

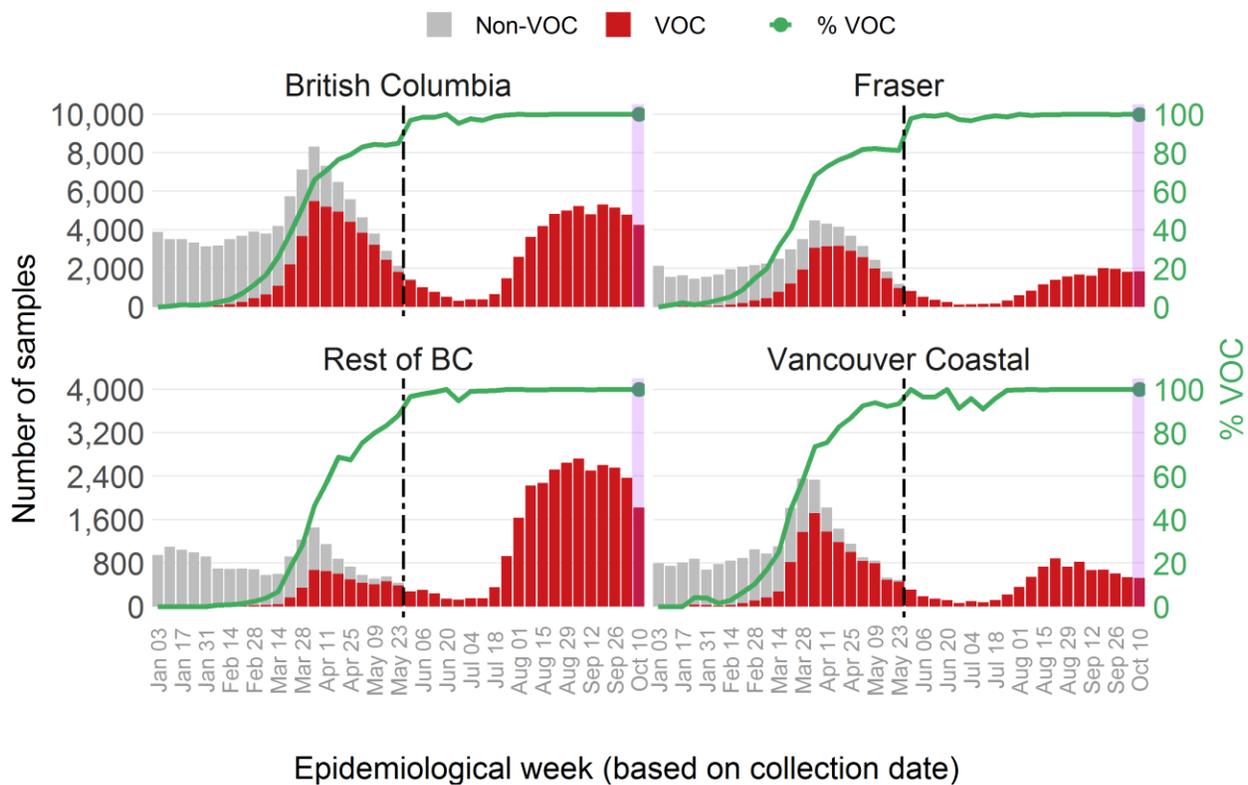
Weekly update on Variants of Concern (VOC)

Oct 29, 2021

Of all positive samples sequenced in epi week 41 (Oct 10 - Oct 16) in BC, ~ 100% were confirmed VOCs (Figure 1).

Data from epi week 41 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 16, 2021



