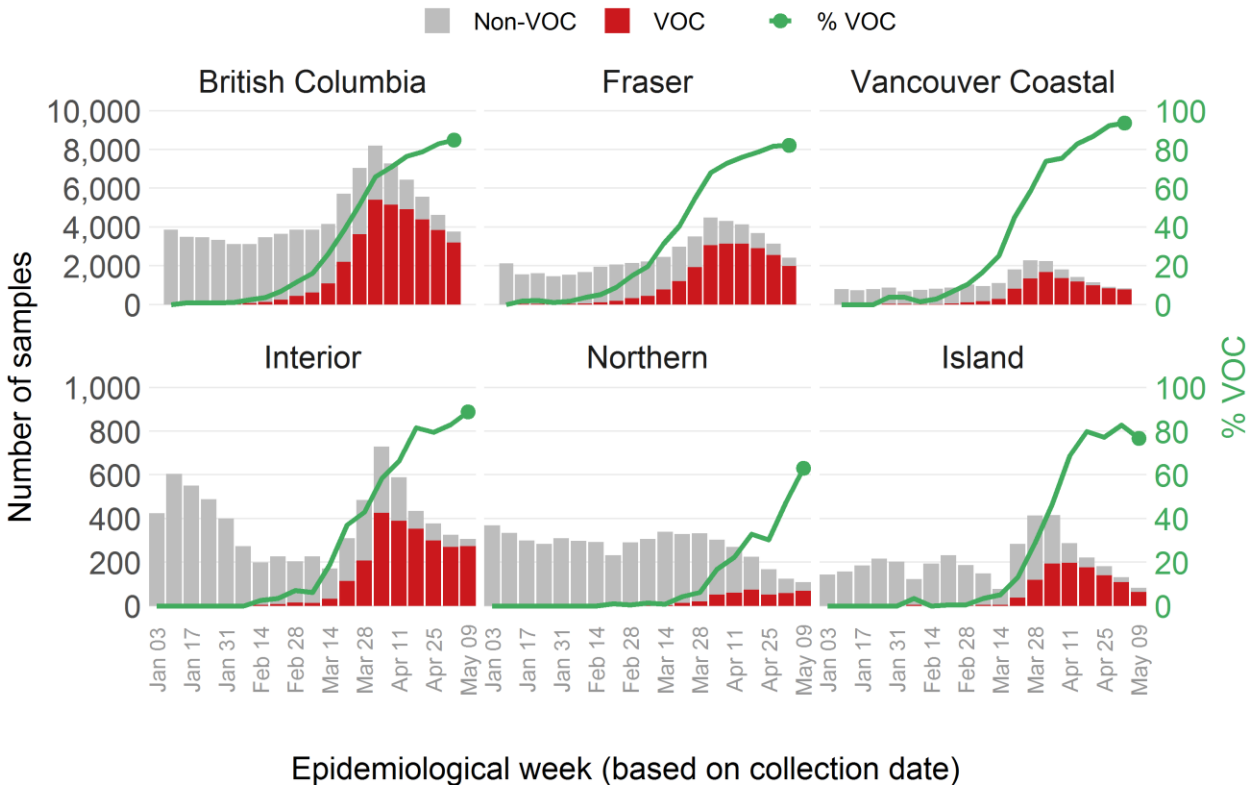
Weekly update on Variants of Concern (VOC)

May 20, 2021

Of all samples tested in epi week 19 (May 09 - May 15) in BC, ~85% were presumptive Variants of Concern (VOC)(Figure 1). VOC prevalence was similar across Health Authorities, except in Northern Health, where it was lower, at 63%.

Figure 1. Prevalence of presumptive VoC, by epi week in BC and Health Authorities, Jan 3- May 15 2021

