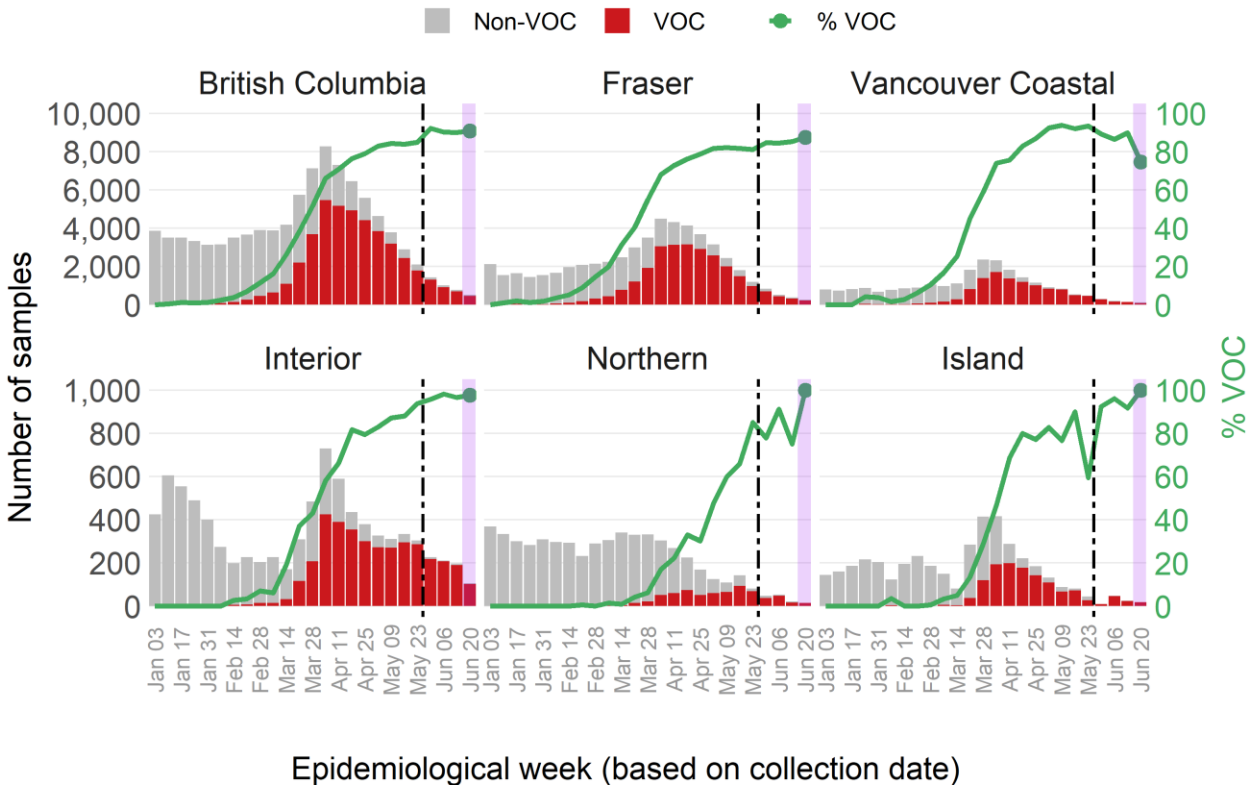
Weekly update on Variants of Concern (VOC)

Jul 02, 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 25 (Jun 20 - Jun 26) in BC, ~ 92% were presumptive VOCs (Figure 1). VOC prevalence was similar across Health Authorities, except in Vancouver Coastal Health, where it was lower, at 80%.