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

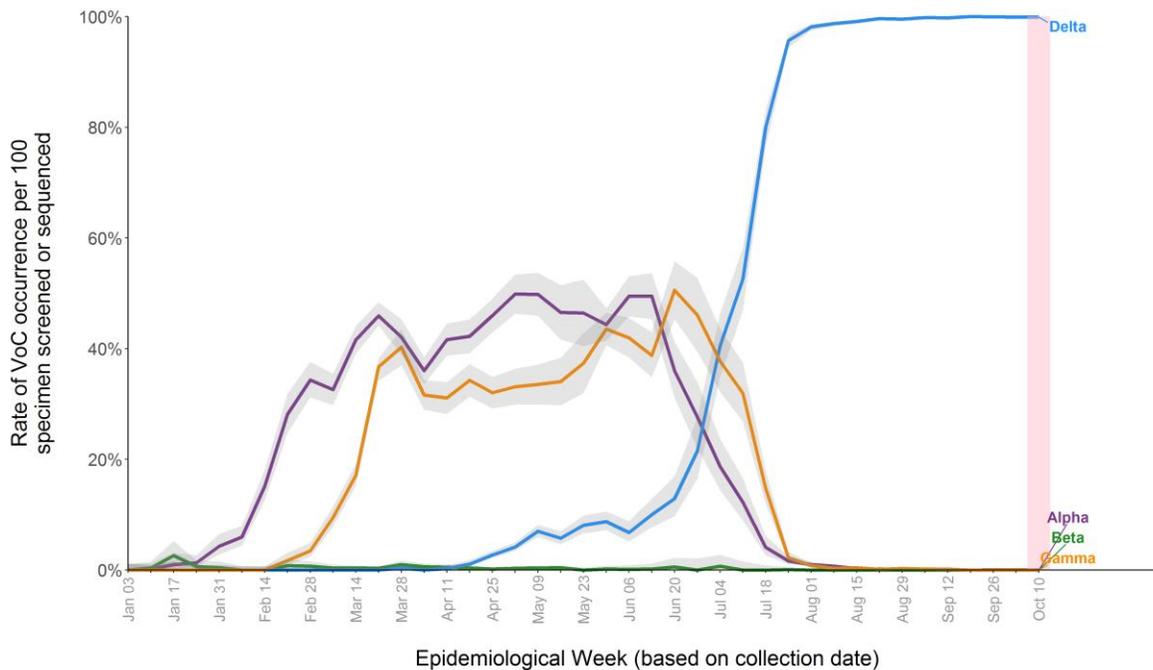
Data from the PLOVER system at the BCCDC Public Health Lab.

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 41 (Oct 10 - Oct 16) 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 16, 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 41 (Oct 10 - Oct 16).

Region	Total positive tests	Sample prevalence** VOCs#			Relative Proportion of VOC***		
		% Alpha	% Delta	% Gamma	% Alpha	% Delta	% Gamma
BC	4254	0	100	0	0	100	0
FHA	1840	0	100	0	0	100	0
IHA	640	0	100	0	0	100	0
NHA	755	0	100	0	0	100	0
VCH	522	0	100	0	0	100	0
VIHA	427	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 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.

