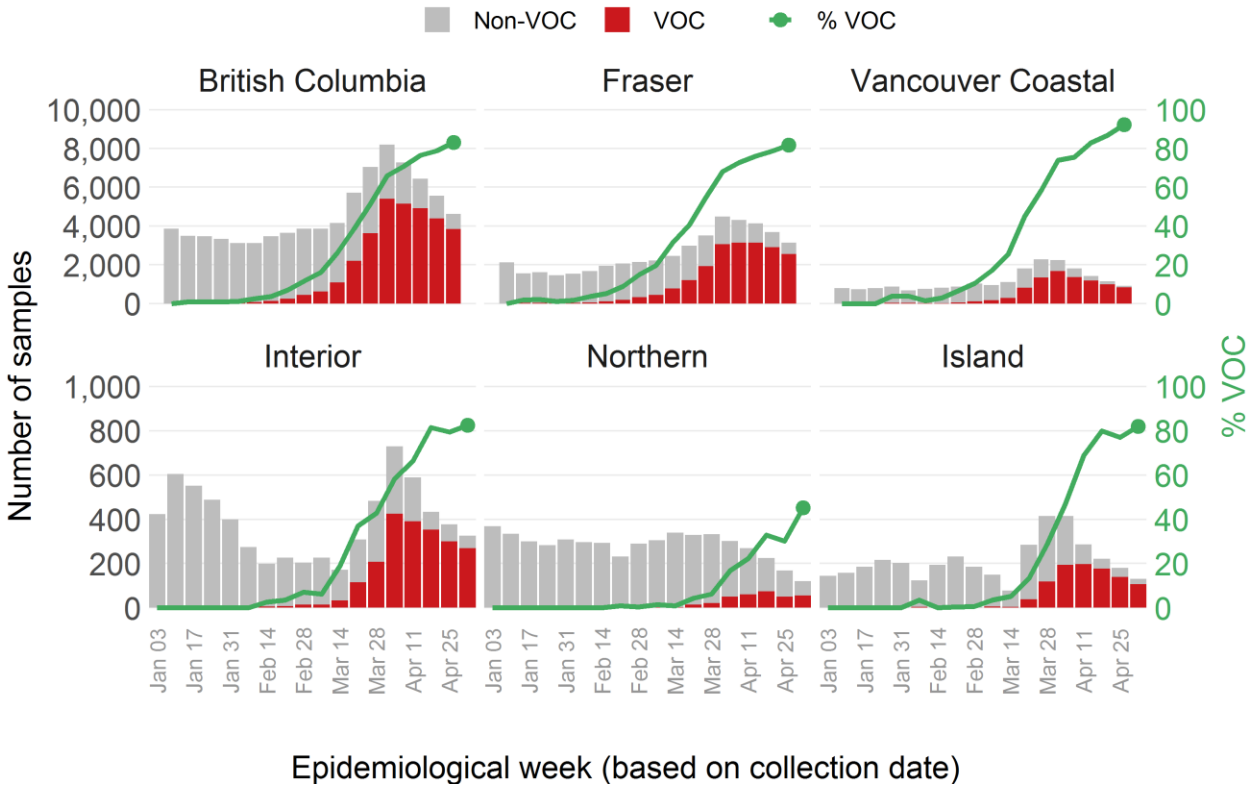
Weekly update on Variants of Concern (VOC)

May 12, 2021

Of all positive samples in epi week 18 (May 02 - May 08) in BC, ~83% were presumptive variants of concern (VOCs) (Figure 1). VOC prevalence was similar across Health Authorities, except in Northern Health, where it was lower, at ~45%.

