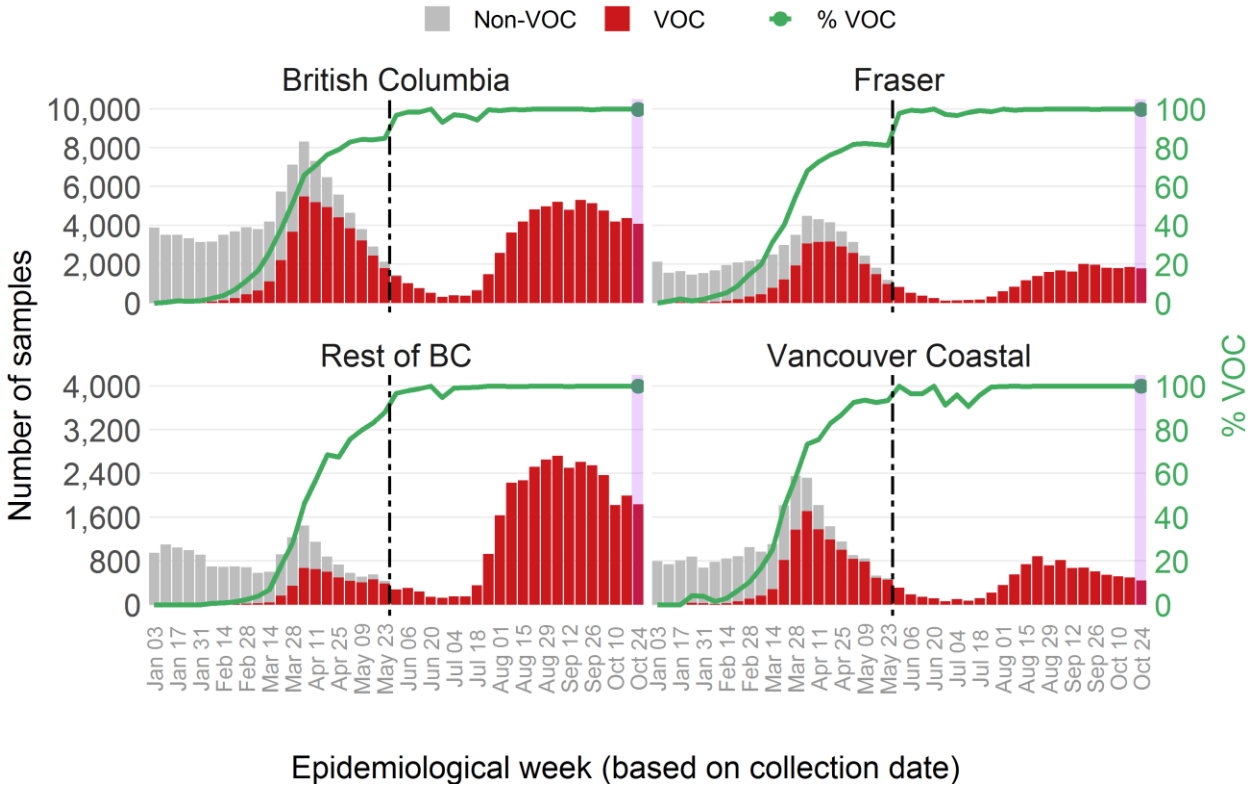
Weekly update on Variants of Concern (VOC)

Nov 12, 2021

Of all positive samples sequenced in epi week 43 (Oct 24 - Oct 30) in BC, ~ 100% were confirmed VOCs (Figure 1). VOC prevalence was similar across Health Authorities.

