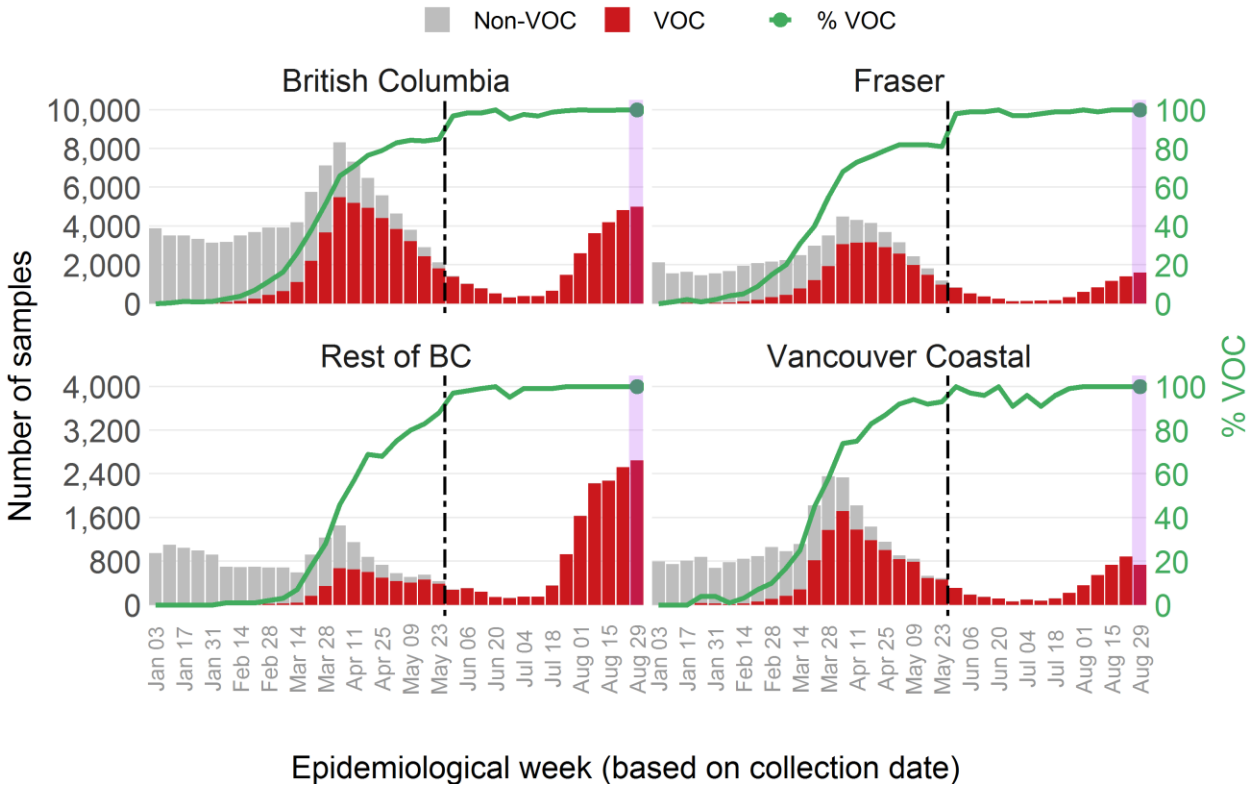
Weekly update on Variants of Concern (VOC)

Sep 10, 2021

Of all positive samples sequenced in epi week 35 (Aug 29 - Sep 04) in BC, ~ 100% were confirmed VOCs (Figure 1). VOC prevalence was similar across Health Authorities.

Data from epi week 35 reflects partial data due to a lag in receipt of positive samples from front line laboratories; 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, Aug 29 - Sep 04