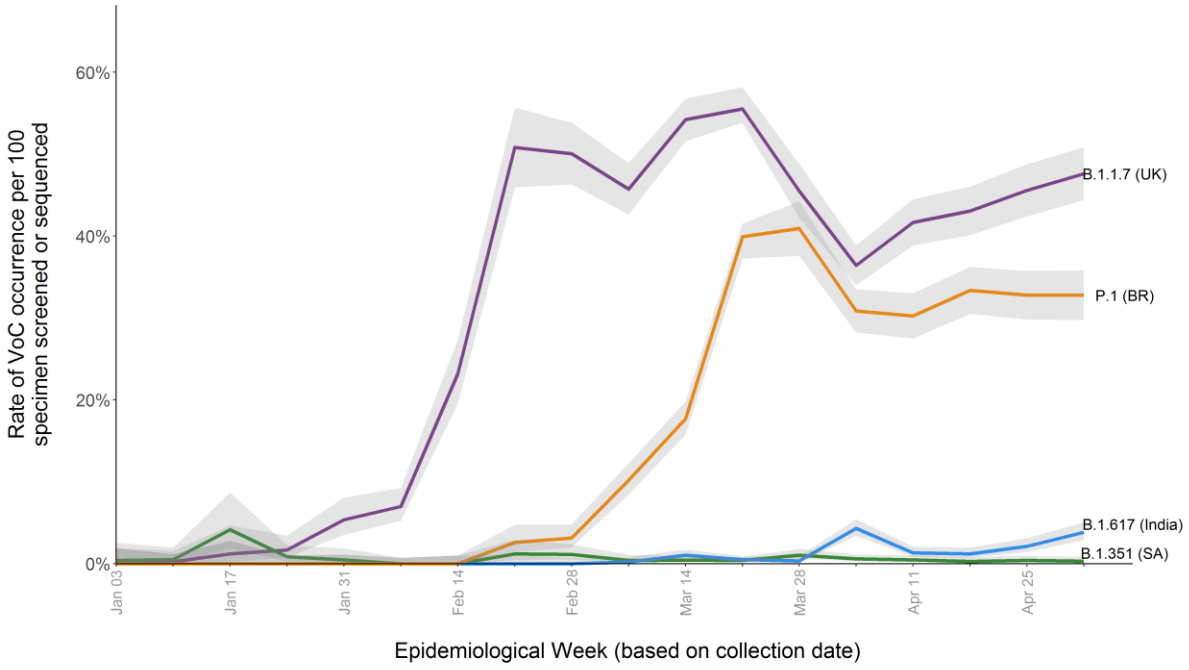


Data from the PLOVER system at the BCCDC Public Health Lab.

The main circulating variants are B.1.1.7 and P.1, respectively accounting for ~ 57% and ~ 41% of positive specimens screened or sequenced.

Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 18 (May 02 - May 08) may change as more sequencing results are analyzed.

Figure 2. Estimated Sample prevalence^ of VOCs by epi week of collection date, Jan 3- May 08 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. The variant B.1.617 has been classified as Variant of Concern by the World Health Organization as of May 10, 2021. The sub-lineages are currently being reviewed in Canada and designation may change.

Table 1. Presumptive VOC prevalence and approximate distribution by VOC lineage in BC and Health Authorities, latest available estimates. VOC counts are generated from VOC qPCR and WGS data.

	Epi week 19 (May 09 - May 15)		Epi week18^ (May 02 - May 08)					
Region	Total positive tests	% presumptive VOC*	Sample prevalence VOC§			Relative Proportion of VOC**		
			B.1.1.7***	B.1.617#	P.1****	B.1.1.7	B.1.617	P.1
BC	3772	85	48	4	33	57	2	41
FHA	2420	82	49	6	30	60	2	38
IHA	307	89	60	0	24	71	0	29
NHA	109	63	64	0	10	87	0	13
VCH	836	94	36	0	49	42	0	58
VIHA	83	77	55	1	25	61	10	29

^ Note that because sequencing results take longer to be analyzed, relative distribution of VOCs is more delayed than % VOC estimate.

** estimated from the proportion of screened samples testing positive for N501Y or E484K mutation.*

§ 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).

***Relative Proportion from the total VOC identified through background surveillance sequencing and non-overlapping screened samples.*

****estimated from the distribution of sequenced samples from background surveillance and non-overlapping subset of screened samples.*

