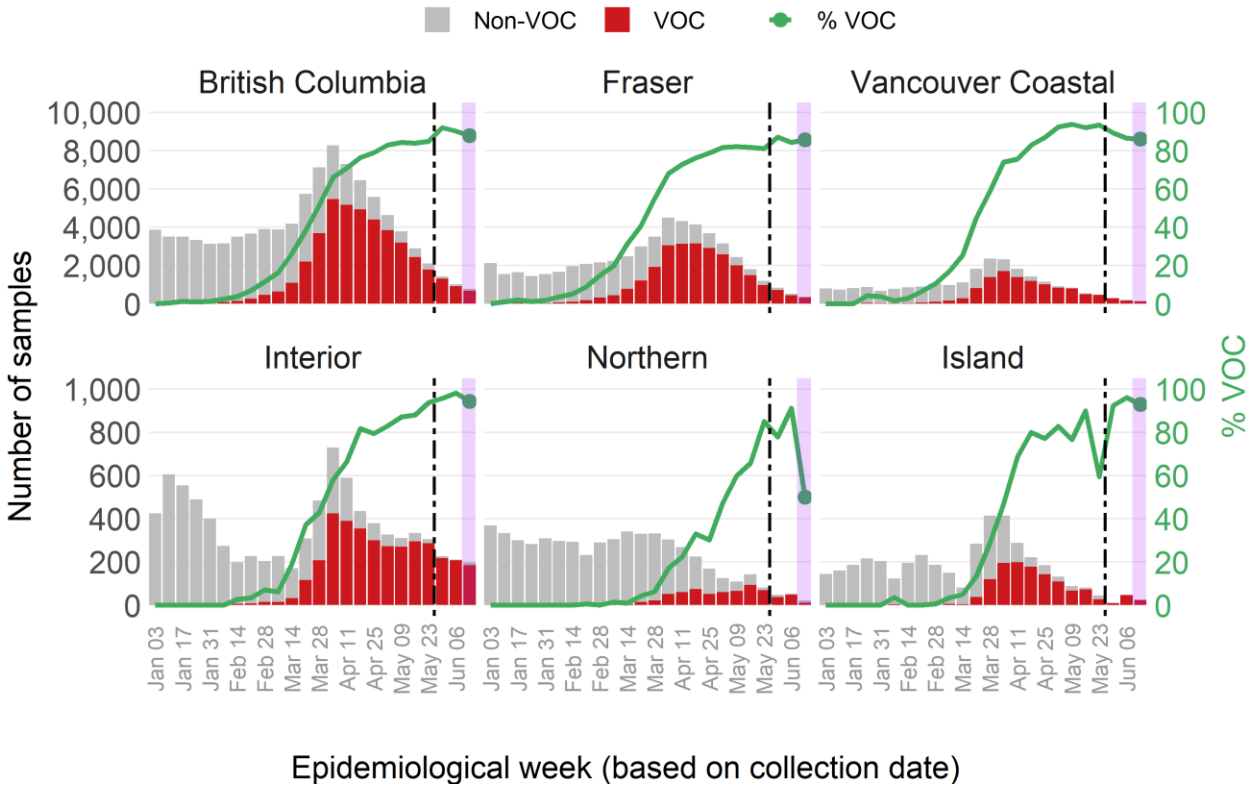
# Weekly update on Variants of Concern (VOC)

## Jun 25, 2021

B.C. has transitioned to whole genome sequencing on all positive samples to provide gold standard analysis to detect VOC and fingerprint details to support outbreak responses. Of all samples tested in epi week 24 (Jun 13 - Jun 19) in BC, ~ 88% were presumptive VOCs (Figure 1). VOC prevalence was similar across Health Authorities, except in Northern Health, where it was lower, at 50%.