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

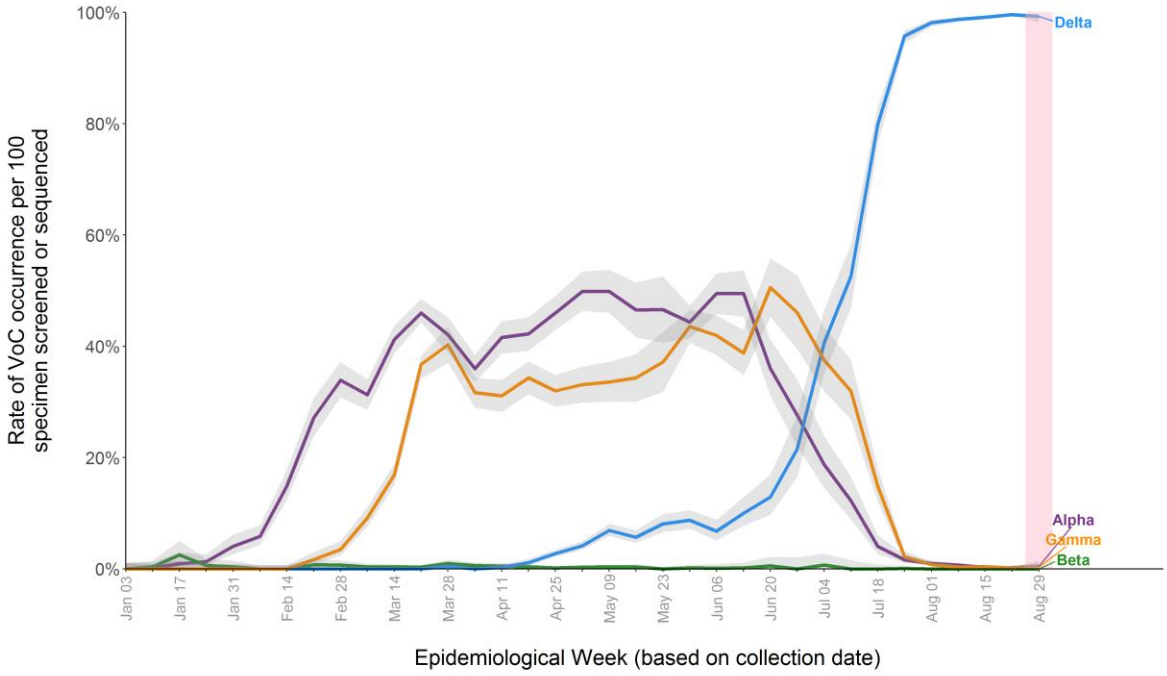
Data from the PLOVER system at the BCCDC Public Health Lab.

Purple shaded box reflects partial data due to the results being available 4-7 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% of positive specimens sequenced.

Please note that the estimate of distribution of VOC lineage[#] (Figure 2) in BC for latest epi week 35 (Aug 29 - Sep 04) 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 - Sep 04, 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 reflects partial data due to a lag in receipt of positive samples from front line laboratories; 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 35 (Aug 29 - Sep 04).

Region	Total positive tests	Sample prevalence** VOCs#			Relative Proportion of VOC***		
		% Alpha	% Delta	% Gamma	% Alpha	% Delta	% Gamma
BC	4997	0.4	99.3	0.3	0	99	0
FHA	1594	1.4	98.6	0	1	99	0
IHA	1631	0.4	99.6	0	0	100	0
NHA	578	0	100	0	0	100	0
VCH	733	0	99.0	1.0	0	99	1
VIHA	438	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 not add up to exactly 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.*