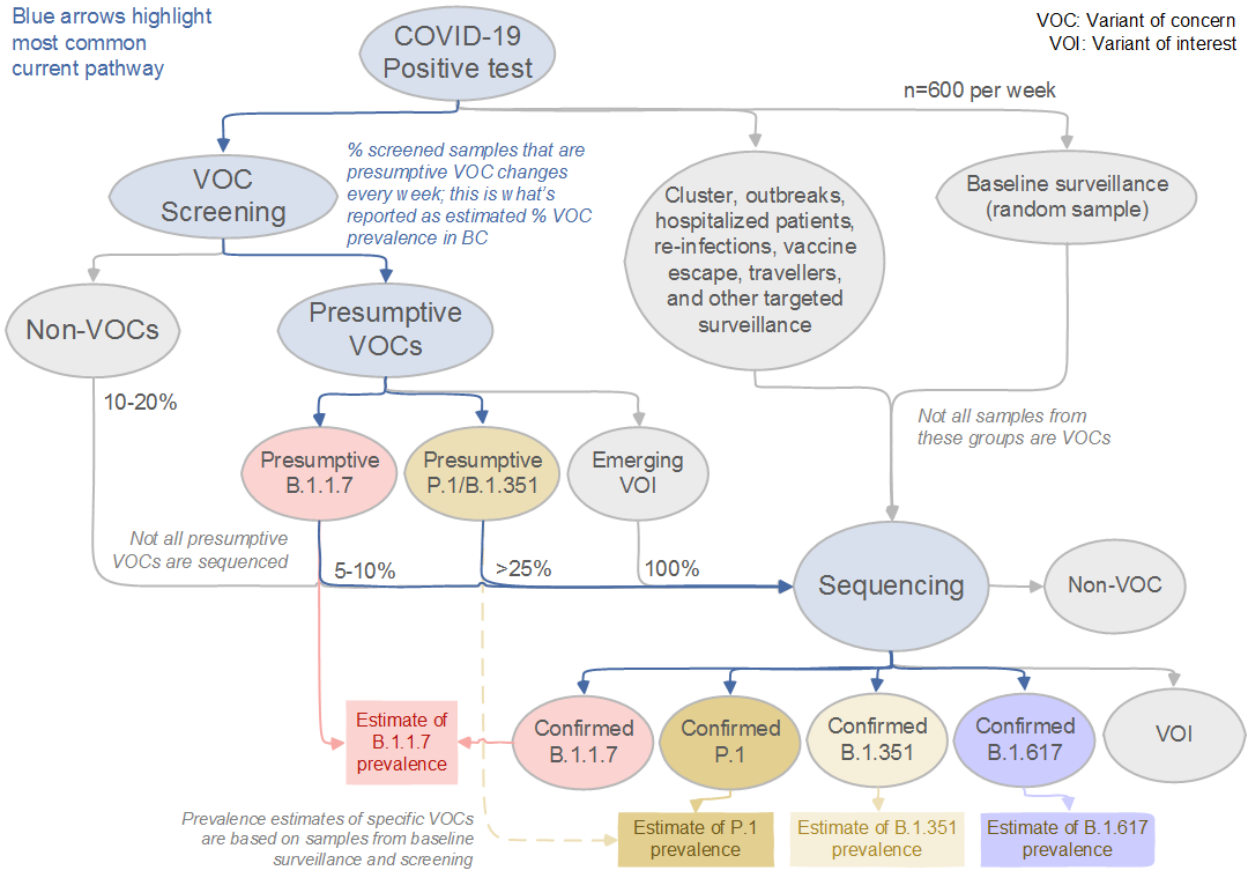
*****estimated from the distribution of sequenced samples from background surveillance and non-overlapping subset of screened samples testing positive for both the N501Y and E484K mutation*

 # Note that B.1.617 has been further divided into 3 sub lineages (B.1.617.1, B.1.617.2, and B.1.617.3) - This variant has been classified as Variant of Concern by the World Health Organization as of May 10, 2021. The sub-lineages are currently being reviewed in Canada and designation may change.

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. Current of as May 2021.



Please note the differences in turnaround time for screening and sequencing: screening results usually come back within 1-2 days, while sequencing results come back after approximately one week, but it could also take longer if there are lab backlogs.

Whole genome sequencing (WGS)

Whole genome sequencing was performed on 27,404 specimens, of which 13,388 came back as variants under closer observation. Table 2 presents the total number of sequenced samples by variant category. Please note that the numbers in this table do not reflect true population prevalence of a given variant in BC nor can they be used to calculate it. As illustrated in Figure 3 above, WGS is performed for a variety of reasons, and the numbers in Table 2 are dependent on changes to sampling strategy and prioritization of particular categories over time.

Identified Lineage* (Pangolin version 2.4.2/ PangoLEARN2021-05-12)	Category**	First Detected/Alternate Name	TOTAL
B.1.1.7	VOC	UK	7289
B.1.351	VOC	South Africa	118
P.1	VOC	Brazil/Japan	5008
B.1.617#	VOC	India (includes double mutant)	378
A.23.1	VOI	TBC	23
B.1.427	VOI	California, USA	4
B.1.429	VOI	California, USA	327
B.1.1.318	VOI	Switzerland	7
B.1.616	VOI	France	0
P.3	VOI	Philippines	0
B.1.526	VOI	New York, USA	2
P.2	VOI	Brazil	145
B.1.525	VOI	Nigeria	57
B.1.526.1	ALM	New York, USA	8
B.1.618	ALM	India; triple mutant	12
P.1.1##	ALM	Brazil	10
TOTAL			13388

** 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*
*** Categories: Variant of Concern (VOC), Variant of Interest (VOI) and Additional Lineages Monitored (ALM)*
 # Note that B.1.617 has been further divided into 3 sub-lineages (B.1.617.1, B.1.617.2, and B.1.617.3) and is recognized as VOC by WHO. The sub-lineages are currently being reviewed in Canada and designation may change.
Note that P.1 has been further divided into 2 lineages (P.1 and P.1.1).