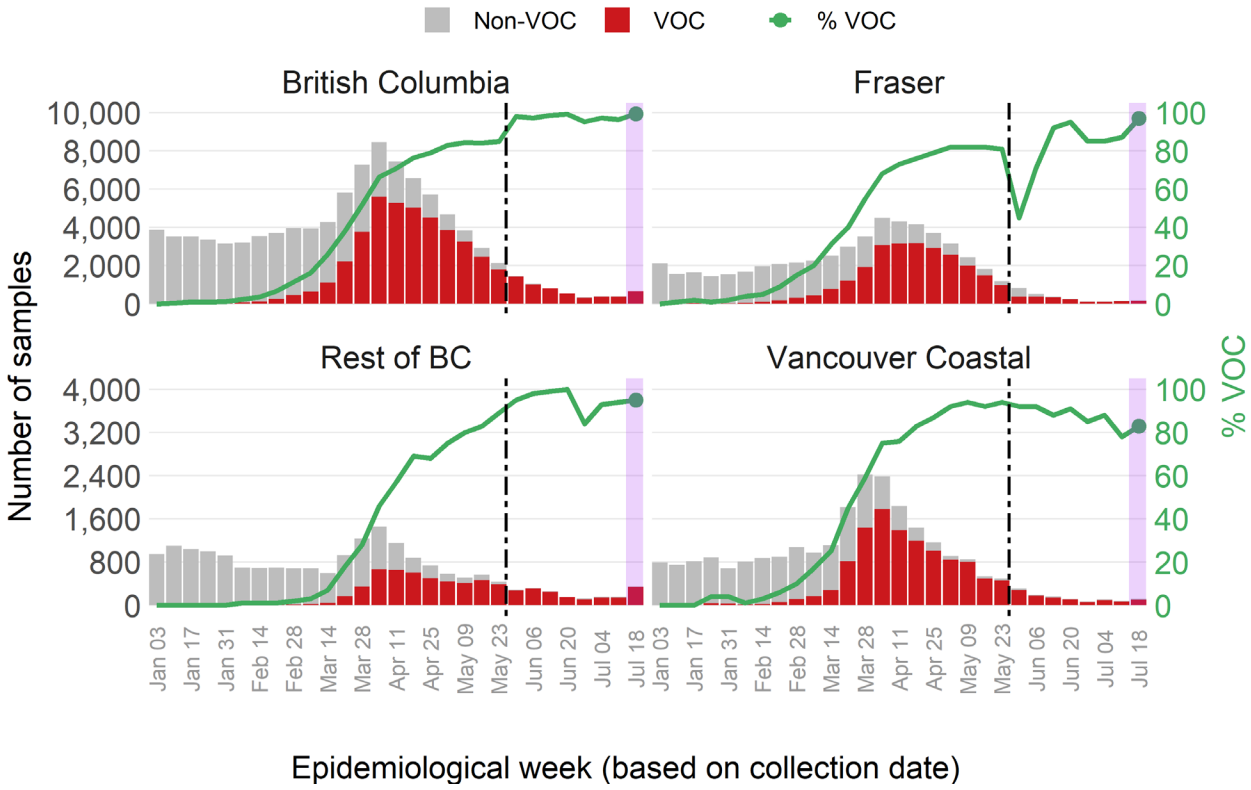
Weekly update on Variants of Concern (VOC)

Jul 30, 2021

Of all positive samples tested in epi week 29 (Jul 18 - Jul 24) in BC, ~ 99% were confirmed VOCs (Figure 1). VOC prevalence was similar across Health Authorities, except in Vancouver Coastal Health, where it was lower, at 83%.

Data from epi week 29 reflects partial data due to a lag in receipt of positive samples from front line laboratories; estimates are expected to change as more specimens are received and sequenced.

Figure 1. Prevalence of VOC, by epi week in BC and Health Authorities, Jul 18 - Jul 24



Dotted line indicates the time of transition to WGS of all positive samples on May 30, 2021 (epi week 22).

