Weekly update on Variants of Concern (VOC)

8 March, 2023

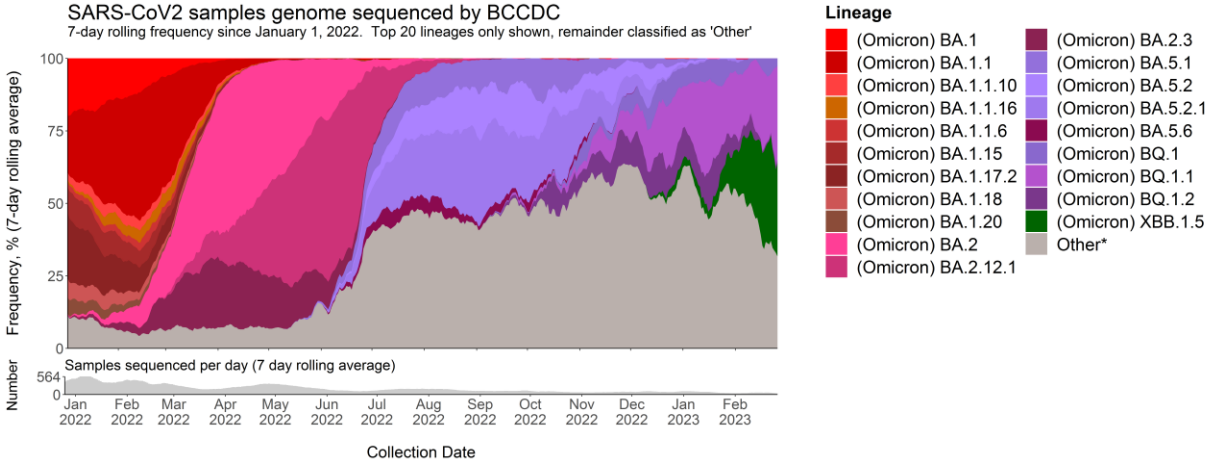
Of all positive samples sequenced* in epi week 8 (February 19 - February 25) in BC, all were confirmed Variants of Concern (VOCs).

Over time, the distribution of variants demonstrate the temporality and changing nature of VOCs circulating as shown in Figure 1. Detection of BA.5, including all descendant sublineages, has stabilized in the most recent epi weeks after a recent decrease increase up to epi week 6 (February 5 – February 12, 2023). Omicron recombinant XBB.1.5 has also stabilized in the most recent epi weeks after a recent increase up to epi week 6.

Due to the large diversity in BA.5 sublineages (>100 descendants), the total sequenced for each individual descendant strain is low and collapsed in the 'Other' category (Figure 1). Lineage sequenced in the most recent week of data categorized as 'Other' are listed in the footnote of the figure. More detail on recent sequenced samples, including those collapsed in 'Other', is available in Figure 5.

Data from epi week 8 may reflect partial data; estimates are expected to change as more specimens are received and sequenced.

Figure 1. Twenty most prevalent lineages in British Columbia, January 1, 2022 - February 25, 2023**



*Other, in the most recent week of data, includes:
BF.7.*, BQ.1.1.*, BQ.1.5, BW.1.1, BW.1.1.1, CH.1.1.1, CH.1.1.2, CK.2.1, CM.12, CM.8.1, ED.2, EF.1, XBB.1, XBB.1.2, XBB.1.5.1
XBB.1.9.1, XBB.2

