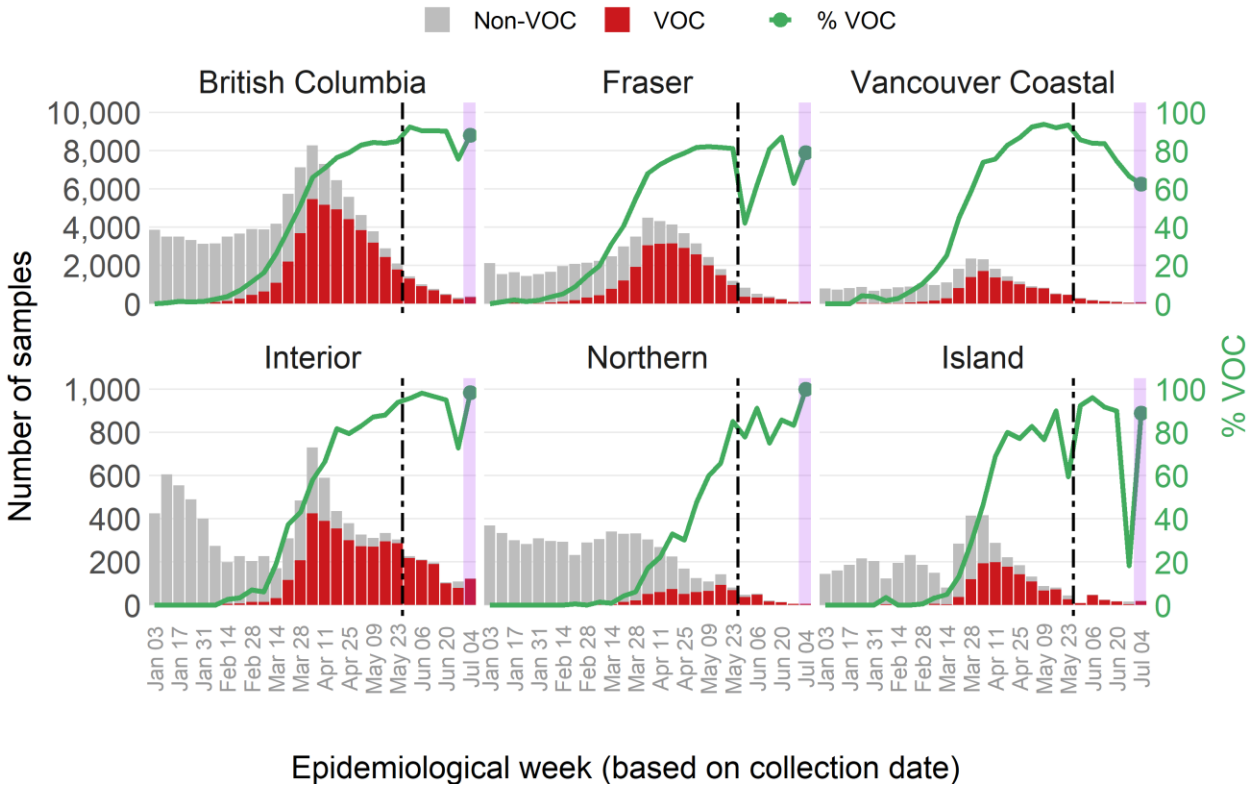
Weekly update on Variants of Concern (VOC)

Jul 16, 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 positive samples tested in epi week 27 (Jul 04 - Jul 10) in BC, ~ 88% were confirmed VOCs (Figure 1). VOC prevalence was similar across Health Authorities, except in Vancouver Coastal Health, where it was lower, at 62%.