Data from epi week 43 may reflect partial data; 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, Jan 3 - Oct 30, 2021



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

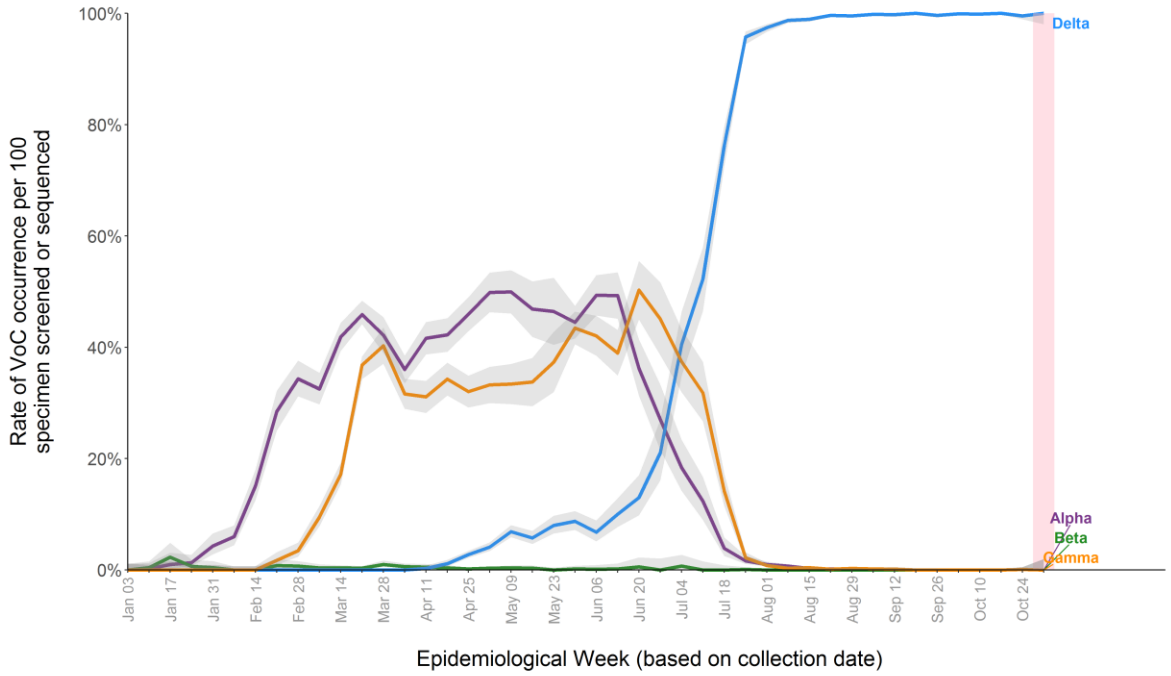
Data from the PLOVER system at the BCCDC Public Health Lab.

Purple shaded box reflects partial data due to the results being available 7-11 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, accounting for about 100% of positive specimens sequenced.

Please note that the estimate of distribution of VOC lineage# (Figure 2) in BC for latest epi week 43 (Oct 24 - Oct 30) 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 - Oct 30, 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), VOC screening results with both E484K and N501Y mutations are assumed to be Gamma, given a very low prevalence of Beta in BC. As of week 22 (May 30, 2021), prevalence of VOC is estimated from sequencing results only.

Pink shaded box can reflect partial data due to a lag in receipt of positive samples from front line laboratories and turn around time of 7 to 11 days from sample collection to WGS analysis; estimates are expected to change as more specimens are received and sequenced.

 # See appendix for the definitions of VOC lineages

Table 1. Sequencing-based VOC prevalence and approximate distribution by VOC lineage in BC and Health Authorities, latest available estimates* on epi week 43 (Oct 24 - Oct 30).

