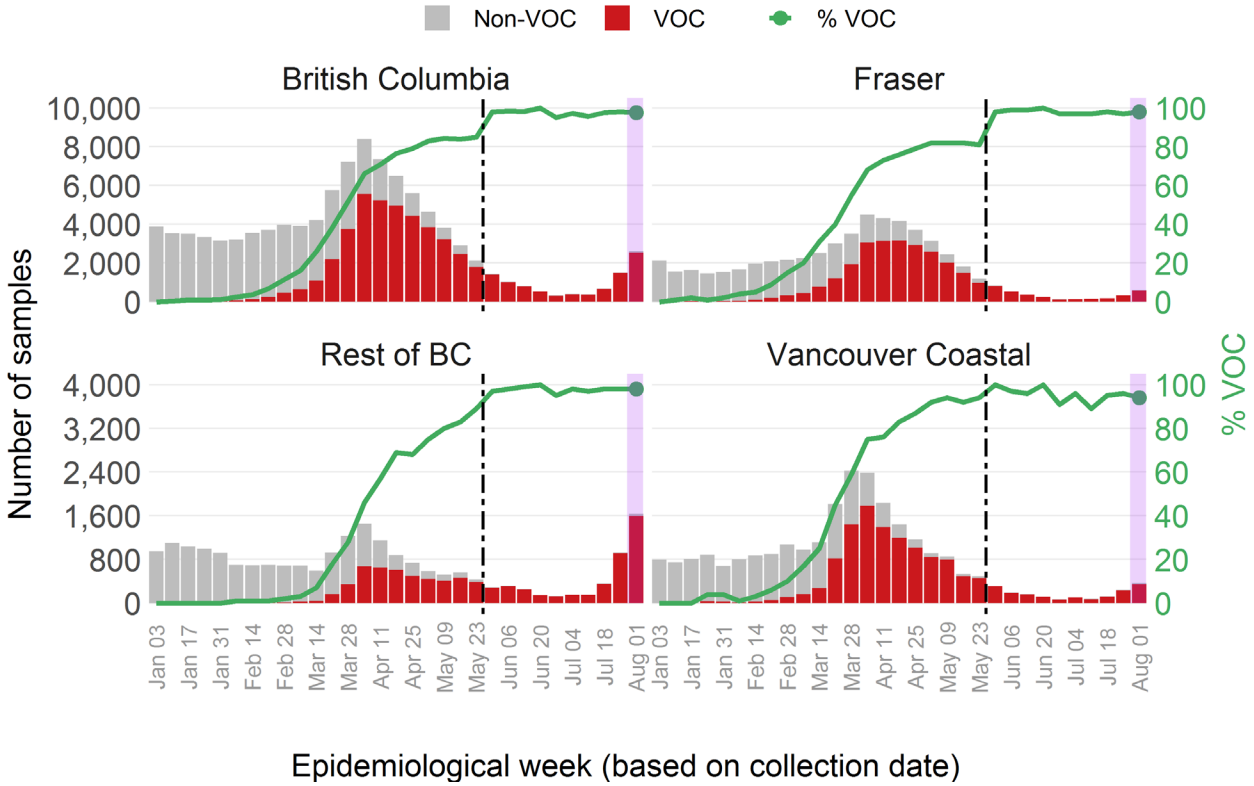
Weekly update on Variants of Concern (VOC)

Aug 13, 2021

Of all positive samples tested in epi week 31 (Aug 1 - 7) in BC, ~ 98% were confirmed VOCs (Figure 1). VOC prevalence was similar across Health Authorities.

Data from epi week 31 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, Aug 1 - Aug 7



