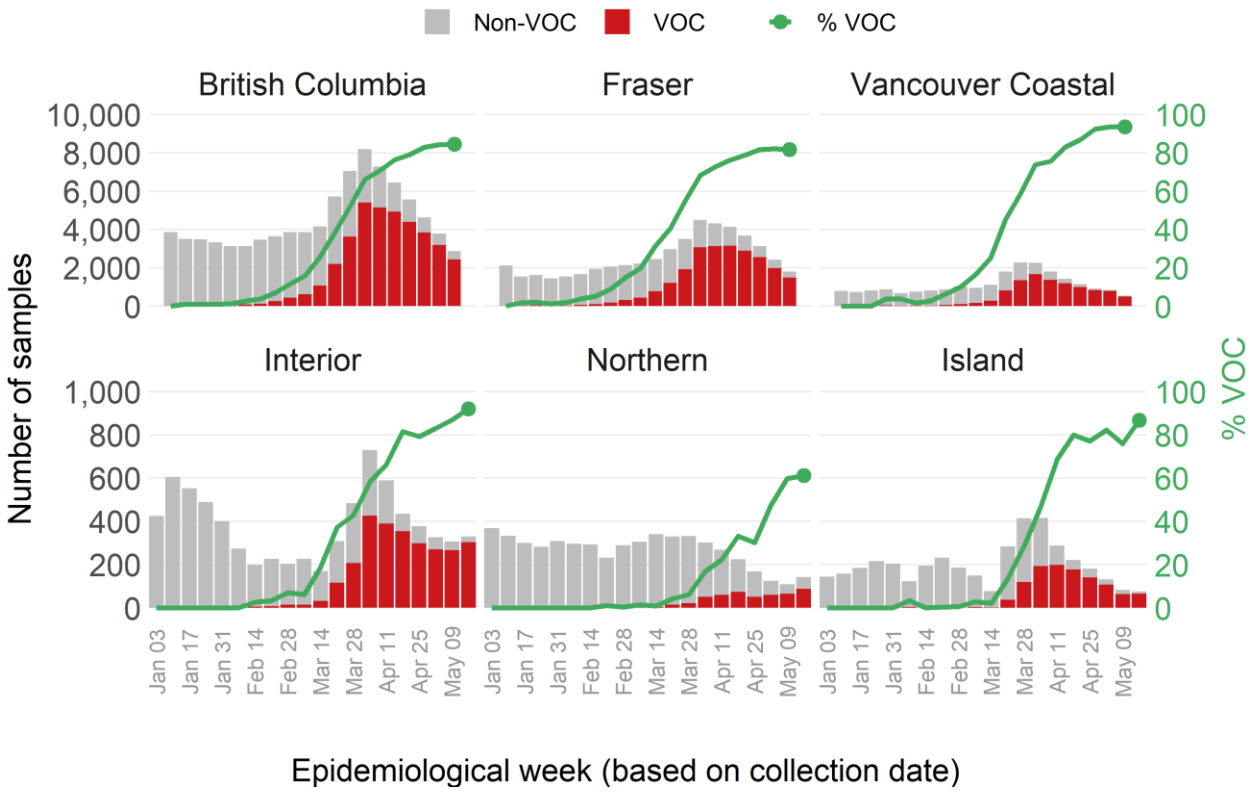
Weekly update on Variants of Concern (VOC)

May 27, 2021

Of all samples tested in epi week 20 (May 16 - May 22) in BC, ~ 84% were presumptive VOCs (Figure 1). VOC prevalence was similar across Health Authorities, except in Northern Health, where it was lower, at 61%.