Region	Total positive tests	Sample prevalence** VOCs#			Relative Proportion of VOC***		
		% Alpha	% Delta	% Gamma	% Alpha	% Delta	% Gamma
BC	4081	0	100	0	0	100	0
FHA	1781	0	100	0	0	100	0
IHA	593	0	100	0	0	100	0
NHA	659	0	100	0	0	100	0
VCH	441	0	100	0	0	100	0
VIHA	583	0	100	0	0	100	0

**Note: Due to 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. Due to rounding, estimates may add to more or less than 100.*

*** 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.*

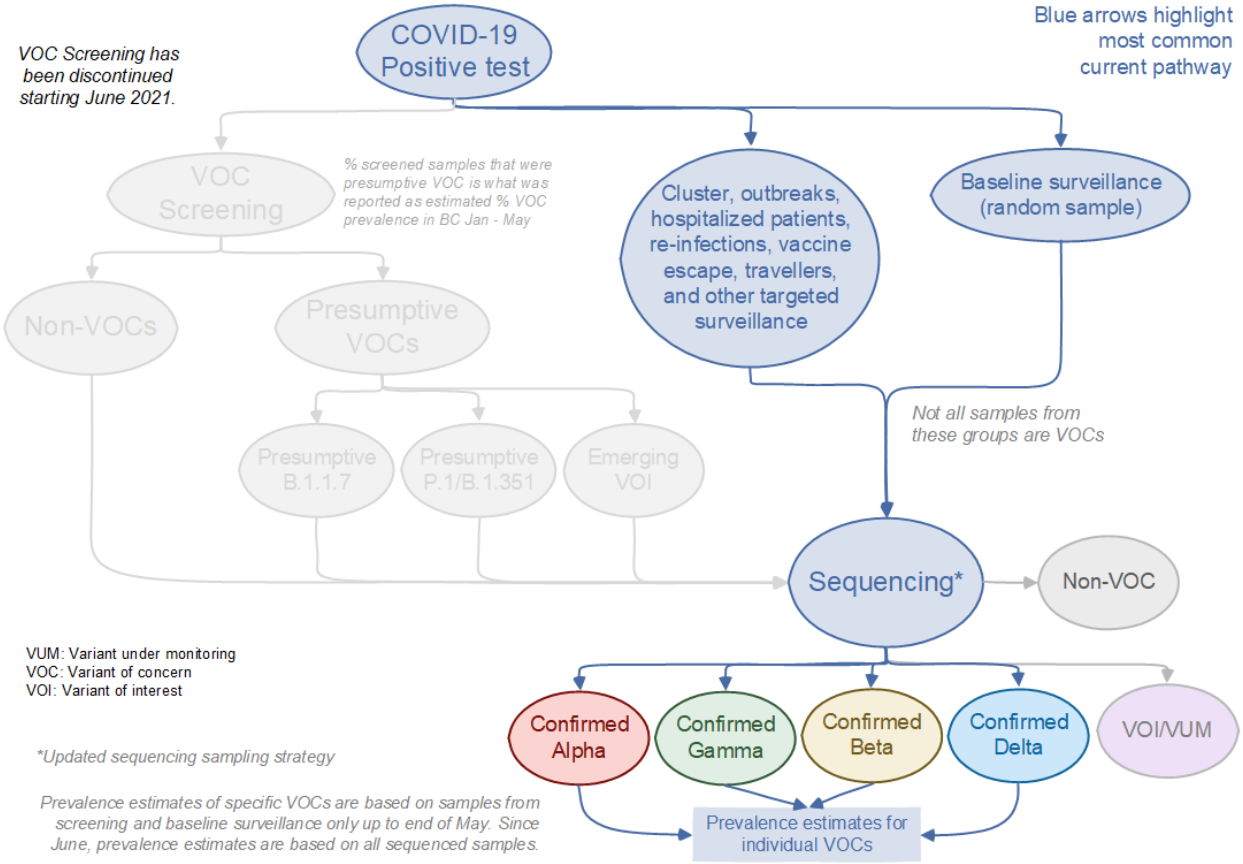
****Relative Proportion from the total VOC identified through sequencing. The proportion for Beta not shown in this table due to small numbers. Note, before epi week 22, relative proportions were previously calculated using both screening and sequencing data. The proportion for Beta not shown in this table due to small numbers.*

 # See appendix for the definitions of VOC lineages

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. Since September 2021 BC has adopted a new sampling strategy for sequencing to report on the provincial number of variants based on weekly point prevalence.