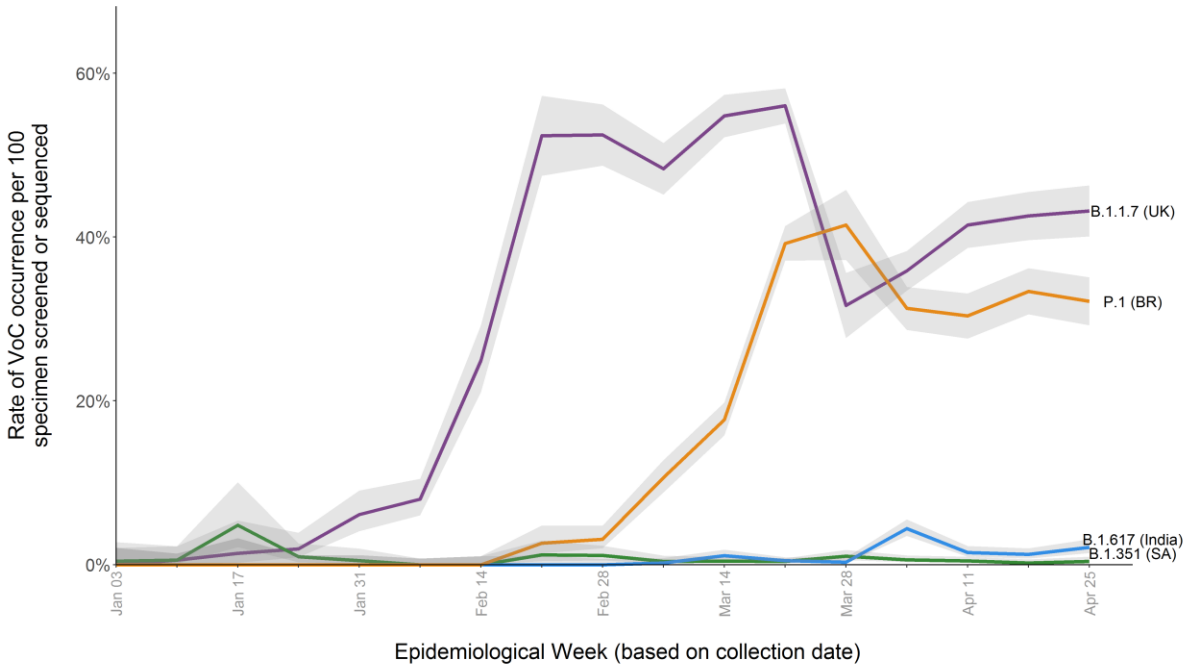
Figure 1. Prevalence of presumptive VOCs, by epi week in BC and Health Authorities, Jan 3 – May 8 2021



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 about ~57% and ~42% of the main VOCs. Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 17 (Apr 25 - May 01) may change as more sequencing results are analyzed.

Figure 2. Estimated sample prevalence^ of VOCs by epi week of collection date, Jan 3 – May 1, 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 12, 2021 and the sub-lineage B.1.617.2 was designated as VOC in the UK, while its designation in Canada is pending.

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

	Epi week 18 (May 02 - May 08)		Epi week 17^ (Apr 25 - May 01)					
Region	Total positive tests	% presumptive VOC*	Sample prevalence VOCs§			Relative Proportion of VOC**		
			B.1.1.7***	B.1.617#	P.1****	B.1.1.7	B.1.617	P.1
BC	4,620	83	43	2	32	57	1	42
FHA	3,134	82	48	4	30	60	1	39
IHA	326	83	31	0	15	67	0	32
NHA	121	45	15	0	1	94	0	6
VCH	906	92	36	1	47	43	0.5	56
VIHA	131	82	28	2	39	41	2	57

^ 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 VOCs 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.*