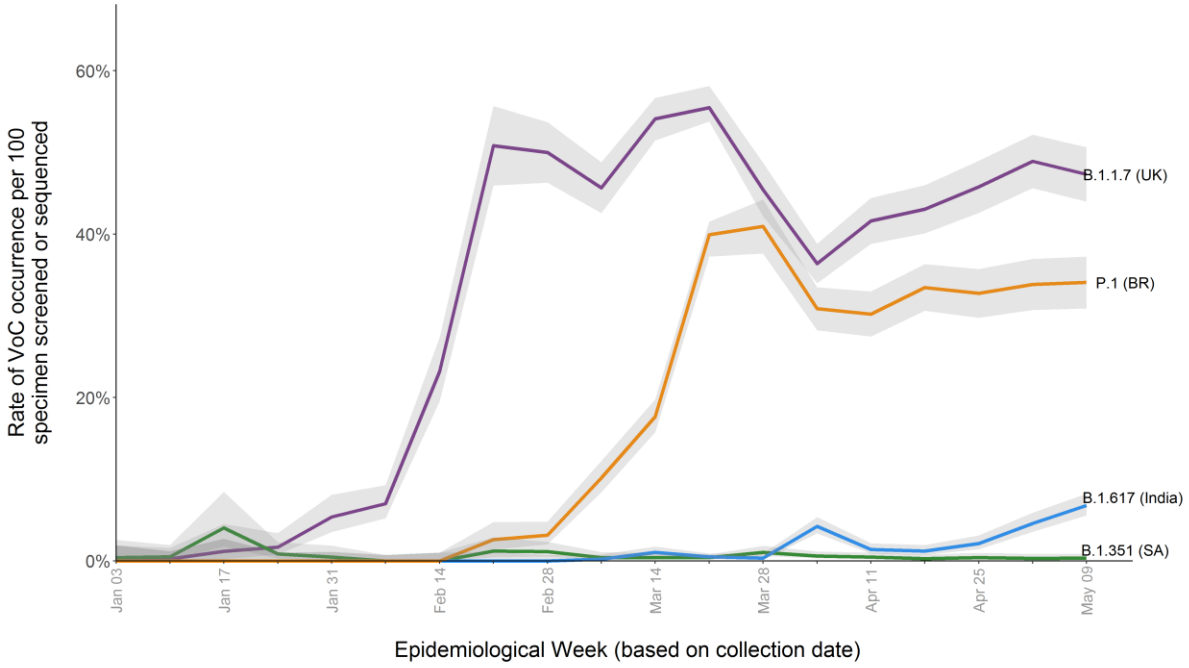
Figure 1. Prevalence of presumptive VOC, by epi week in BC and Health Authorities, Jan 3 – May 16, 2021



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 ~ 56 % and ~ 40% of positive specimens screened or sequenced. Please note that the estimate of distribution of VOC lineages (Figure 2) in BC for latest epi week 19 (May 09 - May 15) may change as more sequencing results are analyzed.

Figure 2. Estimated Sample prevalence^ of VOCs by lineage by epi week of collection date, Jan 3 - May 16 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.

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 20 (May 16 - May 22)		Epi week19^ (May 09 - May 15)					
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	2,878	84	47	7	34	56	3	40
FHA	1,807	82	49	9	30	59	4	37
IHA	329	92	53	0	31	63	0	37
NHA	142	61	76	0	9	90	0	10
VCH	525	94	39	2	48	44	1	54
VIHA	75	87	34	17	33	39	20	38

^ 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. The proportion for B.1.351 not shown in this table due to small numbers (equal or less than 0.5% in most regions except in VIHA where the proportion is 3%)*