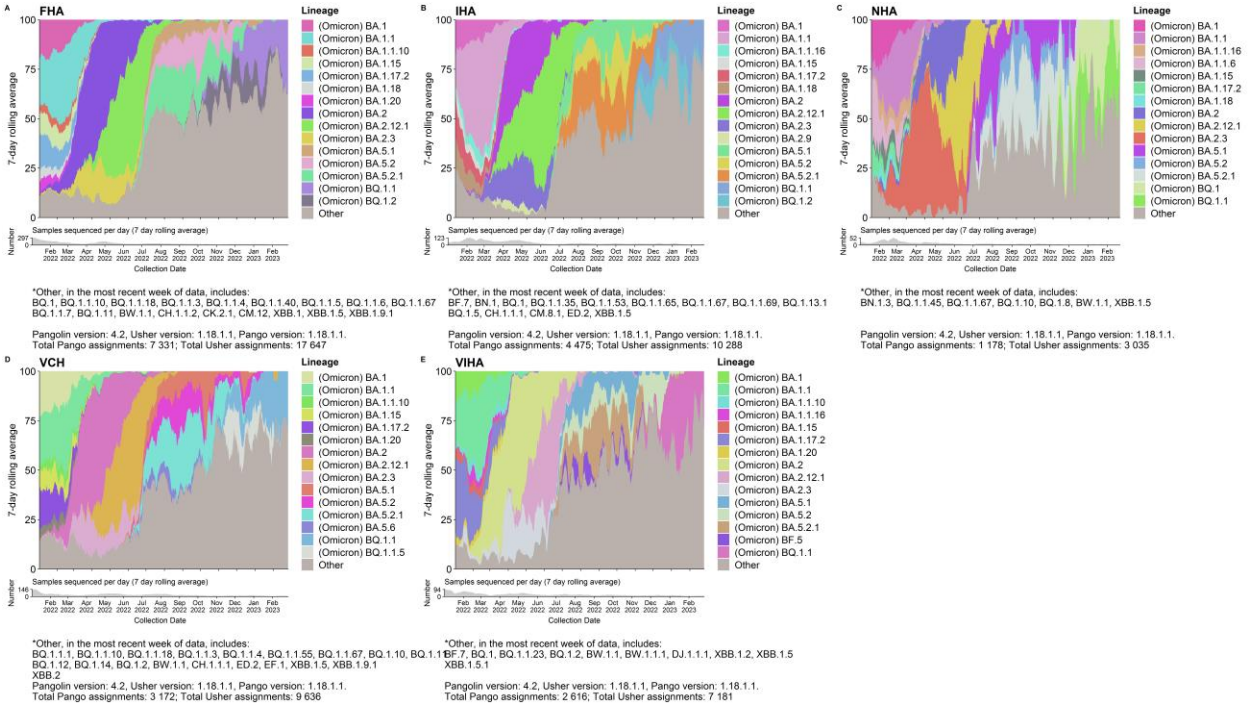
Pangolin version: 4.2, Usher version: 1.18.1.1, Pango version: 1.18.1.1. Total Pango assignments: 21 601; Total Usher assignments: 51 016

*Lineages in the Other category listed with an asterisk * comprise of descendants within the parent variant.*

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

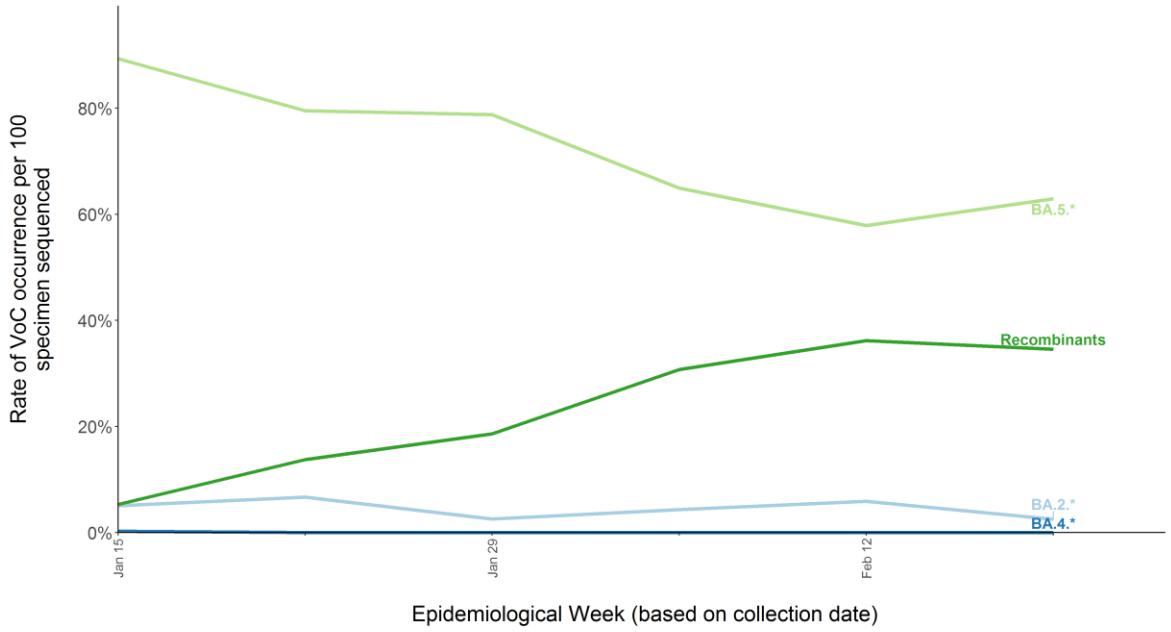
As shown in Figure 2, Omicron sub-lineages have different prevalence distribution in each health authority. Lineages sequenced in the most recent week of data available categorized as 'Other' are listed in the footnote of the figure.

Figure 2. Fifteen most prevalent lineages in British Columbia by Health Authority, January 1, 2022 - February 25, 2023



Pangolin designation beyond three sub-lineages (e.g. BA.5.x.x.x) results in the assignment of a new naming convention whereby a new lineage (e.g. BE) is assigned. These new designations (e.g. BE, BM, etc.) are collapsed in their parental lineage (e.g. BA.5*) in Figure 3.