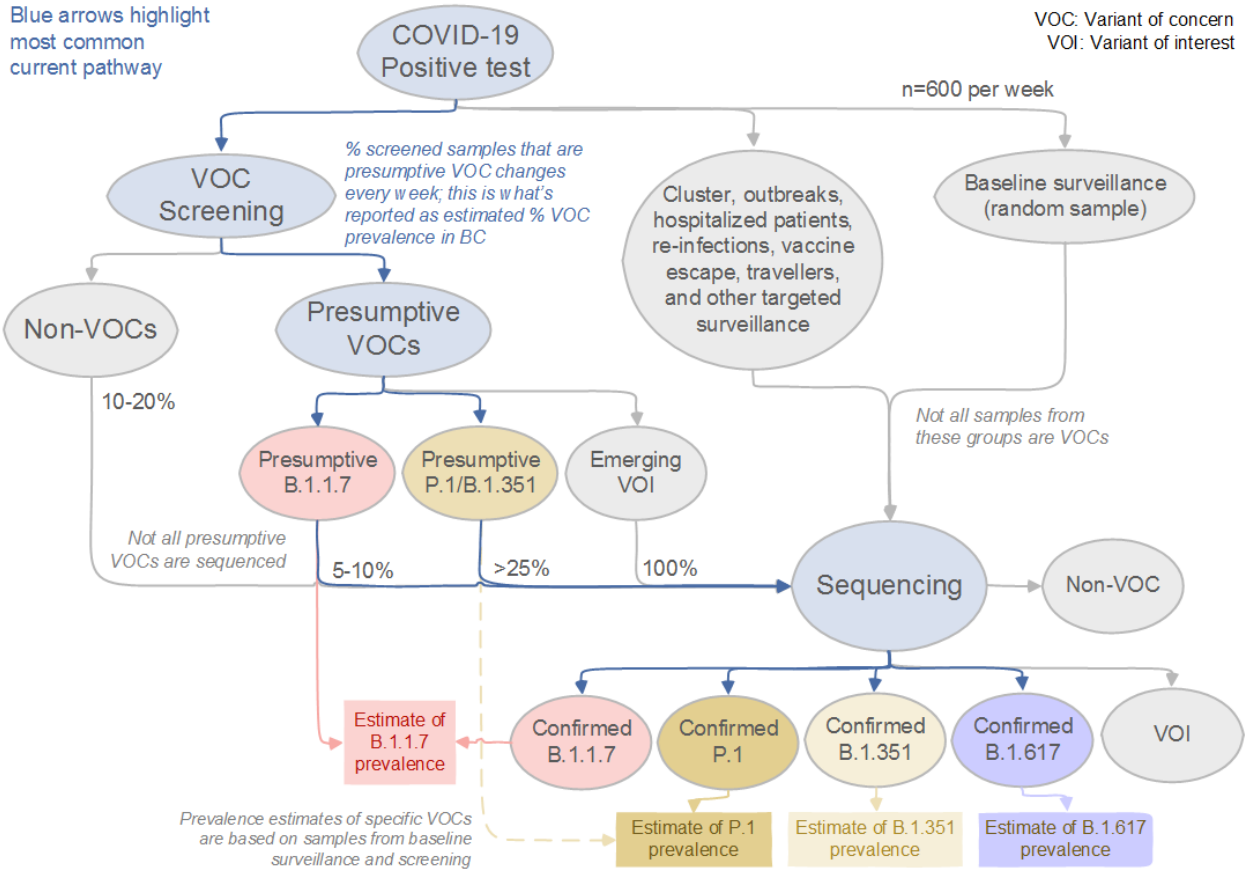
*****Estimated from the distribution of sequenced samples from background surveillance and non-overlapping subset of screened samples testing positive for both the N501Y and E484K mutation.*

 # Note that B.1.617 has been further divided into 4 sub lineages (B.1.617.1, B.1.617.2, B.1.617.3, and B.1.617.4) - This variant has been classified as Variant of Concern by the World Health Organization as of May 12; designation in Canada as VOC is pending

Variants of Interests (VOI)

As illustrated in Figure 3 below, BCCDC Public Health Lab is continuously monitoring for both VOCs and variants of interest (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 as of 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 25,045 specimens, of which 11,760 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.

Table 2. Variant categories confirmed by WGS: frequencies of SARS-CoV-2 genetic lineages.

Identified Lineage* (Pangolin version 2.4.2/ PangoLEARN2021-04-28)	Category**	First Detected/Alternate Name	TOTAL
B.1.1.7	VOC	UK	6,348
B.1.351	VOC	South Africa	109
P.1	VOC	Brazil/Japan	4,427
B.1.617#	VOC	India (includes double mutant)	306
A.23.1	VOI	TBC	23
B.1.427	VOI	California, USA	4
B.1.429	VOI	California, USA	306
B.1.1.318	VOI	Switzerland	6
B.1.616	VOI	France	0
P.3	VOI	Philippines	0
B.1.526	VOI	New York, USA	1
P.2	VOI	Brazil	144
B.1.525	VOI	Nigeria	50
B.1.526.1	ALM	New York, USA	8
B.1.618	ALM	India; triple mutant	15
P.1.1##	ALM	Brazil	13
TOTAL			11,760

** 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 4 sub-lineages (B.1.617.1, B.1.617.2, B.1.617.3, and B.1.617.4) and is recognized as VOC by WHO. The sub-lineages are reviewed to determine the appropriate designation in Canada
Note that P.1 has been further divided into 2 lineages (P.1 and P.1.1).