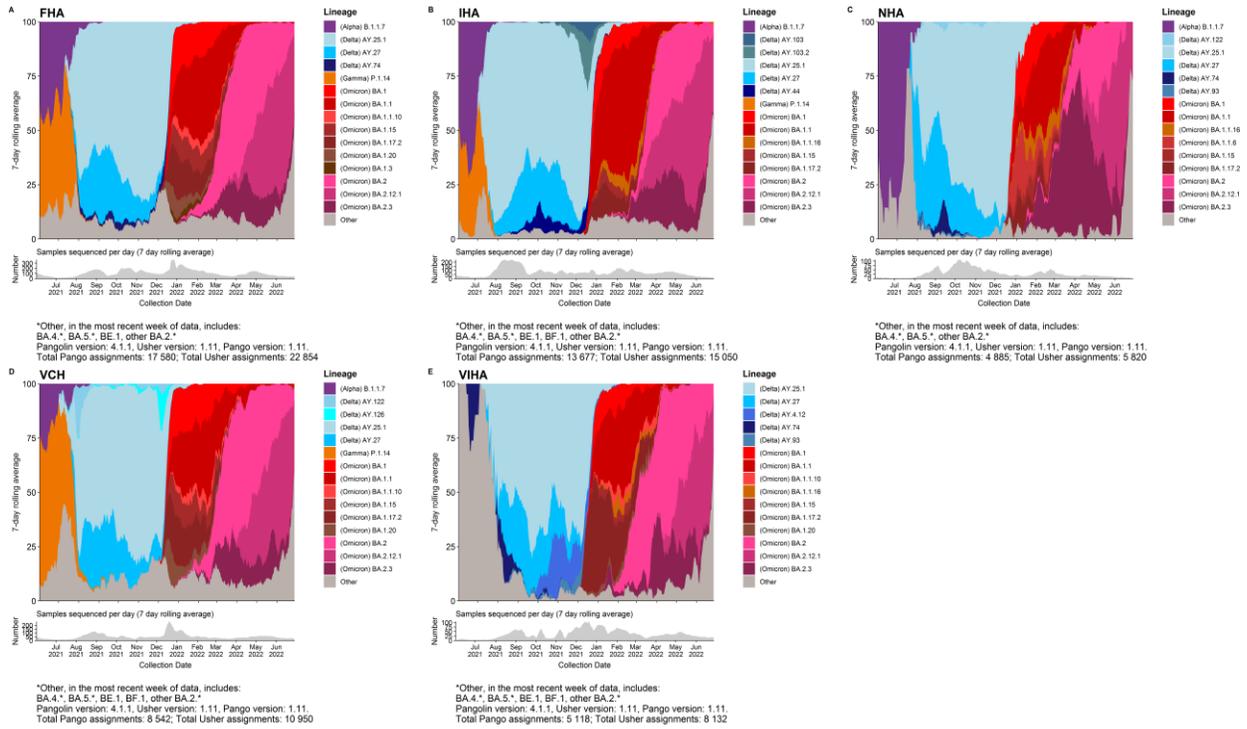
\*Other includes BA.4, BA.4.1, BA.5, BA.5.1, BA.5.2, BA.5.2.1, BA.5.3, BA.5.3.1, BA.5.3.2, BA.5.5, BE.1, BF.1, other BA.2.\* in the most recent week of data. Pangolin version: 4.1.1, Usher version: 1.11, Pango version: 1.11. Total Pango assignments: 51 451; Total Usher assignments: 65 298

\*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)).

