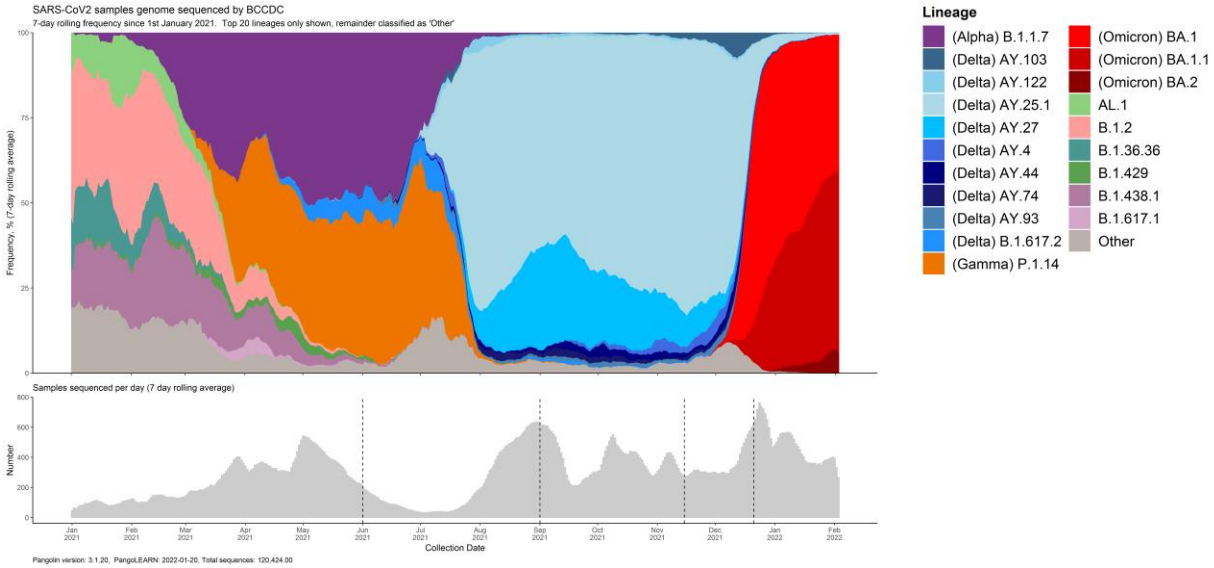
Weekly update on Variants of Concern (VOC)

Feb 11, 2022

Of all positive samples sequenced* in epi week 4 (Jan 23 - Jan 29) in BC, ~ 100% 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.

Data from epi week 4 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, Jan 1 - Jan 29, 2022**

