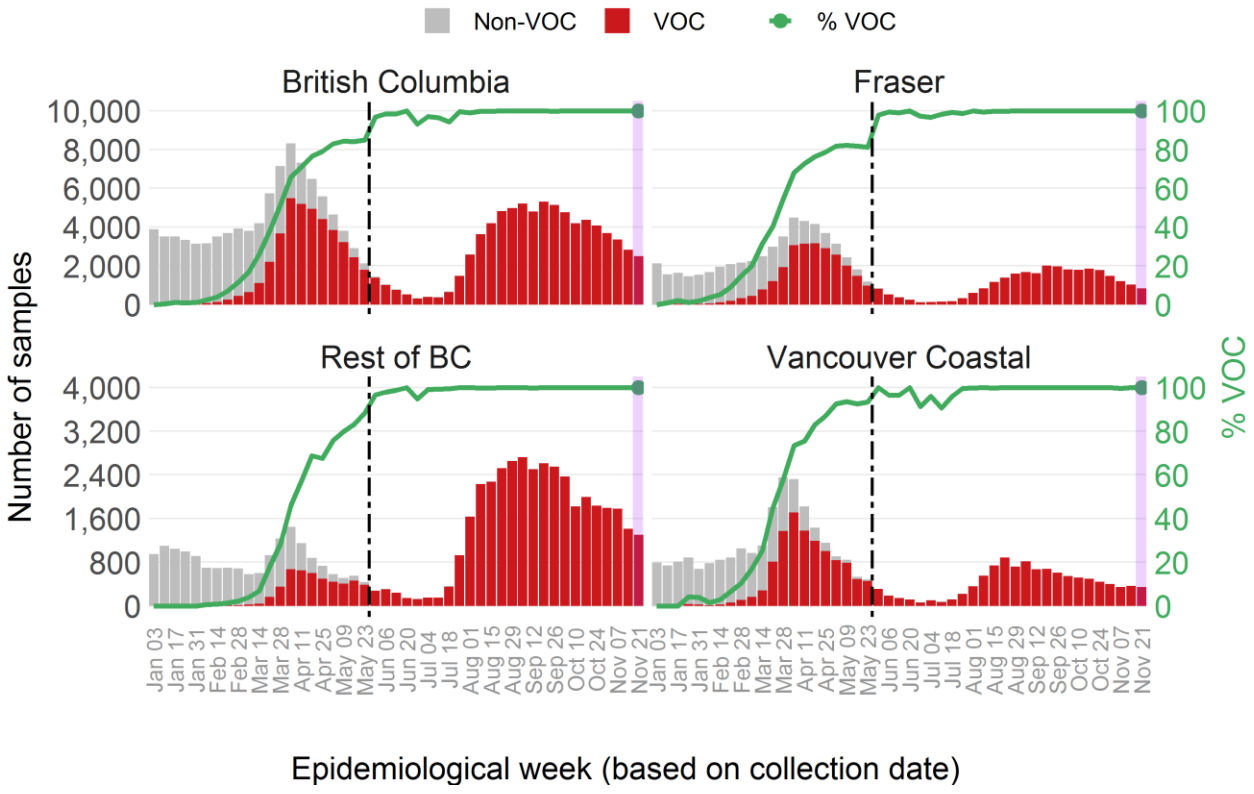
Weekly update on Variants of Concern (VOC)

Dec 10, 2021

Of all positive samples sequenced in epi week 47 (Nov 21 - Nov 27) in BC, ~ 100% were confirmed VOCs (Figure 1).

Data from epi week 47 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 - Nov 27, 2021