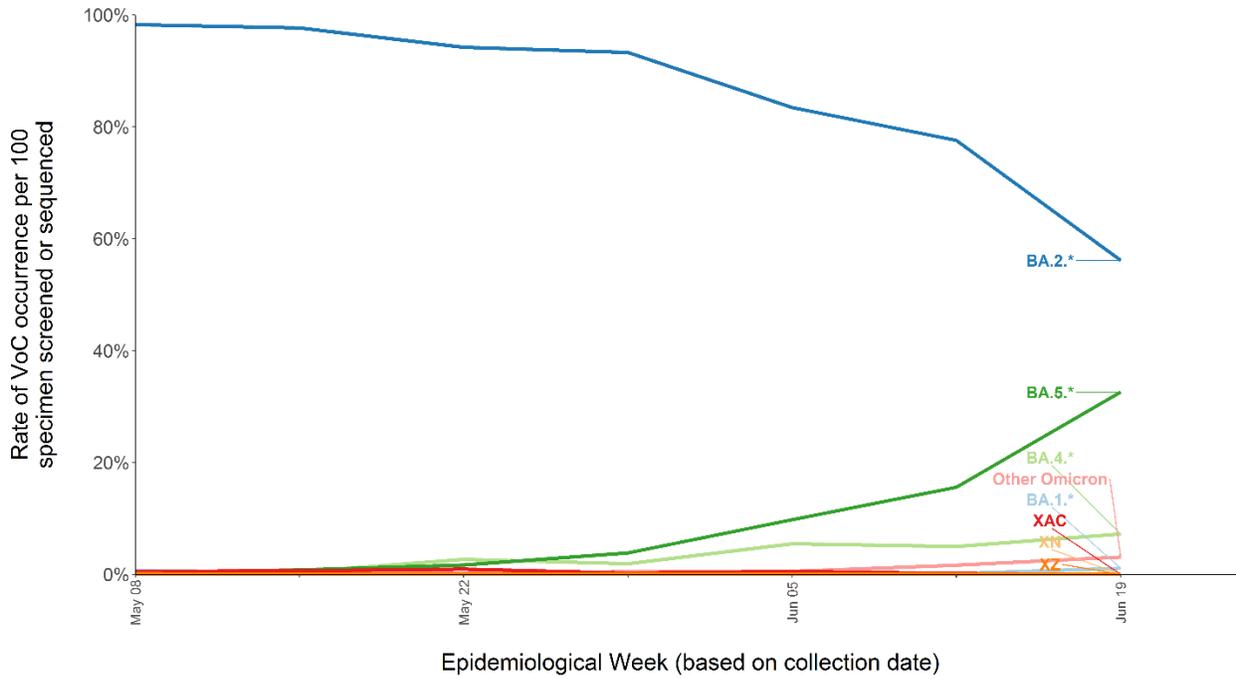
As shown in Figure 2, Omicron sub-lineages have different prevalence distribution in each health authority. In the past week, lineages classified as “Other” include several sub-lineages of BA.2 as well as BA.4 and BA.5 (refer to Figure 3).

Figure 2. Fifteen most prevalent lineages in British Columbia by Health Authority, June 1 - Jun 25, 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 parental lineage (e.g. BE) is assigned. These new designations (e.g. BE, BM, etc.) are collapsed in the "Other Omicron" sublineages category shown in Figure 3.

Figure 3. Proportion of lineages # sequenced over the past 6 weeks from 08 May, 2022 to 19 June, 2022