Figure 1. Prevalence of presumptive VOC, by epi week in BC and Health Authorities, Jun 20 - Jun 26

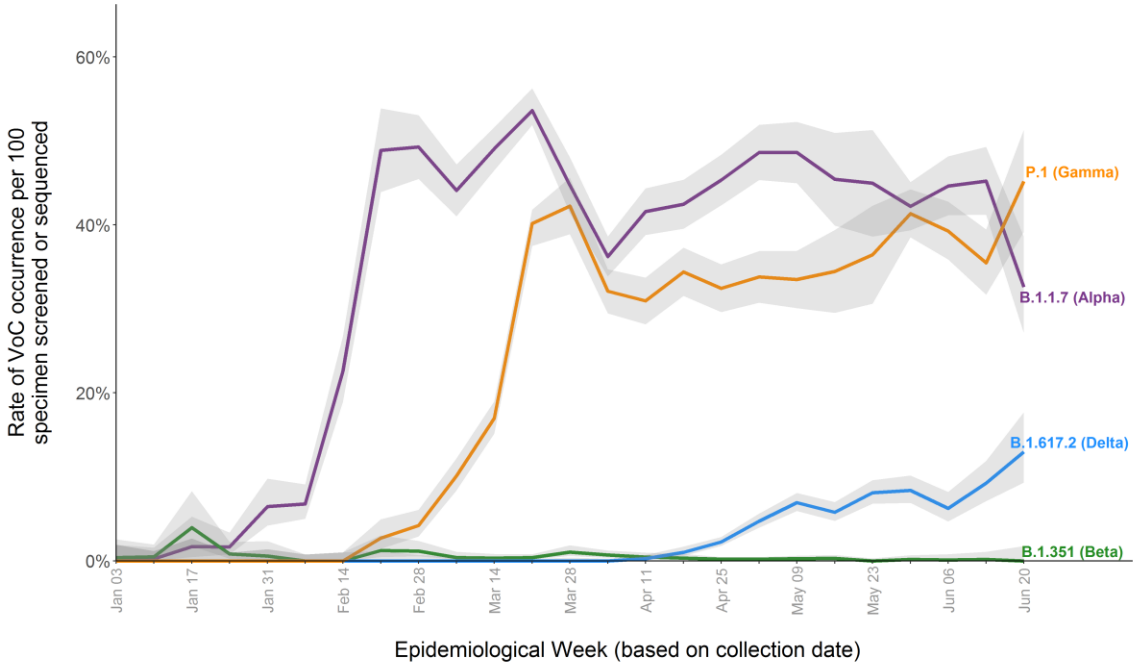


Data from the PLOVER system at the BCCDC Public Health Lab.

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 Alpha (B.1.1.7) and Gamma (P.1), respectively accounting for about 33 % and 50% of positive specimens sequenced. Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 25 (Jun 20 - Jun 26) 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 20 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. Between epi week 13 (March 28, 2021) and epi week 22 (May 30, 2021), 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 25 (Jun 20 - Jun 26).

Region	Total positive tests	Sample prevalence VOCs*			Relative Proportion of VOC**		
		% Alpha (B.1.1.7)	% Delta (B.1.617.2)	% Gamma (P.1)	%Alpha	%Delta	%Gamma
BC	362	33	13	45	36	14	50
FHA	250	30	14	47	33	16	52
IHA	105	69	0	29	71	0	29
NHA	15	80	0	20	80	0	20
VCH	112	10	16	55	12	20	68
VIHA	17	0	60	40	0	60	40