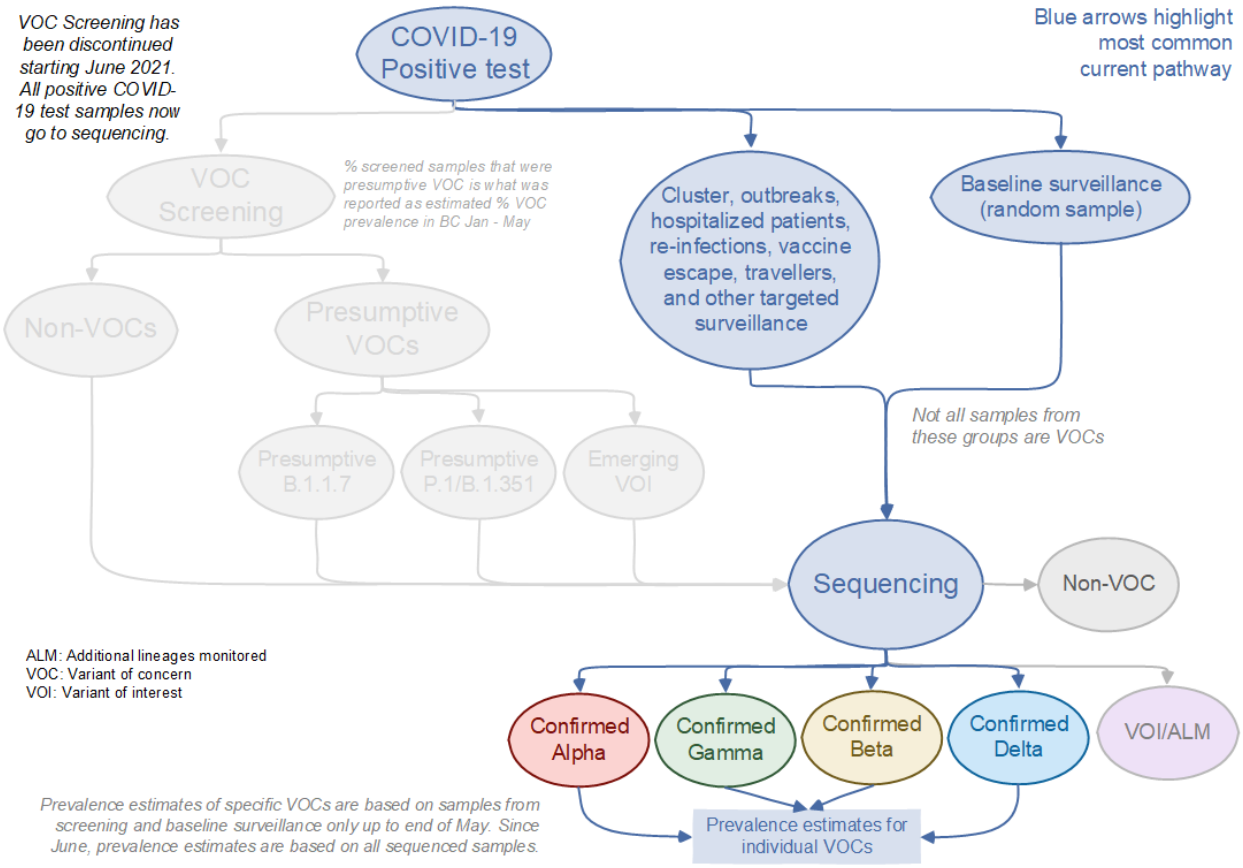
****Relative Proportion from the total VOC identified through sequencing. The proportion for Beta not shown in this table due to small numbers. Note, before epi week 22, relative proportions were previously calculated using both screening and sequencing data. The proportion for Beta not shown in this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

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



*Please note the turnaround time sequencing which takes approximately 4-7 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 66,576 specimens up to epi week 35 (Aug 29 - Sep 04) in BC, of which 46,300 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. As illustrated in Figure 3 above, BC has transitioned to whole genome sequencing on all positive samples.

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

Identified Lineage* (Pangolin version 3.1.11/ PangoLEARN2021-08-24)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
B.1.1.7	Alpha	VOC	UK	14891	0
Q.*	Alpha	VOC	UK	109	16.5
B.1.351	Beta	VOC	South Africa	159	0
B.1.351.*	Beta	VOC	South Africa	2	0
P.1	Gamma	VOC	Brazil/Japan	11678	0.1
P.1.*	Gamma	VOC	Brazil	216	0.5
B.1.617.2	Delta	VOC	India	5581	28.1
AY.*	Delta	VOC	India	11629	27.0
B.1.617.1	Kappa	VOI	India	402	0
B.1.617.3		VOI	India	3	0
A.23.1		VOI	TBC	35	0
B.1.427	Epsilon	VOI	California, USA	4	0
B.1.429	Epsilon	VOI	California, USA	835	0
B.1.1.318		VOI	Switzerland	18	0
B.1.616		VOI	France	0	0
B.1.526	Iota	VOI	New York, USA	12	0
B.1.526.1	Iota	VOI	New York, USA	0	0
B.1.525	Eta	VOI	Nigeria	151	0
C.37	Lambda	VOI	Chile	1	0
P.2	Zeta	VOI	Brazil	194	0
P.3	Theta	VOI	Philippines	4	0
B.1.621	Mu	VOI	Colombia	44	4.5
B.1.621.1	Mu	VOI	Colombia	2	0
B.1.618		ALM	India	46	0

Identified Lineage* (Pangolin version 3.1.11/ PangoLEARN2021-08-24)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
C.1.2		ALM	South Africa	0	0
B.1.466.2		ALM		0	0
B.1.1.519		ALM		282	-0.4
B.1.214.2		ALM		0	0
B.1.1.523		ALM		0	0
B.1.619		ALM		1	100
B.1.620		ALM		0	0
R.1		ALM		1	0
TOTAL		TOTAL	TOTAL	46,300	10.2

** 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 Additional Lineages Monitored (ALM).*

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).*