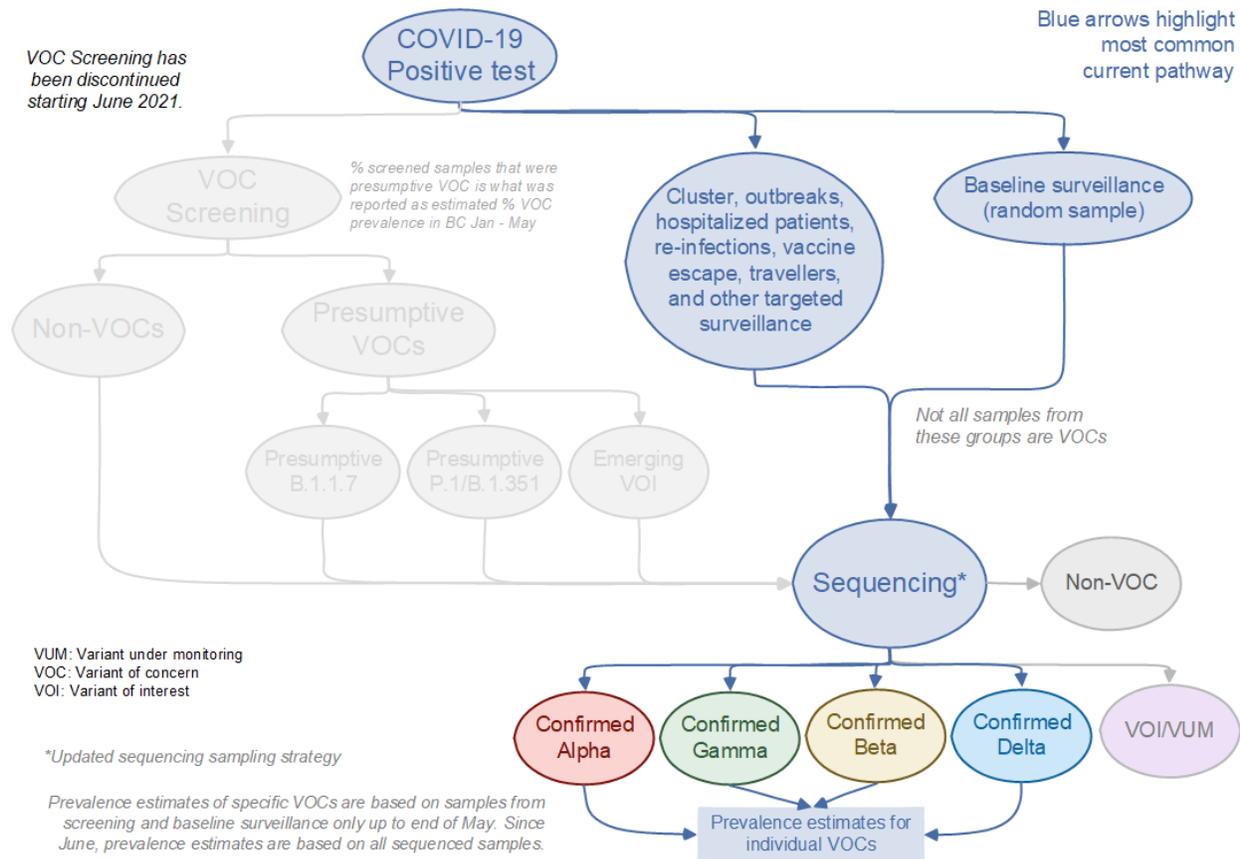
***Relative Proportion from the total VOC identified through sequencing. The proportion for Beta not shown in this table due to small numbers. Note, before epi week 22, relative proportions were previously calculated using both screening and sequencing data. The proportion for Beta not shown in this 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 83,814 specimens up to epi week 41 (Oct 10 - Oct 16) in BC, of which 63,839 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 3.1.15/ PangoLEARN2021-10-15)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
P.1.*	Gamma	VOC	Brazil	11863	99.1
P.1	Gamma	VOC	Brazil/Japan	54	-21,770.4
AY.*	Delta	VOC	India	30396	15.6
B.1.617.2	Delta	VOC	India	3947	10.4
B.1.351	Beta	VOC	South Africa	159	0
B.1.351.*	Beta	VOC	South Africa	2	0
B.1.1.7	Alpha	VOC	UK	14673	-0.5
Q.*	Alpha	VOC	UK	355	20.6
B.1.427	Epsilon	VOI	California, USA	4	0
B.1.429	Epsilon	VOI	California, USA	838	-0.1
C.37	Lambda	VOI	Chile	1	0
B.1.621	Mu	VOI	Colombia	37	0
B.1.621.1	Mu	VOI	Colombia	9	0
B.1.616		VOI	France	0	0
B.1.617.1	Kappa	VOI	India	403	0
B.1.617.3		VOI	India	3	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
P.3	Theta	VOI	Philippines	4	0
B.1.1.318		VOI	Switzerland	20	10.0
A.23.1		VOI	TBC	35	0
AZ.1		VOI		6	0
AZ.2		VOI		0	0

Identified Lineage* (Pangolin version 3.1.15/ PangoLEARN2021-10-15)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
AZ.2.1		VOI		0	0
AZ.3		VOI		0	0
AZ.4		VOI		0	0
AZ.5		VOI		4	0
AZ.6		VOI		0	0
P.2	Zeta	VUM	Brazil	194	0
B.1.618		VUM	India	46	0
B.1.526.2	Iota	VUM	New York, USA	0	0
C.1.2		VUM	South Africa	0	0
A.2.5		VUM		3	0
A.27		VUM		0	0
A.28		VUM		0	0
A.29		VUM		0	0
A.30		VUM		0	0
AT.1		VUM		0	0
AV.1		VUM		0	0
B.1		VUM		127	-2.4
B.1.1.1		VUM		20	0
B.1.1.28		VUM		4	0
B.1.1.519		VUM		284	0.4
B.1.1.523		VUM		0	0
B.1.160		VUM		183	0
B.1.214.2		VUM		0	0
B.1.324		VUM		0	0
B.1.466.2		VUM		0	0
B.1.619		VUM		1	0
B.1.620		VUM		0	0
B.1.628		VUM		0	0
B.1.629		VUM		0	0
B.1.630		VUM		0	0

Identified Lineage* (Pangolin version 3.1.15/ PangoLEARN2021-10-15)	WHO Name	Category**	First Detected	TOTAL	% Change since last report
B.1.631		VUM		0	0
C.16		VUM		0	0
C.36.3		VUM		0	0
C.36.3.1		VUM		0	0
R.1		VUM		1	0
R.2		VUM		0	0
TOTAL				63,839	8.1

* 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).