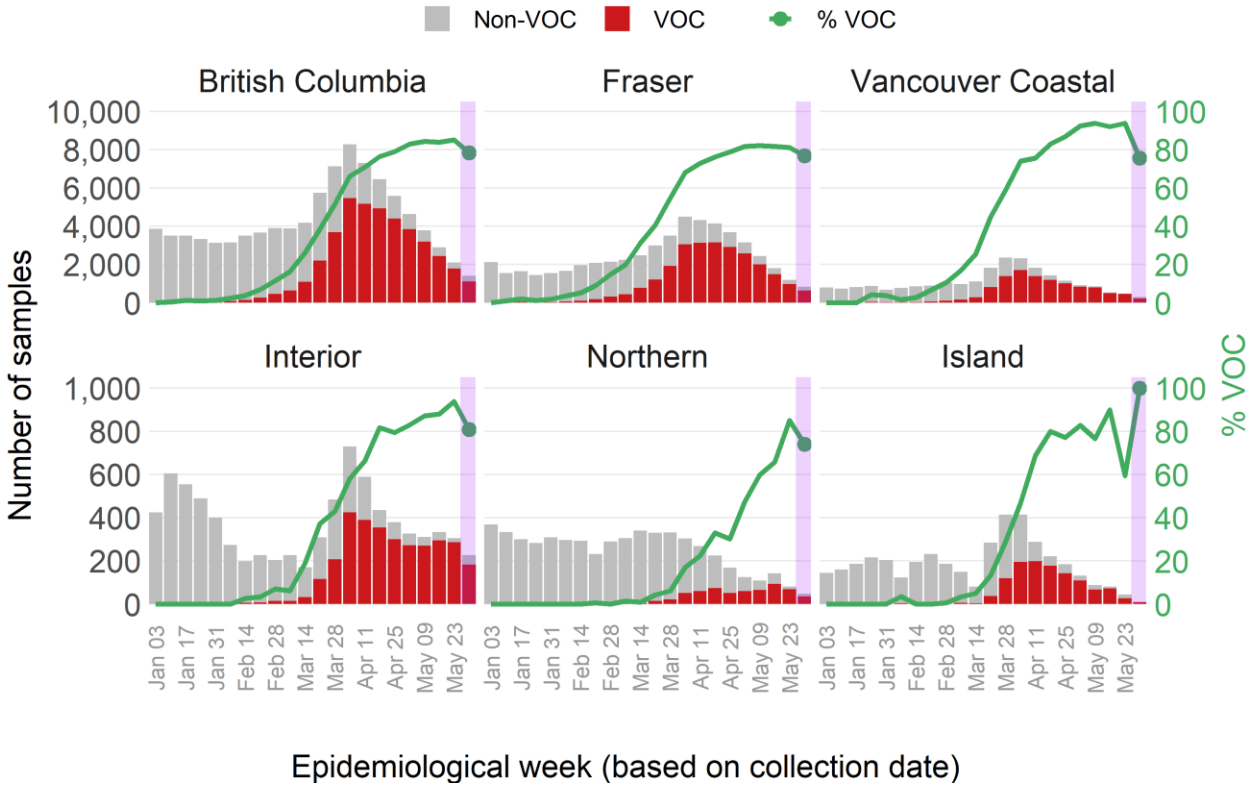
Weekly update on Variants of Concern (VOC)

Jun 11, 2021

B.C. has transitioned to whole genome sequencing on all positive samples to provide gold standard analysis to detect VOC and to support outbreak responses.

Of all samples tested in epi week 22 (May 30 - Jun 05) in BC, ~78% were confirmed VOCs through sequencing (Figure 1). VOC prevalence was similar across Health Authorities, except in Northern Health, where it was lower, at 74%.