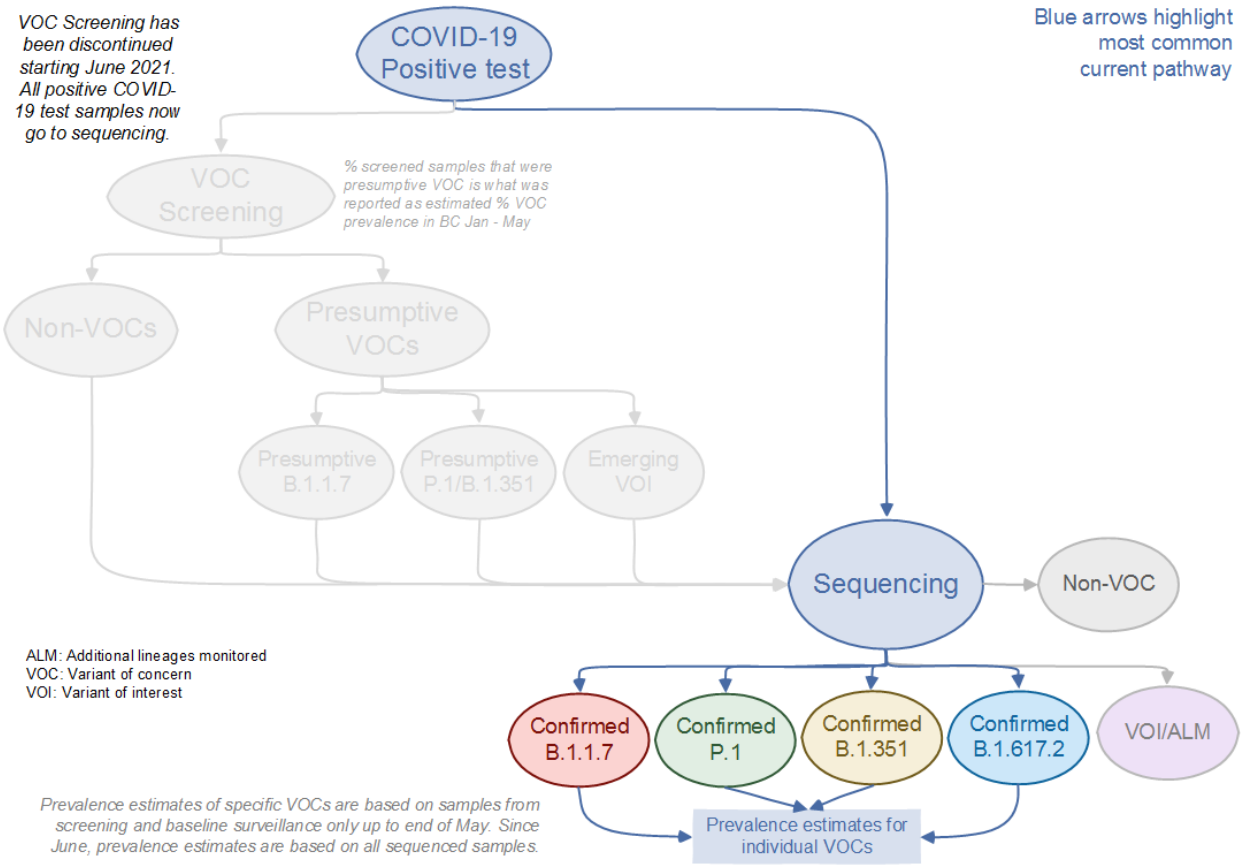
** Sample prevalence is calculated as the rate of occurrence of a given VOC lineage per 100 positive lab samples. It is estimated from the proportion of confirmed VOC via sequencing. Note, before epi week 22, sample prevalence was previously calculated using both screening and sequencing data.*

***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.*

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 41,822 specimens up to epi week 25 (Jun 20 - Jun 26) in BC, of which 26,311 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)	Nomenclature	Category**	First Detected/Alternate Name	TOTAL
B.1.1.7	Alpha	VOC	UK	13,555
B.1.351	Beta	VOC	South Africa	152
P.1	Gamma	VOC	Brazil/Japan	10,273
B.1.617.2	Delta	VOC	India	1,041
B.1.617.1	Kappa	VOI	India; double mutant	285
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	616
B.1.1.318		VOI	Switzerland	16
B.1.616		VOI	France	0
C.37[#]	Lambda	VOI	Chile	1
P.2	Theta	VOI	Brazil	170
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	46
P.1.1[##]		ALM	Brazil	4
AY.1[###]		ALM	India; Delta+	0
B.1.621		ALM	Columbia	6
TOTAL				26,311

** 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).