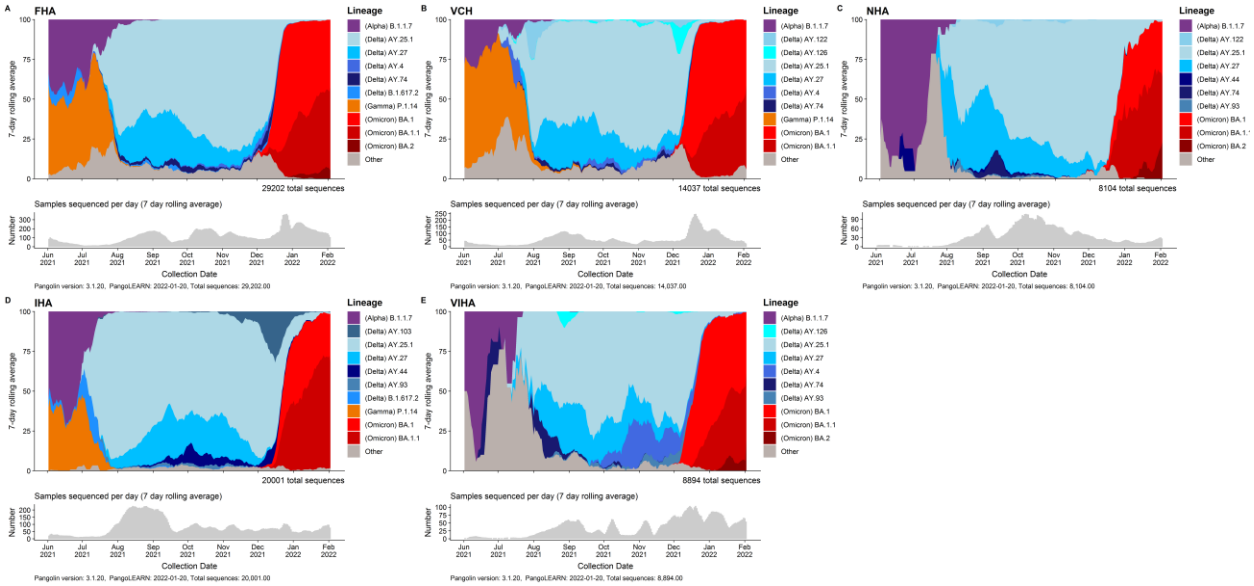


Data from the PLOVER system at the BCCDC Public Health Lab.

***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)).*

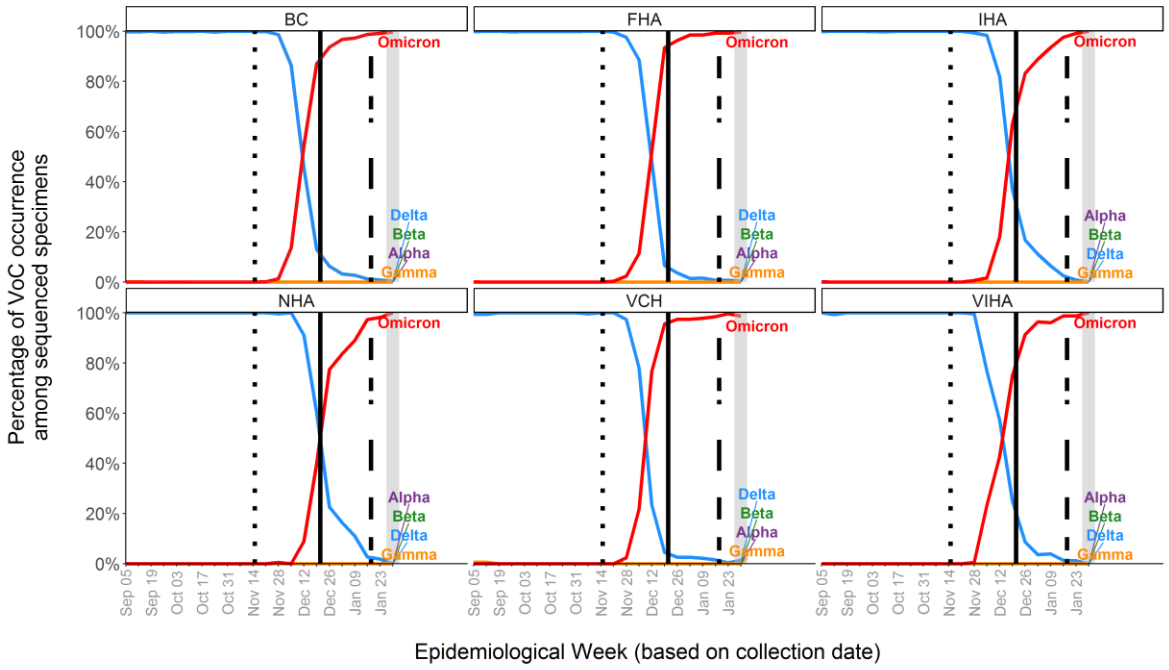
As shown in Figure 1, the main recent circulating variants are Delta and Omicron, respectively accounting for about 0.8% and 99.2% of positive specimens sequenced, with spatial variability within each heath authority (Figure 2).

Figure 2. Ten most prevalent lineages in British Columbia by Health Authority, June 1 - Jan 29, 2022



As shown in figure 3, the estimate of the distribution of VOC lineages# varies by health authority. Please note that these estimates for latest epi week 4 (Jan 23 - Jan 29) may change as more sequencing results are analyzed and given the lag in receipt of positive samples from frontline laboratories.

Figure 3. Estimated Sample prevalence^ of VOCs by lineage by epi week of collection date



 # See appendix for the definitions of VOC lineages

^ Sample prevalence is calculated as the rate of occurrence of a given VOC lineage per 100 positive lab samples. It was estimated from the proportion of presumptive VOC from screening and the proportion of confirmed VOC via sequencing (excluding outbreaks and targeted surveillance) until May 30th, 2021 when BC transitioned to WGS on all positive cases. From week 13 (March 28, 2021), VOC screening results with both E484K and N501Y mutations are assumed to be Gamma, given a very low prevalence of Beta in BC. As of week 22 (May 30, 2021), prevalence of VOC is estimated from sequencing results only.