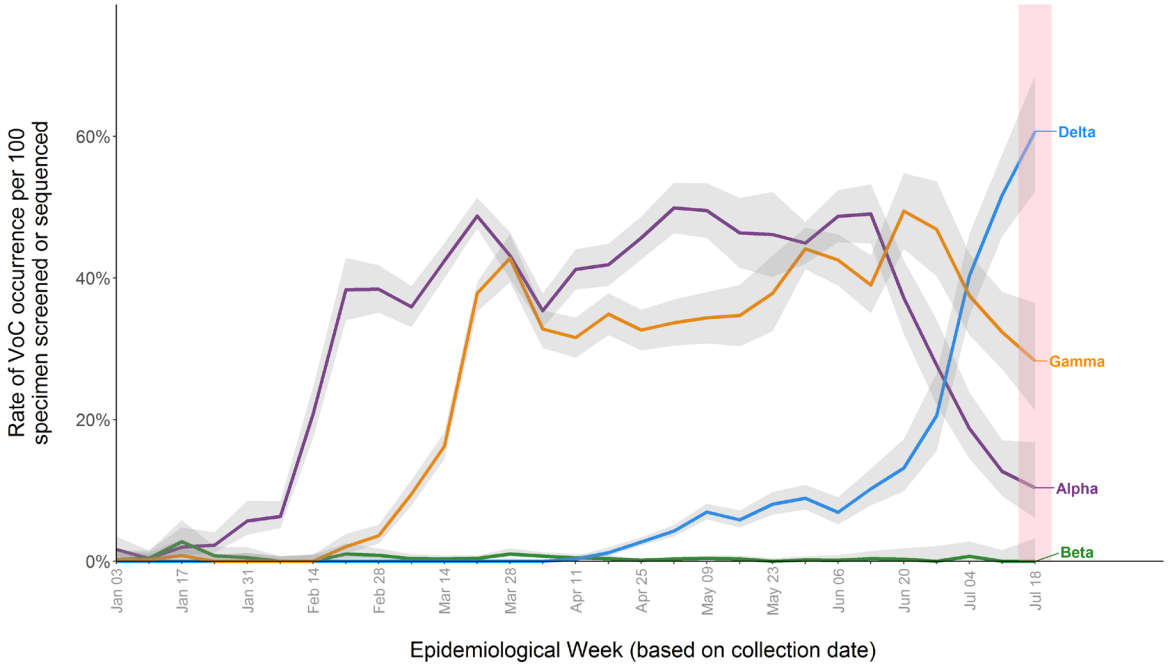
Data from the PLOVER system at the BCCDC Public Health Lab.

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 Delta (B.1.617.2) and Gamma (P.1), respectively accounting for about 61% and 28% of positive specimens sequenced.

Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 29 (Jul 18 - Jul 24) may change as more sequencing results are analyzed and given the lag in receipt of positive samples from front line laboratories.

Figure 2. Estimated Sample prevalence^ of VOCs by lineage by epi week of collection date, Jan 3 - Jul 24, 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.

Pink shaded box reflects partial data due to a lag in receipt of positive samples from front line laboratories; estimates are expected to change as more specimens are received and sequenced.

Table 1. Sequencing-based VOC prevalence and approximate distribution by VOC lineage in BC and Health Authorities, latest available estimates on epi week 29 (Jul 18 - Jul 24).

Region	Total positive tests	Sample prevalence VOCs*			Relative Proportion of VOC**		
		%B.1.1.7 (Alpha)	%B.1.617.2 (Delta)	%P.1 (Gamma)	%B.1.1.7	%B.1.617.2	%P.1
BC	654	10	61	28	10	61	29
FHA	168	16	44	40	16	44	40
IHA	314	0	89	11	0	89	11
NHA***	11	0	0	0	0	0	0
VCH	122	13	54	29	13	57	30
VIHA***	30	0	100	0	0	100	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.*

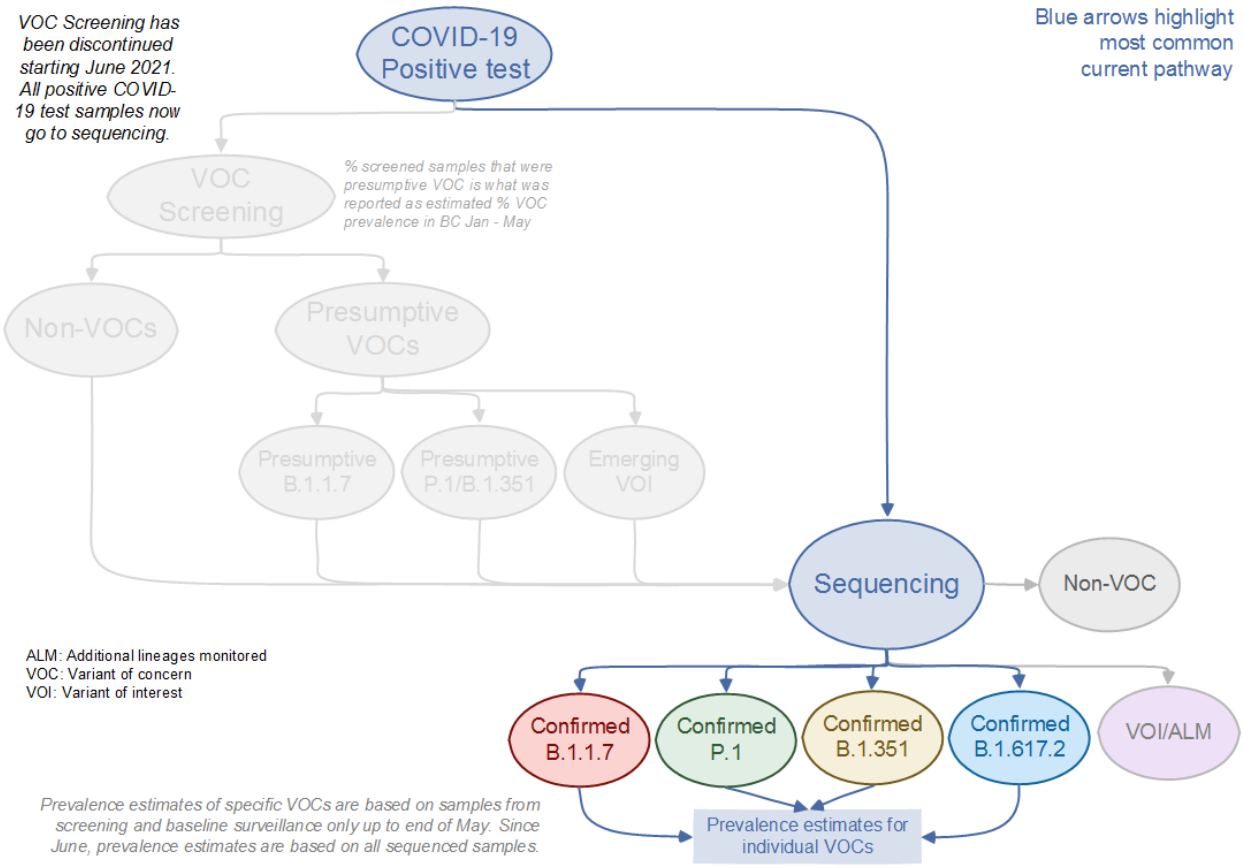
*** Relative Proportion from the total VOC identified through sequencing. The proportion for B.1.351 not shown in this table due to small numbers. Note, before epi week 22, relative proportions were previously calculated using both screening and sequencing data. The proportion for B.1.351 not shown in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