Data from epi week 27 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 04 - Jul 10



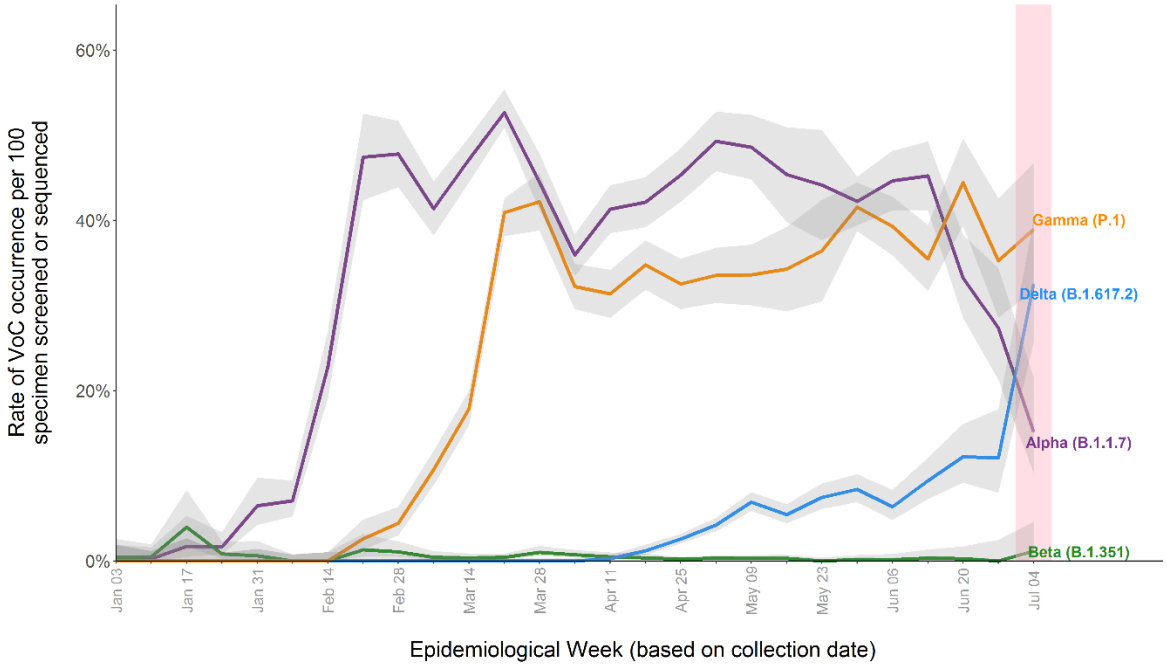
Data from the PLOVER system at the BCCDC Public Health Lab.

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), Delta (B.1.617.2) and Gamma (P.1), respectively accounting for about 15%, 33% and 39% of positive specimens sequenced.

Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 27 (Jul 04 - Jul 10) 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 10, 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 27 (Jul 04 - Jul 10).

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	362	15	33	39	17	37	44
FHA	250	13	11	60	15	13	70
IHA	105	24	54	20	24	55	21
NHA	15	50	0	50	50	0	50
VCH	112	3	30	40	3	40	53
VIHA	17	22	56	11	25	63	13