Figure 1. Prevalence of presumptive VOC, by epi week in BC and Health Authorities, Jun 13 - Jun 19

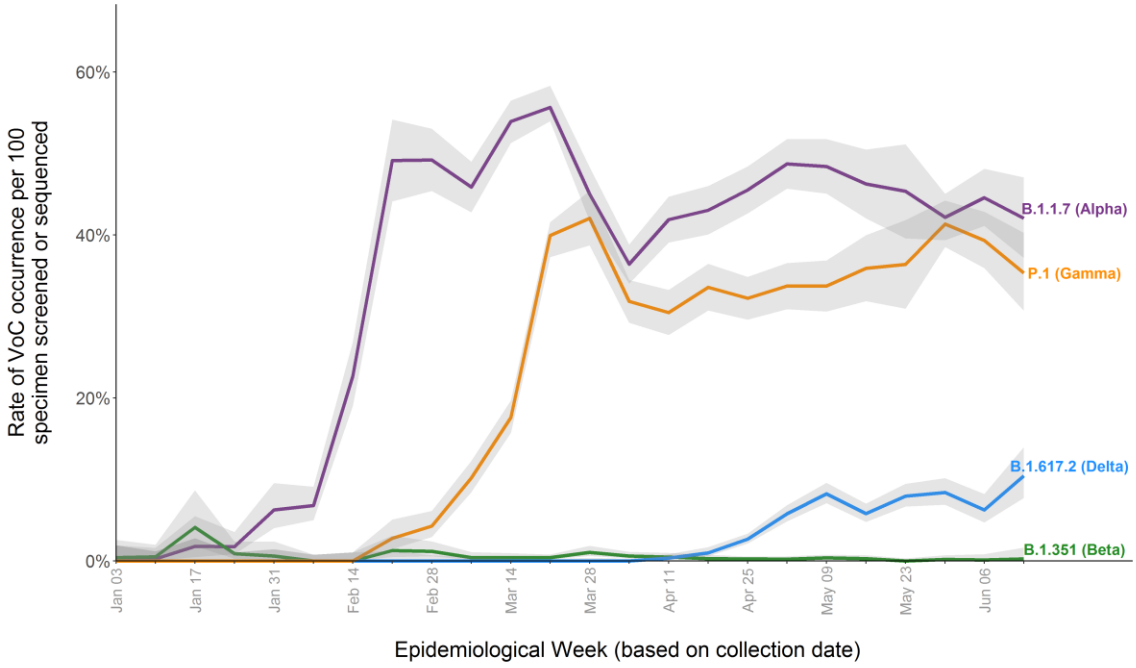



*Data from the PLOVER system at the BCCDC Public Health Lab.*

*Purple shaded box reflects partial data due to the results being available 4-7 days after the sample is received by the BCCDC Public Health Lab, and estimates for the latest epi week may change as more sequencing results come back.*

The main circulating variants are B.1.1.7 (Alpha) and P.1 (Gamma), respectively accounting for ~ 48 % and ~ 40% of positive specimens screened or sequenced. Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 24 (Jun 13 - Jun 19) may change as more sequencing results are analyzed.

Figure 2. Estimated Sample prevalence^ of VOCs by lineage by epi week of collection date, Jan 3 - Jun 13 2021.




*^ 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) , based on current prevalence, VOC screening results with both E484K and N501Y mutations are assumed to be P.1, given a very low prevalence of B.1.351 in BC. As of week 22 (May 30, 2021), prevalence of VOC is estimated from sequencing results only.*

Table 1. Sequencing-based VOC prevalence and approximate distribution by VOC lineage in BC and Health Authorities, latest available estimates on epi week epi week 24 (Jun 13 - Jun 19).