Figure 1. Prevalence of presumptive and sequenced VOC¨, by start of epi week of collection date in BC and Health Authorities, Jan 3 - May 30, 2021

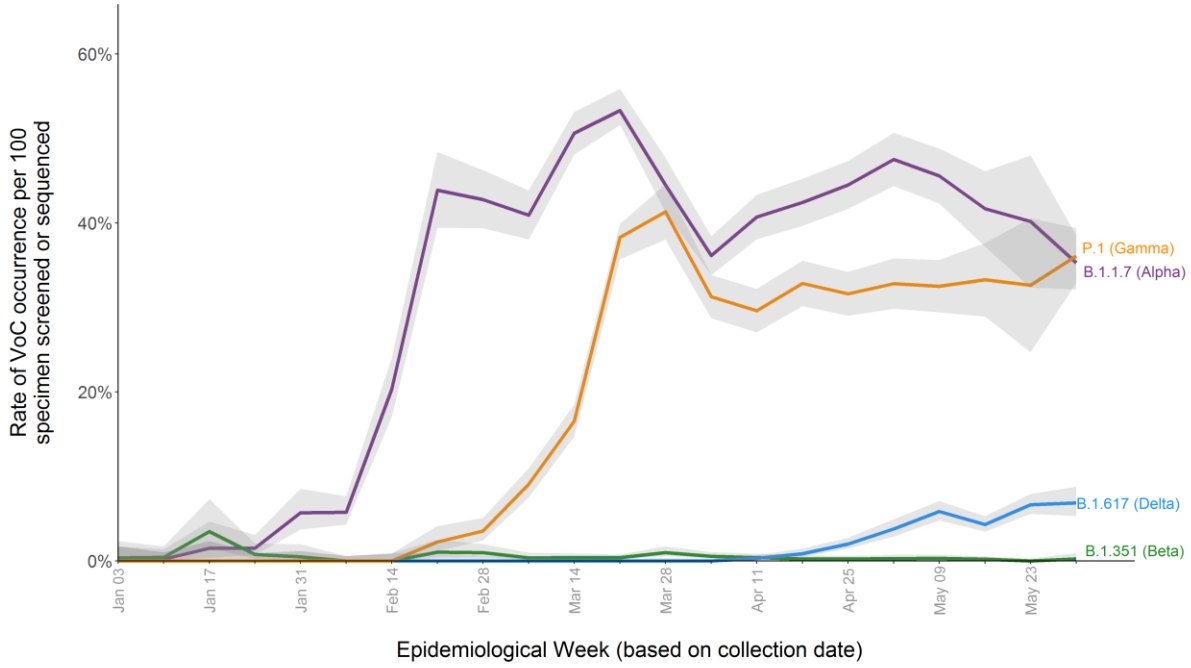


Data from the PLOVER system at the BCCDC Public Health Lab.

¨ *Purple shaded box reflects partial data due to the results being available four to seven 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 and P.1, respectively accounting for ~45 % and ~46% of positive specimens screened or sequenced. Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 22 (May 30 - Jun 05) 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 - May 30 2021.



^ 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 presumptive VOC from screening and the proportion of confirmed VOC via sequencing (excluding outbreaks and targeted surveillance).

As of 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 for epi week 22 (May 30 - Jun 05).

Region	Total positive tests	Sample prevalence VOCs*			Relative Proportion of VOC**		
		%B.1.1.7***	%B.1.617.2#	%P.1****	%B.1.1.7	%B.1.617.2	%P.1
BC	1,415	35	7	36	45	9	46
FHA	829	35	7	34	46	10	45
IHA	226	54	2	29	63	2	35
NHA	47	52	9	13	71	12	18
VCH	300	23	7	48	30	9	60
VIHA	9¥	100¥	0	0	100¥	0	0

* *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 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 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*