Figure 3. Overview of the screening and sequencing process applied to positive COVID-19 tests in BC, Oct 2021.



Please note the turnaround time sequencing which takes approximately 7-11 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 90,391 specimens up to epi week 43 (Oct 24 - Oct 30) in BC, of which 70,425 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. Figure 3 above illustrates BC's whole genome sequencing strategy of COVID cases.

Table 2: Frequencies of SARS-CoV-2 monitored genetic lineages confirmed by WGS.

Identified Lineage* (Pangolin version 3.1.16/ PangoLEARN2021-10-18)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
B.1.1.7	Alpha	VOC	UK	14758	0.6
Q.*	Alpha	VOC	UK	266	-33.5
B.1.351	Beta	VOC	South Africa	160	0.6
B.1.351.*	Beta	VOC	South Africa	2	0
B.1.617.2	Delta	VOC	India	3101	-34.0
AY.*	Delta	VOC	India	37784	10.0
P.1	Gamma	VOC	Brazil/Japan	53	-1.9
P.1.*	Gamma	VOC	Brazil	11865	0
A.23.1		VOI	TBC	35	0
AZ.1		VOI		6	0
AZ.2		VOI		0	
AZ.2.1		VOI		0	
AZ.3		VOI		0	
AZ.4		VOI		0	
AZ.5		VOI		4	0
AZ.6		VOI		0	
B.1.1.318		VOI	Switzerland	20	0
B.1.427	Epsilon	VOI	California, USA	4	0
B.1.429	Epsilon	VOI	California, USA	838	0
B.1.525	Eta	VOI	Nigeria	152	0.7
B.1.526	Iota	VOI	New York, USA	12	0
B.1.526.1	Iota	VOI	New York, USA	0	
B.1.616		VOI	France	0	
B.1.617.1	Kappa	VOI	India	403	0

Identified Lineage* (Pangolin version 3.1.16/ PangoLEARN2021-10-18)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
B.1.617.3		VOI	India	3	0
B.1.621	Mu	VOI	Colombia	37	0
B.1.621.1	Mu	VOI	Colombia	9	0
C.37	Lambda	VOI	Chile	1	0
P.3	Theta	VOI	Philippines	4	0
A.2.5		VUM		3	0
A.27		VUM		0	
A.28		VUM		0	
A.29		VUM		0	
A.30		VUM		0	
AT.1		VUM		0	
AV.1		VUM		0	
B.1		VUM		133	0.8
B.1.1.1		VUM		20	0
B.1.1.28		VUM		4	0
B.1.1.519		VUM		284	0
B.1.1.523		VUM		0	
B.1.160		VUM		183	0
B.1.214.2		VUM		0	
B.1.324		VUM		0	
B.1.466.2		VUM		0	
B.1.526.2	Iota	VUM	New York, USA	0	
B.1.618		VUM	India	85	0
B.1.619		VUM		1	0
B.1.620		VUM		0	
B.1.628		VUM		0	
B.1.629		VUM		0	
B.1.630		VUM		0	
B.1.631		VUM		0	
C.1.2		VUM	South Africa	0	
C.16		VUM		0	

Identified Lineage* (Pangolin version 3.1.16/ PangoLEARN2021-10-18)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
C.36.3		VUM		0	
C.36.3.1		VUM		0	
P.2	Zeta	VUM	Brazil	194	0
R.1		VUM		1	0
R.2		VUM		0	
TOTAL				70425	3.9

** 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 updates of the Pangolin tool may also result in the refinement of lineage and sublineage designations. See appendix for the definitions of VOC lineages*

*** Variant category includes: Variant of Concern (VoC), Variant of Interest (VoI) and Variants under Monitoring (VuM).*

Appendix – VOC Lineages Table

VOC	Associated Lineages
Alpha	B.1.1.7, Q.*
Beta	B.1.351, B.1.351.*
Gamma	P.1, P.1.*
Delta	B.1.617.2, AY.*

**indicates an additional numerical value (e.g. Q.1).*