| Region | Total positive tests | Sample prevalence VOCs* | | | Relative Proportion of VOC** | | |
|---|---|---|---|---|---|---|---|
| | | %B.1.1.7 (Alpha)*** | %B.1.617 (Delta) | %P.1 (Gamma)**** | %B.1. 1.7 | %B.1.617 | %P.1 |
| BC | 765 | 42 | 10 | 35 | 48 | 12 | 40 |
| FHA | 368 | 38 | 14 | 34 | 44 | 16 | 39 |
| IHA | 196 | 71 | 0 | 24 | 75 | 0 | 25 |
| NHA | 22 | 50 | 0 | 0 | 100 | 0 | 0 |
| VCH | 146 | 14 | 11 | 63 | 16 | 13 | 71 |
| VIHA | 25 | 64 | 21 | 7 | 69 | 23 | 8 |

** Sample prevalence is calculated as the rate of occurrence of a given VOC lineage per 100 positive lab samples. It is estimated from the proportion of confirmed VOC via sequencing. Note, before epi week 22, sample prevalence was previously calculated using both screening and sequencing data.*

***Relative Proportion from the total VOC identified through sequencing. The proportion for B.1.351 not shown in this table due to small numbers. Note, before epi week 22, relative proportions were previously calculated using both screening and sequencing data. The proportion for B.1.351 not shown in this table due to small numbers.*

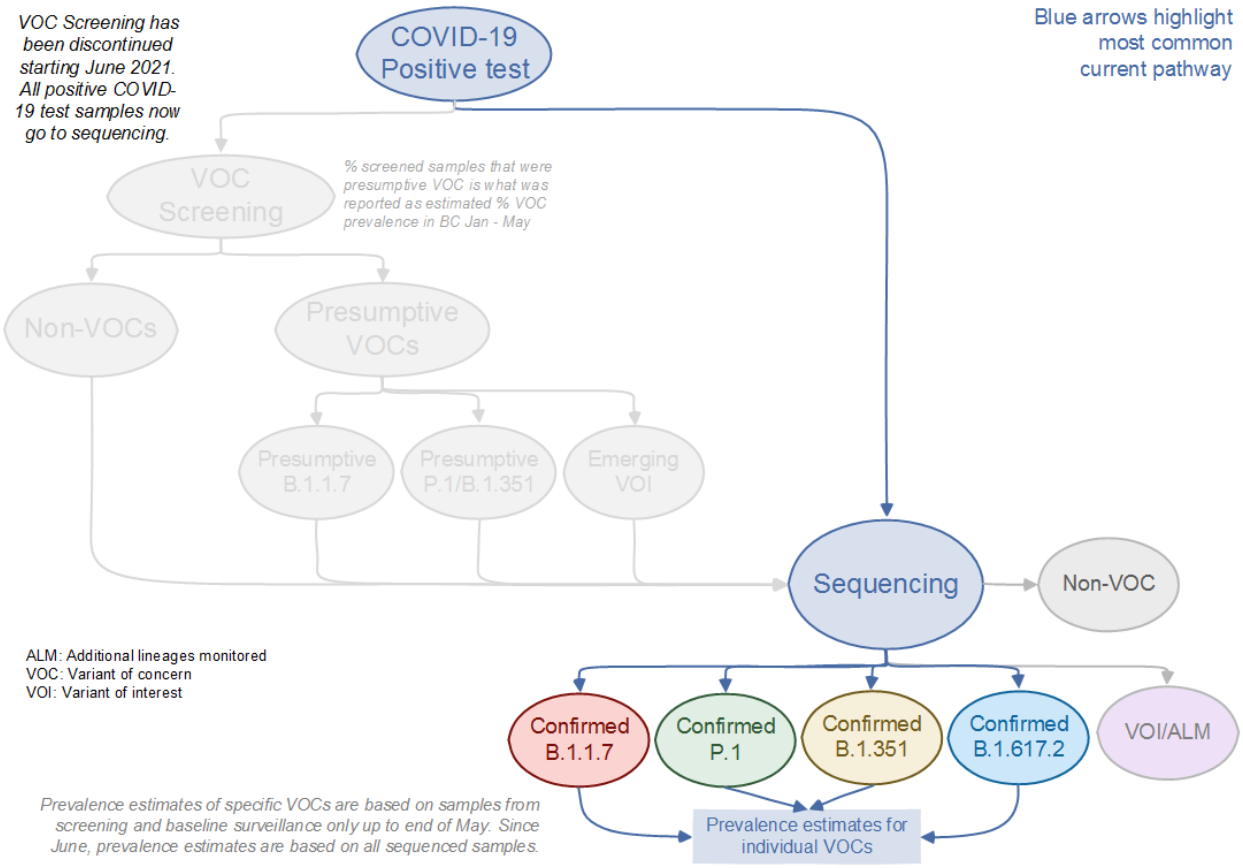
****Estimated from whole genome sequencing (WSG) starting epi week 22, and prior to this week the prevalence was estimated from the distribution of sequenced samples from background surveillance and non-overlapping subset of screened sample up to May 30, 2021.*