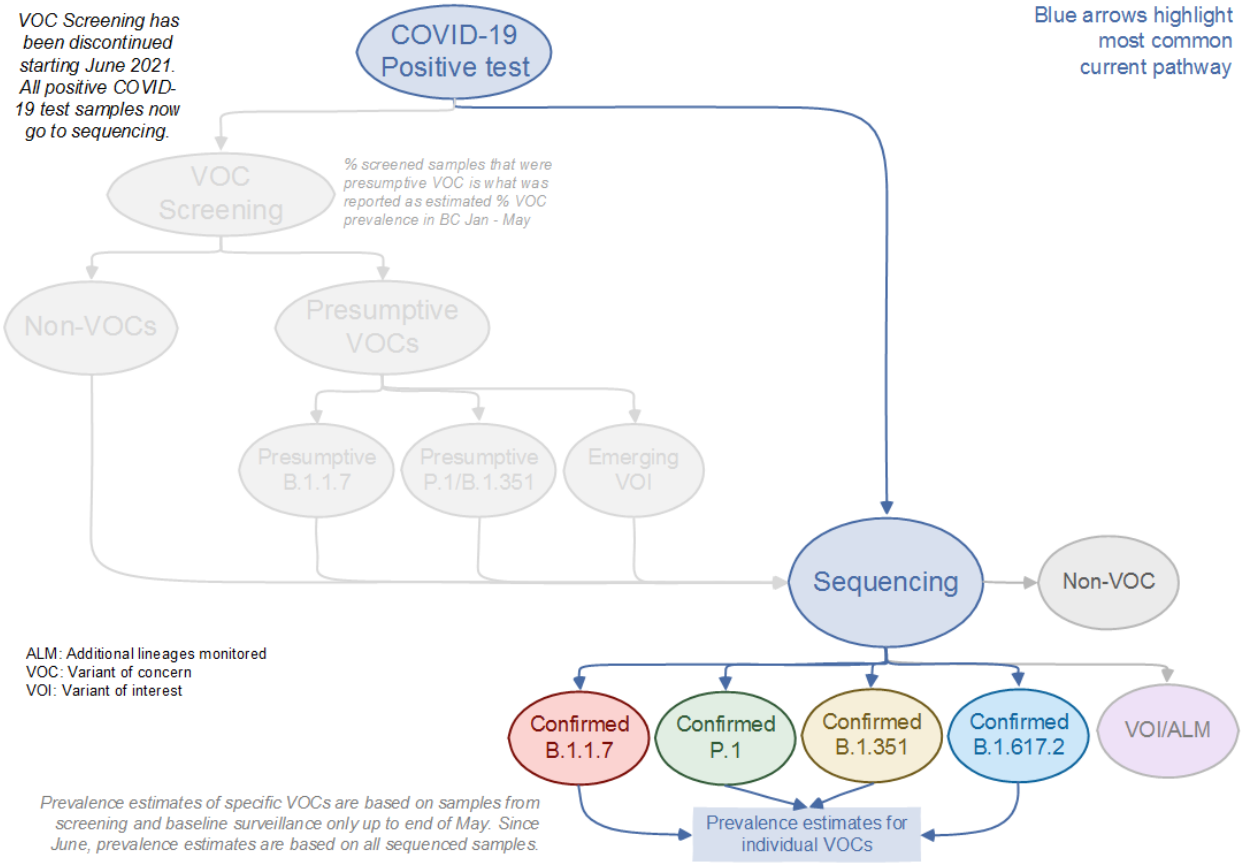
 # Note that B.1.617 has been further divided into 3 sub lineages (B.1.617.1 (Kappa), B.1.617.2 (Delta), B.1.617.3) – B.1.617.2 (Delta) has been designated as a VOC

¥ *Note the low number of positive tests that were sequenced from VIHA over the past epi week. Low numbers lead to unstable estimates of prevalence and relative proportions.*

Variants of Interests (VOI)

B.C. has transitioned to whole genome sequencing on all positive samples to provide gold-standard analysis to detect variants of concern and fingerprint details to support outbreak responses, as illustrated in the updated 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, June 2021.



Please note the turnaround time sequencing which takes approximately one week, but it could also take longer if there are lab backlogs.

Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 33,861 specimens up to epi week 22 (May 30 - Jun 05) in BC, of which came 19,439 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)*	*Nomenclature*	*Category***	*First Detected/Alternate Name*	*TOTAL*
B.1.1.7	Alpha	VOC	UK	10,118
B.1.351	Beta	VOC	South Africa	135
P.1	Gamma	VOC	Brazil/Japan	7,551
B.1.617.2#	Delta	VOC	India	614
B.1.617.1#	Kappa	VOI	India; double mutant	264
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	417
B.1.1.318		VOI	Switzerland	16
B.1.616		VOI	France	0
P.2	Theta	VOI	Brazil	147
P.3	Iota	VOI	Philippines	0
B.1.526	Zeta	VOI	New York, USA	12
B.1.525	Eta	VOI	Nigeria	91
B.1.526.1		ALM	New York, USA	8
B.1.618		ALM	India; triple mutant	31
P.1.1##		ALM	Brazil	4
TOTAL				19,439

** 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 B.1.617 has been further divided into 3 sub lineages with new designation: B.1.617.1 Kappa, B.1.617.2 (Delta), and B.1.617.3.

Note that P.1 has been further divided into 2 lineages (P.1 and P.1.1).