**** Note: Due to decline in positive cases and the lag in receipt of positive samples from front line laboratories the reported estimates for VoC by Health Authorities are expected to change as more specimens are received and sequenced*

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, Jul 2021.



Please note the turnaround time sequencing which takes approximately 4-7 days, but it could also take longer if there are lab backlogs or if there are delays in receiving current positive samples from front line laboratories.

Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 47,755 specimens up to epi week 29 (Jul 18 - Jul 24) in BC, of which 29,999 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 since May 30, 2021.

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

Identified Lineage* (Pangolin version 3.1.7/ PangoLEARN2021-07-09)	Nomenclature	Category**	First Detected/Alternate Name	TOTAL	% Change since last report
B.1.1.7	Alpha	VOC	UK	14,850	0.3
B.1.351#	Beta	VOC	South Africa	160	0
B.1.351.1#	Beta	VOC	South Africa	0	0
B.1.351.2#	Beta	VOC	South Africa	0	0
B.1.351.3#	Beta	VOC	South Africa	2	0
B.1.351.4#	Beta	VOC	South Africa	0	0
P.1##	Gamma	VOC	Brazil/Japan	11,579	1.6
P.1.1##	Gamma	VOC	Brazil	15	0
P.1.2	Gamma	VOC	Brazil	0	0
B.1.617.2	Delta	VOC	India	1,688	0
AY.1###	Delta	VOC	India	0	0
AY.2###	Delta	VOC	India	0	0
B.1.617.1	Kappa	VOI	India	387	25.1
B.1.617.3		VOI	India	4	0
A.23.1		VOI	TBC	35	34.3
B.1.427	Epsilon	VOI	California, USA	4	0
B.1.429	Epsilon	VOI	California, USA	804	4.4
B.1.1.318		VOI	Switzerland	24	0
B.1.616		VOI	France	0	0
B.1.526	Iota	VOI	New York, USA	21	0
B.1.526.1	Iota	VOI	New York, USA	0	0
B.1.525	Eta	VOI	Nigeria	153	1.3

Identified Lineage* (Pangolin version 3.1.7/ PangoLEARN2021-07-09)	Nomenclature	Category**	First Detected/Alternate Name	TOTAL	% Change since last report
C.37	Lambda	VOI	Chile	1	0
P.2	Zeta	VOI	Brazil	191	3.1
P.3	Theta	VOI	Philippines	2	0.0
B.1.618		ALM	India	58	-12.1
B.1.621		ALM	Columbia	21	14.3
TOTAL				29,999	2.3

** 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.*

Please note that a new version of Pangolin is being used. As a result, some samples have had their lineages reassigned.

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

 # Note that Beta variant, B.1.351, has been further divided into 4 sub lineages (B.1.351.1, B.1.351.2, B.1.351.3, B.1.351.4).

Note that Gamma (P.1) variant has been divided into one sub-lineage (P.1.1).

Note that Delta (B.1.617.2) variant has been further divided into 2 sub-lineages (AY.1 and AY.2).