*****Estimated from WGS starting epi week 22, and prior to this week, the prevalence was estimated from the distribution of sequenced samples from background surveillance and non-overlapping subset of screened samples testing positive for both the N501Y and E484K mutation up to May 30, 2021.*

## Variants of Interests (VOI)

As illustrated in Figure 3 below, BCCDC Public Health Lab is continuously monitoring for both VOCs and VOIs. 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.

Figure 3. Overview of the screening and sequencing process applied to positive COVID-19 tests in BC, Jun 2021.




*Please note the turnaround time sequencing which takes approximately 4-7 days, but it could also take longer if there are lab backlogs.*

## Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 39127 specimens up to epi week 24 (Jun 13 - Jun 19) in BC, of which came back as variants under closer observation. Table 2 below presents the number of variant samples sequenced; it does not represent the number of variant COVID cases. As illustrated in Figure 3 above, BC has transitioned to whole genome sequencing on all positive samples.

Table 2: Frequencies of SARS-CoV-2 monitored genetic lineages confirmed by WGS

| Identified Lineage* (Pangolin version 2.4.2/ PangoLEARN2021-05-19) | WHO label | Category** | First Detected | TOTAL |
|---|---|---|---|---|
| B.1.1.7 | Alpha | VOC | UK | 12,054 |
| B.1.351 | Beta | VOC | South Africa | 151 |
| P.1 | Gamma | VOC | Brazil/Japan | 9,709 |
| B.1.617.2# | Delta | VOC | India | 970 |
| B.1.617.1# | Kappa | VOI | India; double mutant | 284 |
| B.1.617.3# | | VOI | India | 4 |
| A.23.1 | | VOI | TBC | 23 |
| B.1.427 | Epsilon | VOI | California, USA | 4 |
| B.1.429 | Epsilon | VOI | California, USA | 591 |
| B.1.1.318 | | VOI | Switzerland | 16 |
| B.1.616 | | VOI | France | 0 |
| C.37 | | VOI | Chile | 1 |
| P.2 | Theta | VOI | Brazil | 151 |
| P.3 | Iota | VOI | Philippines | 1 |
| B.1.526 | Zeta | VOI | New York, USA | 12 |
| B.1.525 | Eta | VOI | Nigeria | 94 |
| B.1.526.1 | | ALM | New York, USA | 8 |
| B.1.618 | | ALM | India; triple mutant | 44 |
| P.1.1## | | ALM | Brazil | 4 |
| AY.1 | | ALM | India; Delta+ | 0 |
| TOTAL | | | | 24,121 |

** 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.*

*** Variant category includes: Variant of Concern (VoC), Variant of Interest (VoI) and Additional Lineages Monitored (ALM).*

**** Other surveillance categories include: vaccine breakthrough, reinfections, hospitalized and other requests for sequencing.*

*# Note that a new lineage, C.37 (Lambda) has been designated (VOI) as Variant of Interest and added to the list of variants that are closely monitored.*
*## Note that P.1 has been further divided into 2 lineages (P.1 and P.1.1).*
*## Note that AY.1 is a new sub-lineage of B.1.617.2 (Delta) with the addition of a mutation also found in B.1.351 (Beta).*