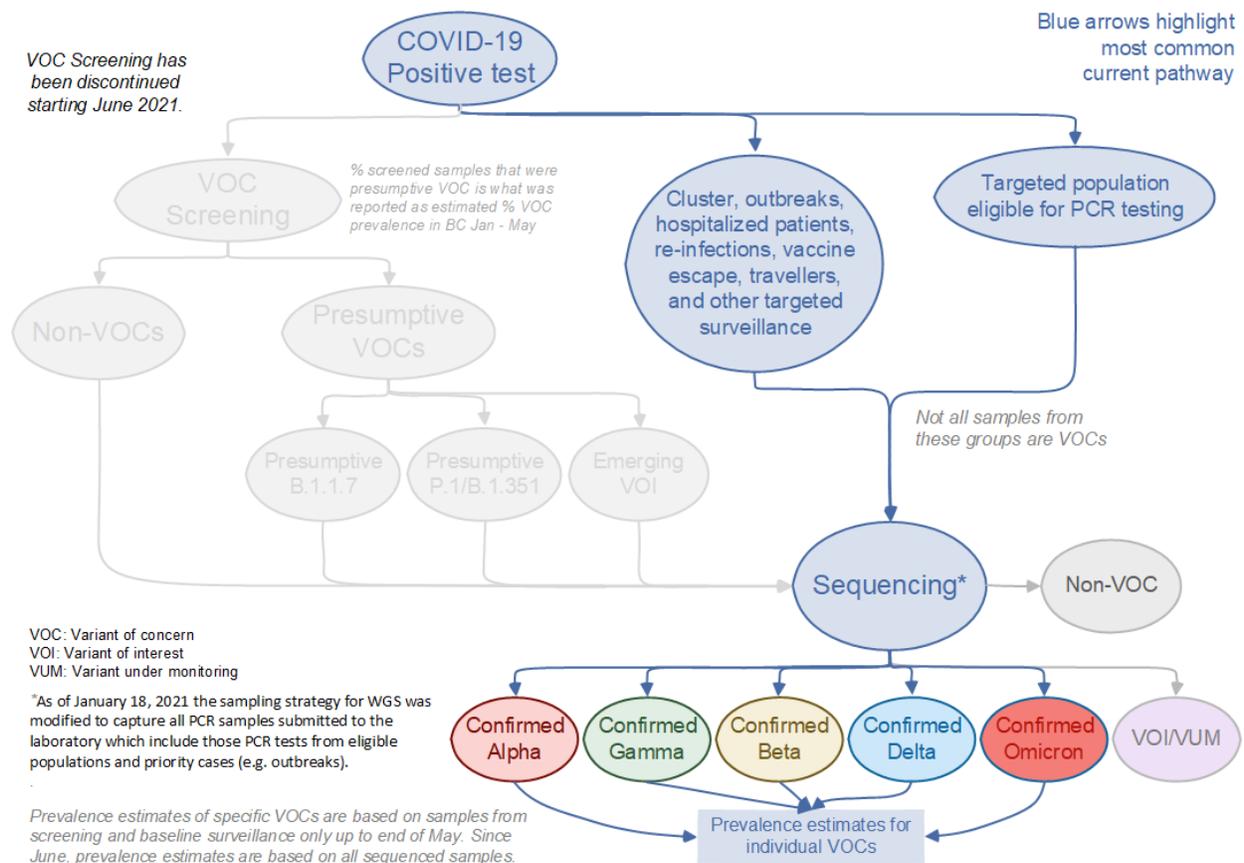


# See appendix for the definitions of VOC lineages

## 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). There are numerous VOIs, and they may not necessarily become VOCs. Once a VOI becomes a VOC, it will be added to our VOC reporting. As of September 2021 BC changed its sampling strategy for sequencing to report on the provincial number of variants based on weekly point prevalence. To address the latests VOC Omicron, sequencing of all positives samples was resumed with retrospective specimens collected from November 15th 2021 - December 20th 2021. Due to the rising number of cases in the province, 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) as shown in Figure 4. **Note:** As of June 11, 2021 border testing samples will no longer be in the pool of priority cases for sequencing given the pause of the federal program of random testing of vaccinated travelers arriving by air.

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

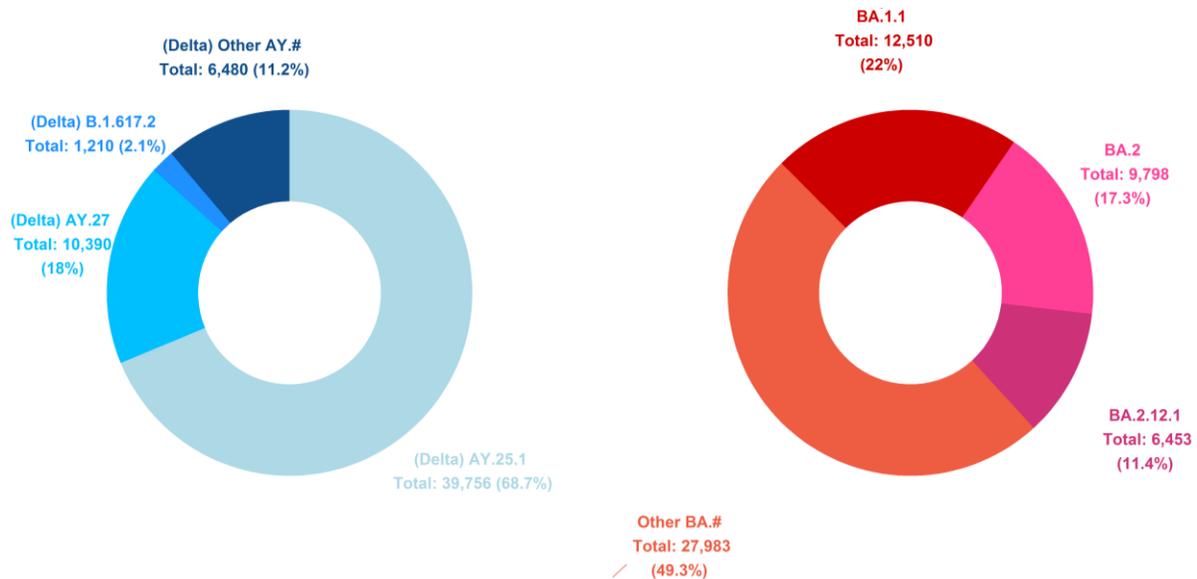
## Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 165157 specimens up to epi week 25 (Jun 19 - Jun 25) in BC, of which 143779 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 98.2% of all the variants that were detected in the province (see [WGS frequency of lineages table](#) on BCCDC website).

The Delta (n = 57836) and Omicron (n = 56744) variants account for largest proportion of the VOCs. Delta includes B.1.617.2, the parent lineage, and many AY sub-lineages, while Omicron includes B.1.1.529, the parent lineage, and BA sub-lineages (Figure 5 and appendix Table).

Figure 5. Cumulative Distribution of the three most prevalent Delta and Omicron lineages\*\*



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



# 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.*

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

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