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

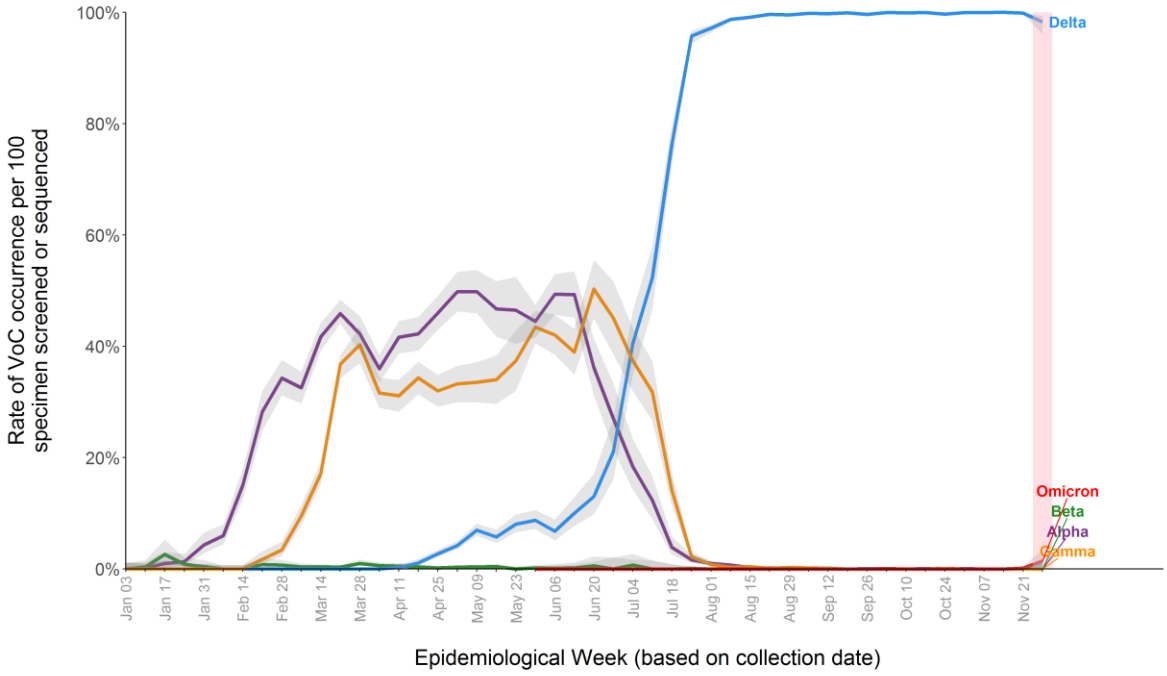
Data from the PLOVER system at the BCCDC Public Health Lab.

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 99.9% of positive specimens sequenced.

Please note that the estimate of distribution of VOC lineage# (Figure 2) in BC for latest epi week 47 (Nov 21 - Nov 27) may change as more sequencing results are analyzed and given the lag in receipt of positive samples from frontline laboratories.

Figure 2. Estimated Sample prevalence^ of VOCs by lineage by epi week of collection date, Jan 3 - Nov 27, 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 47 (Nov 21 - Nov 27).

Region	Total positive tests	Sample prevalence** VOCs#			Relative Proportion of VOC***		
		% Alpha	% Delta	% Gamma	% Alpha	% Delta	% Gamma
BC	2499	0	100	0	0	100	0
FHA	843	0	100	0	0	100	0
IHA	475	0	100	0	0	100	0
NHA	376	0	100	0	0	100	0
VCH	342	0	100	0	0	100	0
VIHA	452	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 and Omicron not shown in this table due to small numbers.*

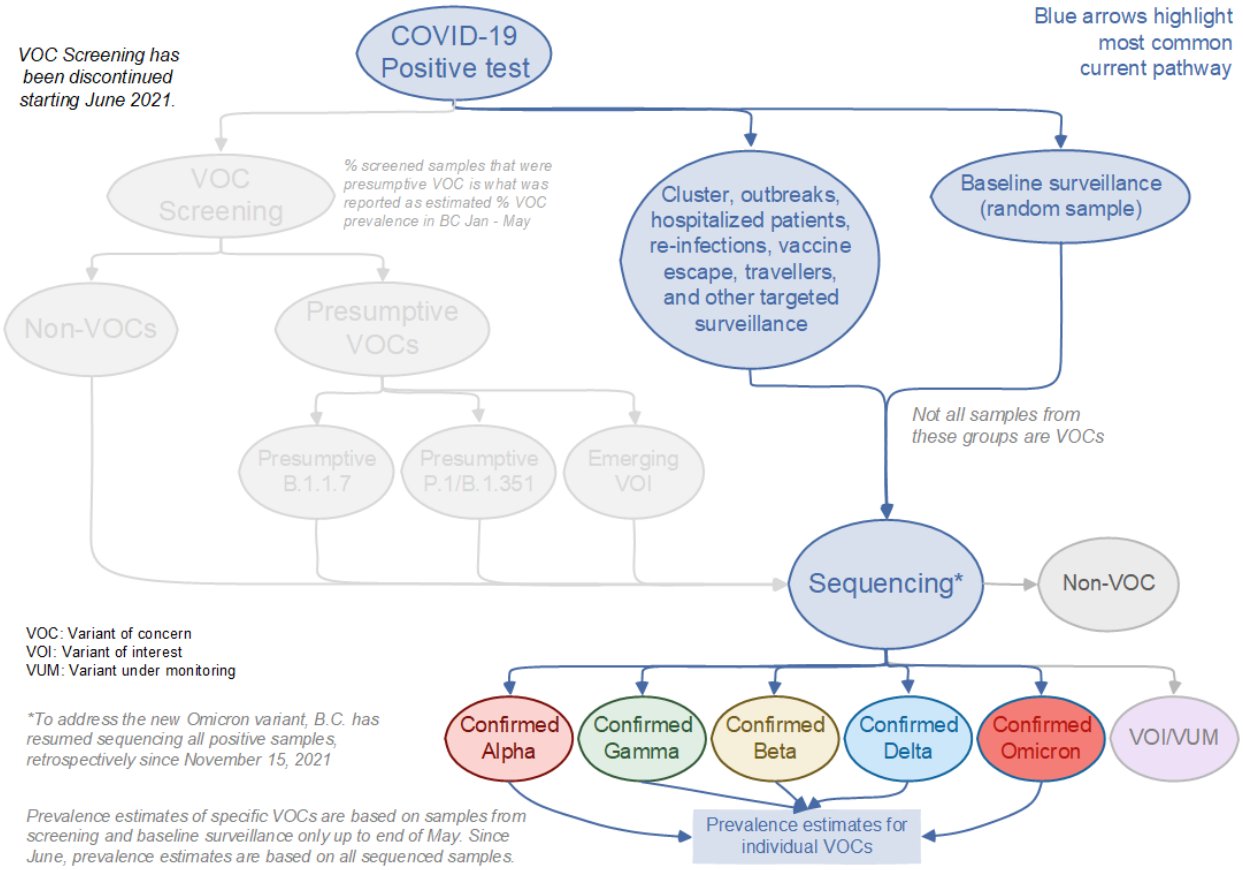
 # See appendix for the definitions of VOC lineages