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

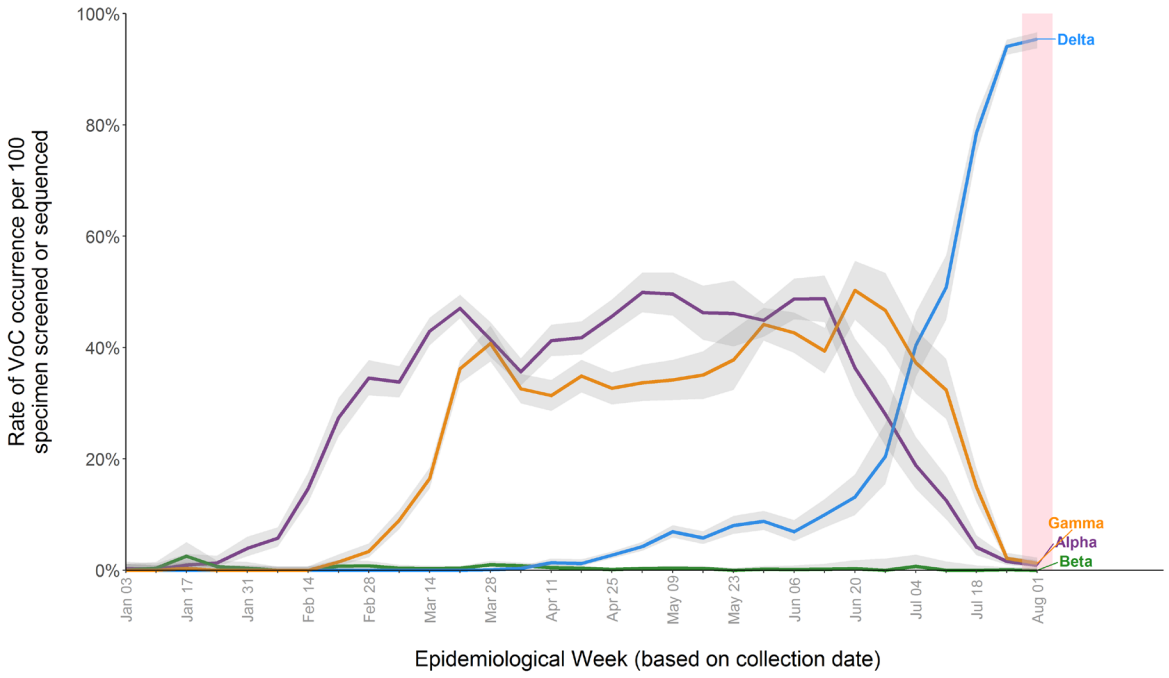
Data from the PLOVER system at the BCCDC Public Health Lab.

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 variant is Delta (B.1.617.2), accounting for about 95% of positive specimens sequenced.

Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 31 (Aug 01 - Aug 07) 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 - Aug 7, 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 31 (Aug 1 - Aug 7).

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	2602	1	95	1	1	98	1
FHA	594	3	93	2	3	96	2
IHA	1369	0	98	0	0	100	0
NHA	108	0	95	5	0	95	5
VCH	363	0	85	9	0	90	10
VIHA	158	0	93	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. Due to rounding, individual VoC estimates may not match the overall VoC prevalence.*