Grey shaded box can reflect partial data due to a lag in receipt of positive samples from front line laboratories and turn around time of 7 to 11 days from sample collection to WGS analysis; estimates are expected to change as more specimens are received and sequenced.

Dotted line indicates the time of transition to WGS of all positive samples on November 15, 2021 (epi week 46).

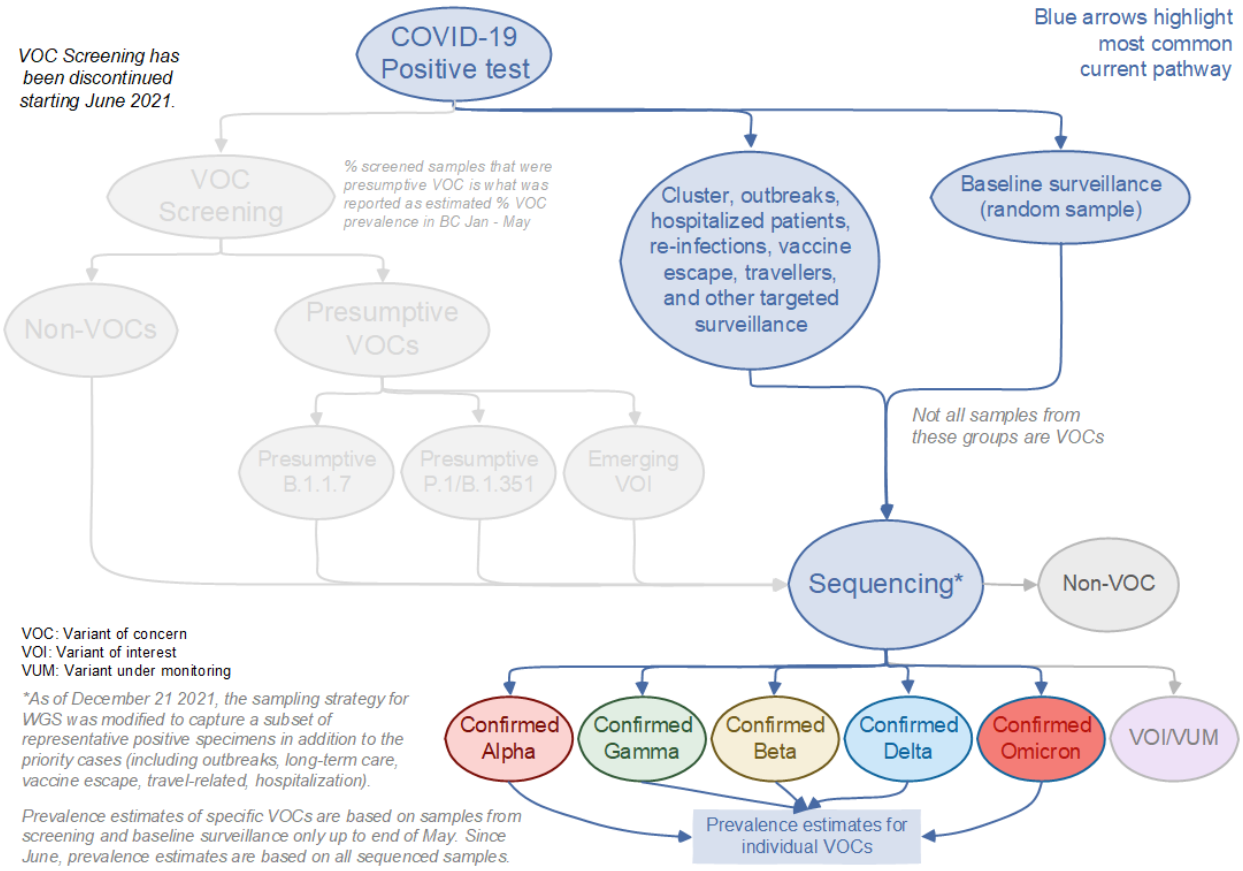
Solid line indicates the time of transition to WGS of a subset of representative positive samples in addition to priority cases (including outbreaks, long-term care, vaccine escape, travel-related, hospitalization) on December 21st, 2021 (epi week 51). This time corresponds to the roll out of Rapid Antigen Tests (RAT) which are not sequenced.