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

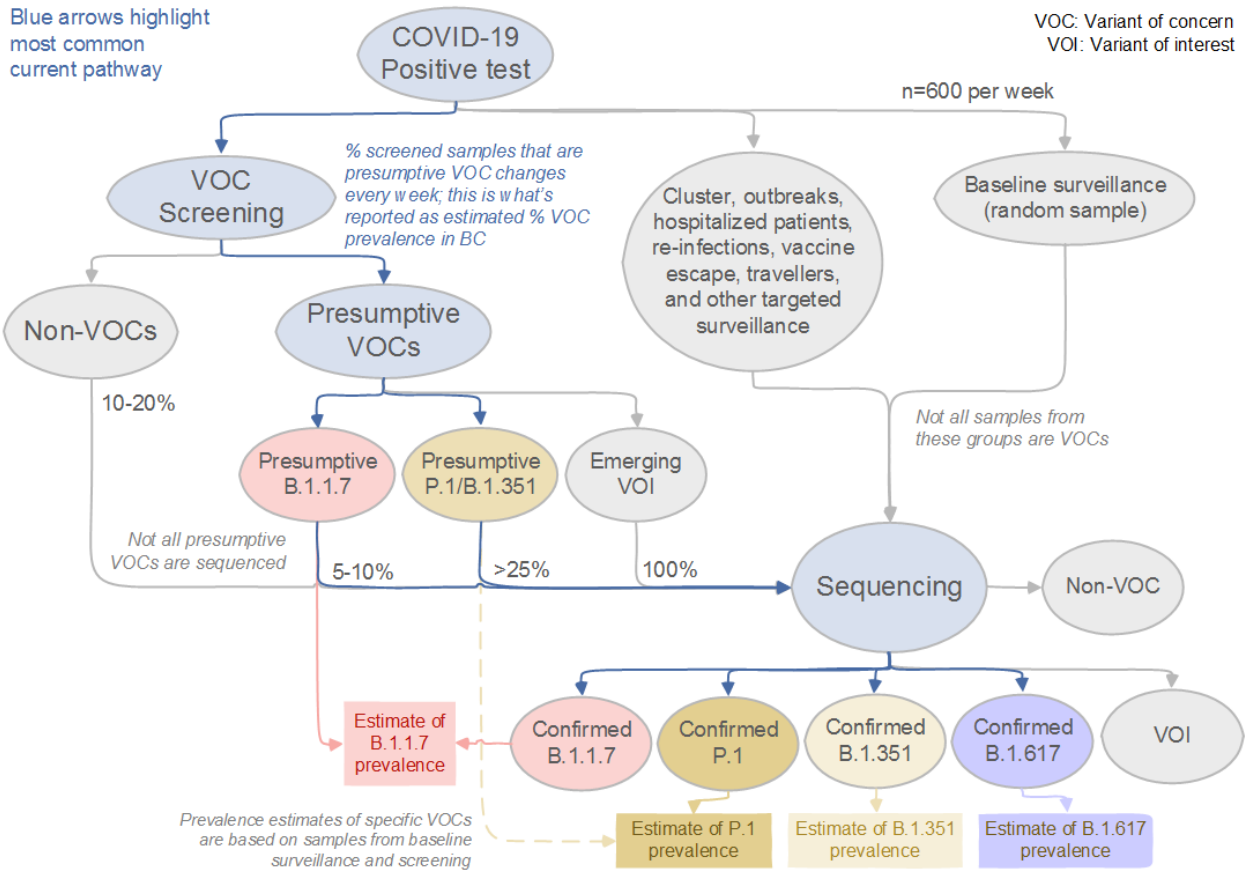
*****estimated from the distribution of sequenced samples from background surveillance and non-overlapping subset of screened samples testing positive for both the N501Y and E484K mutation*

 # 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 12,2021

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, 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 successfully performed on 29,207 specimens, of which 15,063 came back as variants under closer observation. Table 2 presents the number of sequenced samples by variant category; it does not represent the number of variant COVID cases. 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	8015
B.1.351	VOC	South Africa	130
P.1	VOC	Brazil/Japan	5761
B.1.617#	VOC	India (includes double mutant)	541
A.23.1	VOI	TBC	23
B.1.427	VOI	California, USA	4
B.1.429	VOI	California, USA	348
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	2
P.2	VOI	Brazil	145
B.1.525	VOI	Nigeria	62
B.1.526.1	ALM	New York, USA	8
B.1.618	ALM	India; triple mutant	14
P.1.1##	ALM	Brazil	4
TOTAL			15063

** 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).