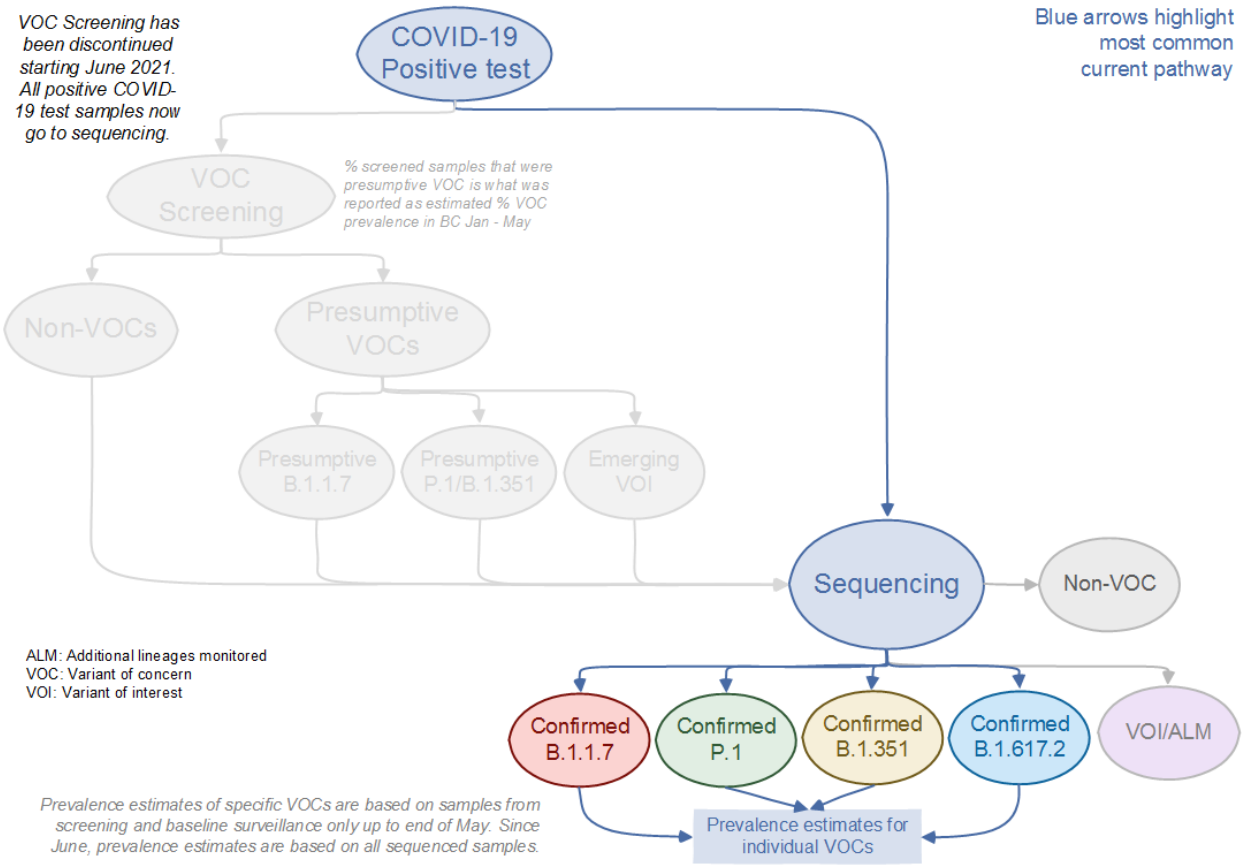
***Relative Proportion from the total VOC identified through sequencing. The proportion for B.1.351 not shown in this table due to small numbers. Note, before epi week 22, relative proportions were previously calculated using both screening and sequencing data. The proportion for B.1.351 not shown in this table due to small numbers. Due to rounding, totals may be more or less than 100%.*

****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 53,018 specimens up to epi week 31 (Aug 1 - Aug 7) in BC, of which 32,586 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 3.1.10/ PangoLEARN2021-07-28)	Name	Category**	First Detected/Alternate Name	TOTAL	% Change since last report
B.1.1.7	Alpha	VOC	UK	14,940	0.1
B.1.351#	Beta	VOC	South Africa	161	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	11,611	-1.4
P.1.1##	Gamma	VOC	Brazil	187	92
P.1.2##	Gamma	VOC	Brazil	1	100
B.1.617.2	Delta	VOC	India	3,949	33.9
AY.1###	Delta	VOC	India	0	0
AY.2###	Delta	VOC	India	0	0
B.1.617.1	Kappa	VOI	India	402	0.7
B.1.617.3		VOI	India	4	0
A.23.1		VOI	TBC	35	0
B.1.427	Epsilon	VOI	California, USA	4	0
B.1.429	Epsilon	VOI	California, USA	826	-0.2
B.1.1.318		VOI	Switzerland	28	3.6
B.1.616		VOI	France	0	0
B.1.526	Iota	VOI	New York, USA	12	-75
B.1.526.1	Iota	VOI	New York, USA	0	0
B.1.525	Eta	VOI	Nigeria	153	0
C.37	Lambda	VOI	Chile	1	0
P.2	Zeta	VOI	Brazil	193	0.5

Identified Lineage* (Pangolin version 3.1.10/ PangoLEARN2021-07-28)	Name	Category**	First Detected/Alternate Name	TOTAL	% Change since last report
P.3	Theta	VOI	Philippines	2	0
B.1.621		VOI	Columbia	27	14.8
B.1.621.1		VOI	Columbia	2	100
B.1.618		ALM	India	46	-26.1
TOTAL				32,586	4.1

** 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.*

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 P.1 has been further divided into 3 lineages (P.1, P.1.1 and P.1.2).

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