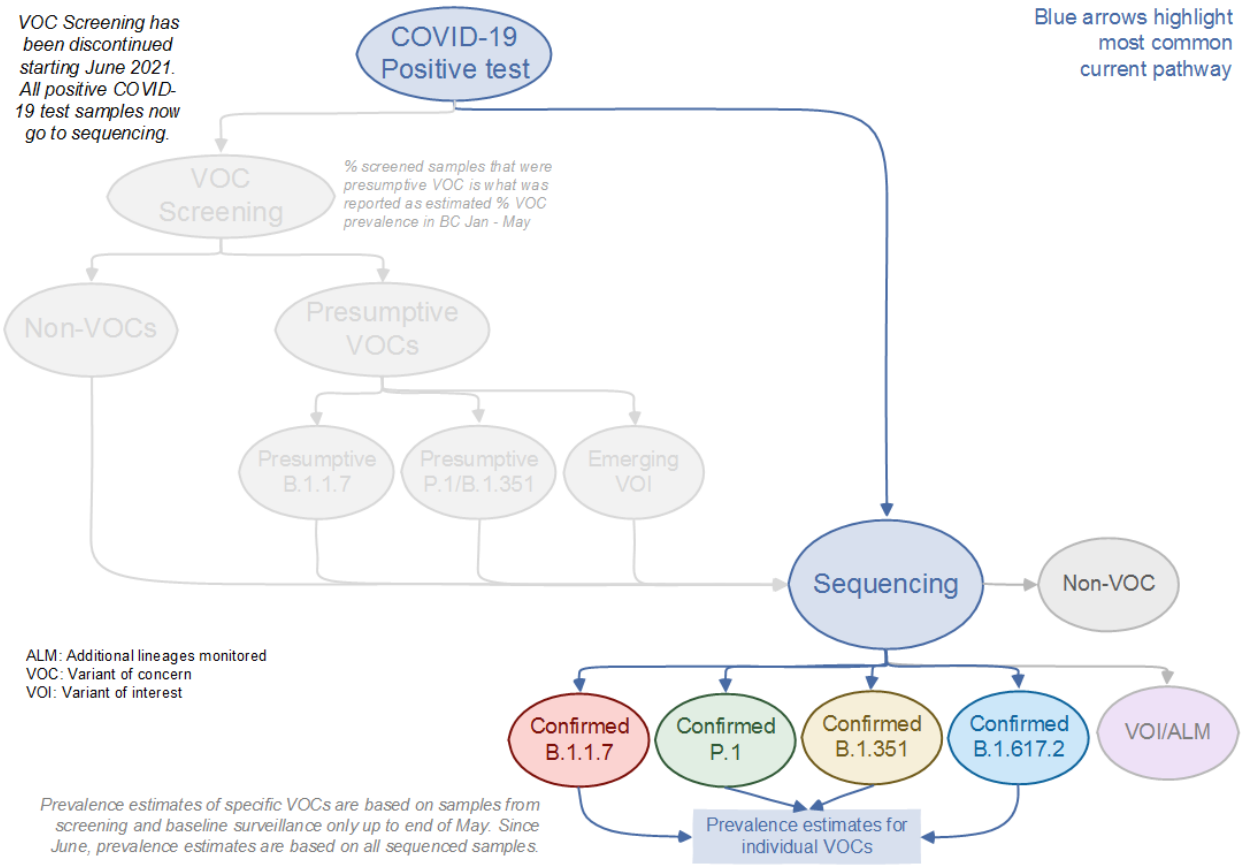
** Sample prevalence is calculated as the rate of occurrence of a given VOC lineage per 100 positive lab samples. It is estimated from the proportion of confirmed VOC via sequencing. Note, before epi week 22, sample prevalence was previously calculated using both screening and sequencing data.*

***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, 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 43,814 specimens up to epi week 27 (Jul 04 - Jul 10) in BC, of which 27,991 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 3.1.7/ PangoLEARN2021-07-09)	Nomenclature	Category**	First Detected/Alternate Name	TOTAL
B.1.1.7	Alpha	VOC	UK	14,170
B.1.351	Beta	VOC	South Africa	157
P.1	Gamma	VOC	Brazil/Japan	10,963
B.1.617.2	Delta	VOC	India	1,219
B.1.617.1	Kappa	VOI	India; double mutant	291
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	700
B.1.1.318		VOI	Switzerland	24
B.1.616		VOI	France	0
C.37#		VOI	Chile	1
P.2	Lambda	VOI	Brazil	181
P.3	Theta	VOI	Philippines	2
B.1.526*	Iota	VOI	New York, USA	20
B.1.525	Zeta	VOI	Nigeria	151
B.1.526.1*	Eta	ALM	New York, USA	0
B.1.618		ALM	India; triple mutant	58
P.1.1##		ALM	Brazil	12
AY.1###		ALM	India; Delta+	0
B.1.621		ALM	Colombia	11
TOTAL				27,991

** 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).*

**** 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).