Monitoring of Variants

As illustrated in Figure 3 below, BCCDC Public Health Lab is continuously monitoring for both VOCs and VOIs and it is tracking a regularly updated Variants Under Monitoring (VUMs). 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. To address the new Omicron (B.1.1.529) sequencing of all positives samples has resumed with retrospective specimens collected from November 15th 2021 onwards.

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



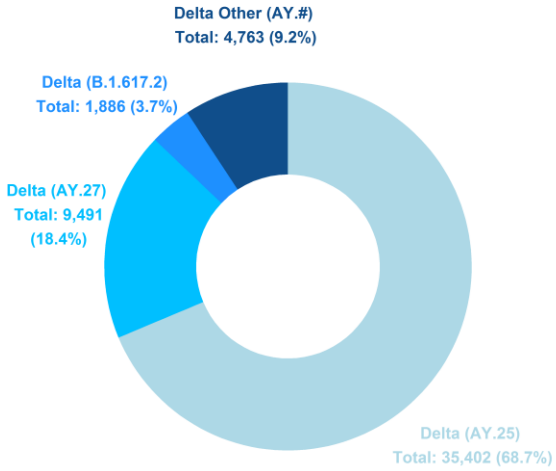
Please note the turnaround time sequencing which takes approximately 7-11 days, but it could also take longer if there are lab backlogs or if there are delays in receiving current positive samples from frontline laboratories.

Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 100,663 specimens up to epi week 47 (Nov 21 - Nov 27) in BC, of which 80,665 came back as variants under closer observation. Figure 3 above illustrates BC's whole genome sequencing strategy of COVID cases.