Dashed-dotted line indicates transition to the most recent change in testing guidelines. Trends from Jan 18th 2022 onwards represent those in targeted populations (health care workers, clinically extremely vulnerable, etc).

Monitoring of Variants

As illustrated in Figure 4 below, 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. Since September 2021 BC has adopted a new sampling strategy for sequencing to report on the provincial number of variants based on weekly point prevalence. To address the new Omicron (B.1.1.529 and BA.*) 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, as of December 21 2021, the sampling strategy for WGS was modified to capture a subset of representative positive specimens in addition to the priority cases (including outbreaks, long-term care, vaccine escape, travel-related, hospitalization). This strategy is subject to change depending on case count and variant distribution.

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



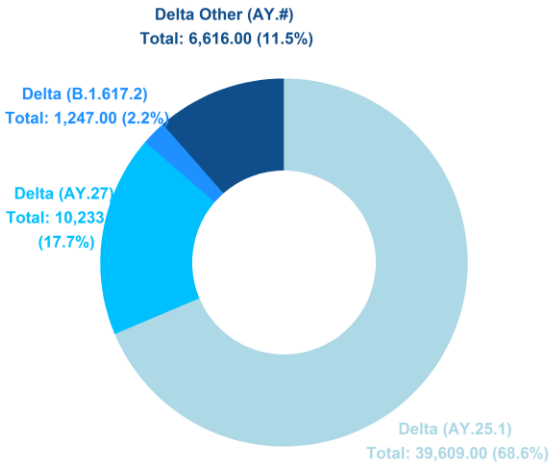
Please note the turnaround time sequencing which takes approximately 7-11 days, but it could also take longer if there are lab backlogs or if there are delays in receiving current positive samples from frontline laboratories.

Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 130,025 specimens up to epi week 4 (Jan 23 - Jan 29) in BC, of which 110,047 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 97.7% of all the variants that were detected in the province (see WGS frequency of lineages table on BCCDC website). The Delta (n = 57,705) and Omicron (n = 23,237) variants account for largest proportion of the VOCs. Delta includes B.1.617.2, the parent lineage, and many sub-lineages AY.* (Figure 5 and appendix Table).

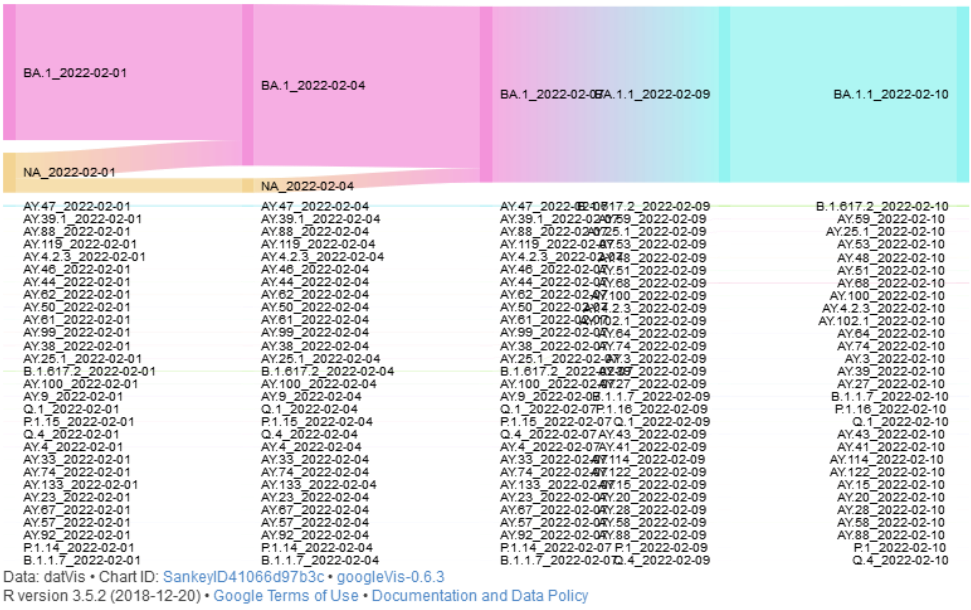
Figure 5. Cumulative Distribution of the three most prevalent Delta lineages**



*** 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 some VOCs from one sub-lineage to another over time. In the past week, we note the most recent change of a subset of Omicron BA.1 to its sub-lineage BA.1.1

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.*

** 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); these may change with time as new SARS-CoV-2 genomic data becomes available.*