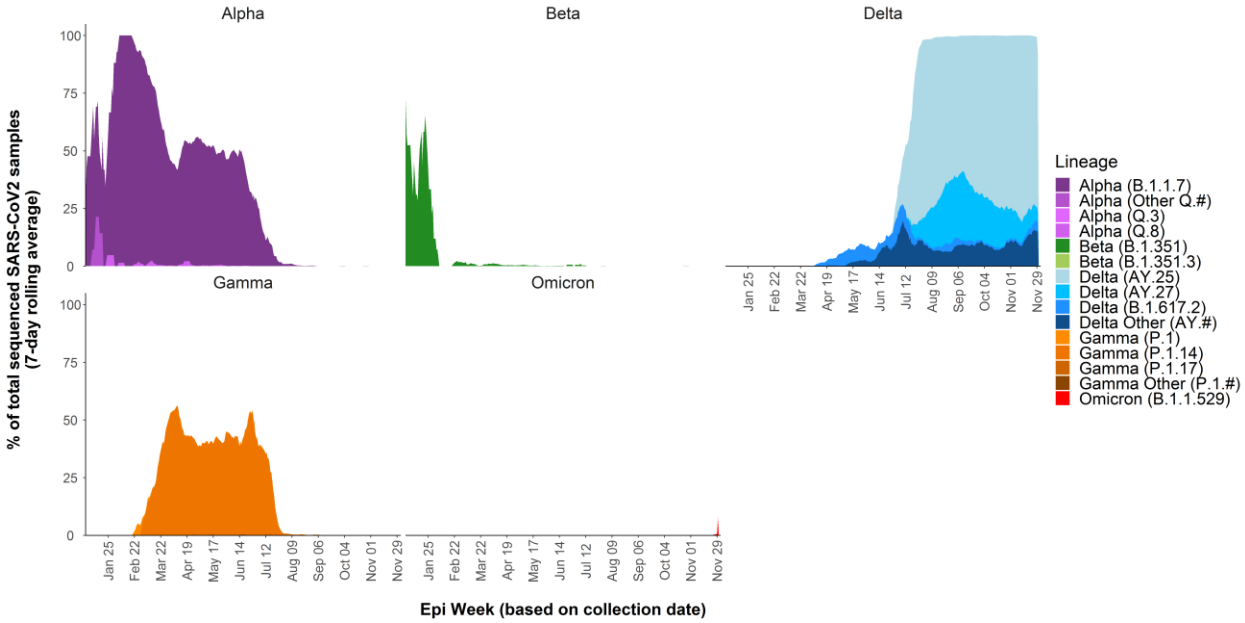
The VOCs represent 96.9% of all the variants that were detected in the province (Table 2). The Delta variant accounts for largest proportion of the VOCs and includes B.1.617.2, the parent lineage, and two sub-lineages AY.25 and AY.27 (Figure 4).

Figure 4. Cumulative Distribution of the three most prevalent Delta lineages



Over time, the distribution of variants of concern (VOCs) demonstrates the temporality and changing nature of circulating VOCs as shown in Figure 5.

Figure 5. Temporal distribution of the three most prevalent lineages within each Variant of Concern



 # indicates an additional numerical value (e.g. AY.1)

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

Identified Lineage* (Pangolin version 3.1.16/ PangoLEARN 2021-11-18)	WHO Name	Category**	TOTAL	% Change since last report
B.1.1.7	Alpha	VOC	14886	0.0
Q.*	Alpha	VOC	141	0.0
B.1.351	Beta	VOC	162	1.2
B.1.351.*	Beta	VOC	2	0.0
AY.*	Delta	VOC	49697	8.0
B.1.617.2	Delta	VOC	1886	5.6
P.1.*	Gamma	VOC	11384	0.0
P.1	Gamma	VOC	56	0.0
B.1.1.529	Omicron	VOC	10	90.0
A.23.1		VOI	35	0.0
AZ.*		VOI	12	0.0
B.1.1.318		VOI	18	0.0
B.1.427	Epsilon	VOI	4	0.0
B.1.429	Epsilon	VOI	839	0.1
B.1.525	Eta	VOI	152	0.0
B.1.526	Iota	VOI	12	0.0
B.1.526.*		VOI	0	
B.1.616		VOI	0	
B.1.617.1	Kappa	VOI	404	0.2
B.1.617.3		VOI	3	0.0
B.1.621	Mu	VOI	44	0.0
B.1.621.1	Mu	VOI	2	0.0
C.37	Lambda	VOI	1	0.0
P.3	Theta	VOI	4	0.0
A.2.5		VUM	3	0.0
A.27		VUM	0	
A.28		VUM	0	
A.29		VUM	0	
A.30		VUM	0	
AT.1		VUM	0	

Identified Lineage* (Pangolin version 3.1.16/ PangoLEARN 2021-11-18)	WHO Name	Category**	TOTAL	% Change since last report
AV.1		VUM	0	
B.1		VUM	132	0.0
B.1.1.1		VUM	20	0.0
B.1.1.28		VUM	4	0.0
B.1.1.519		VUM	285	0.0
B.1.1.523		VUM	0	
B.1.160		VUM	183	0.0
B.1.214.2		VUM	0	
B.1.324		VUM	0	
B.1.466.2		VUM	0	
B.1.618		VUM	85	0.0
B.1.619		VUM	1	0.0
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	
B.1.640		VUM	0	
C.1.2		VUM	0	
C.16		VUM	0	
C.36.*		VUM	0	
P.2	Zeta	VUM	197	1.5
R.1		VUM	1	0.0
R.2		VUM	0	
TOTAL			80665	5.1

** 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).*