Figure 3. Proportion of lineages # sequenced over the past 6 weeks from 08 January, 2023 to February 25, 2023



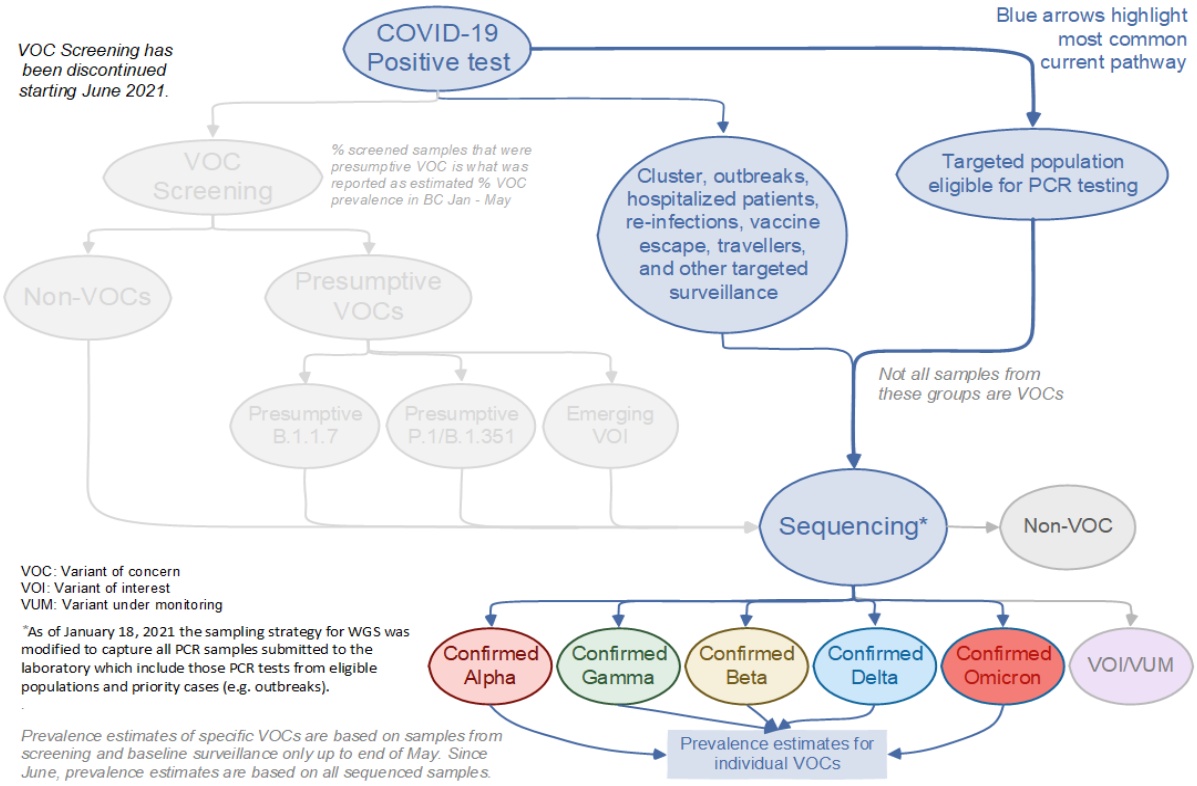
 # See appendix for the definitions of VOC lineages

Monitoring of Variants

BCCDC Public Health Laboratory is continuously monitoring for new SARS-CoV-2 lineages by Whole Genome Sequencing (WGS). Sequencing strategy was optimized based on available capacity and clinical and public health needs, and changed over the course of the SARS-CoV-2 pandemic.

In brief, VOC screening and confirmation by whole genome sequencing (WGS) was performed at the BCCDC PHL in the earlier phase of the pandemic (January-May 2021). From June 2021 onward, sample VOC status was detected by WGS alone until September 2021. The strategy transitioned from September 1, 2021 (epi-week 35) to WGS being applied to a subset only (10% random sample in addition to prioritized cases including all hospitalized, vaccinated or outbreak-associated) in addition to a monthly point prevalence of all positive samples. In the context of Omicron's emergence, the strategy resumed to WGS of all samples starting in November 15, 2021, and was rapidly revised by epi week 50, 2021 due to Omicron's high case load. Thereafter, with the switch to targeted PCR testing beginning January 18, 2022 (epi-week 3), sequencing of all PCR confirmed cases in BC was again routinely attempted, as shown in Figure 4. As of October, 2022 sequenced samples no longer include travel testing due to the ending of COVID-19 emergency border measures.

Figure 4. Overview of the screening and sequencing process applied to positive COVID-19 tests in BC, Feb 2023.

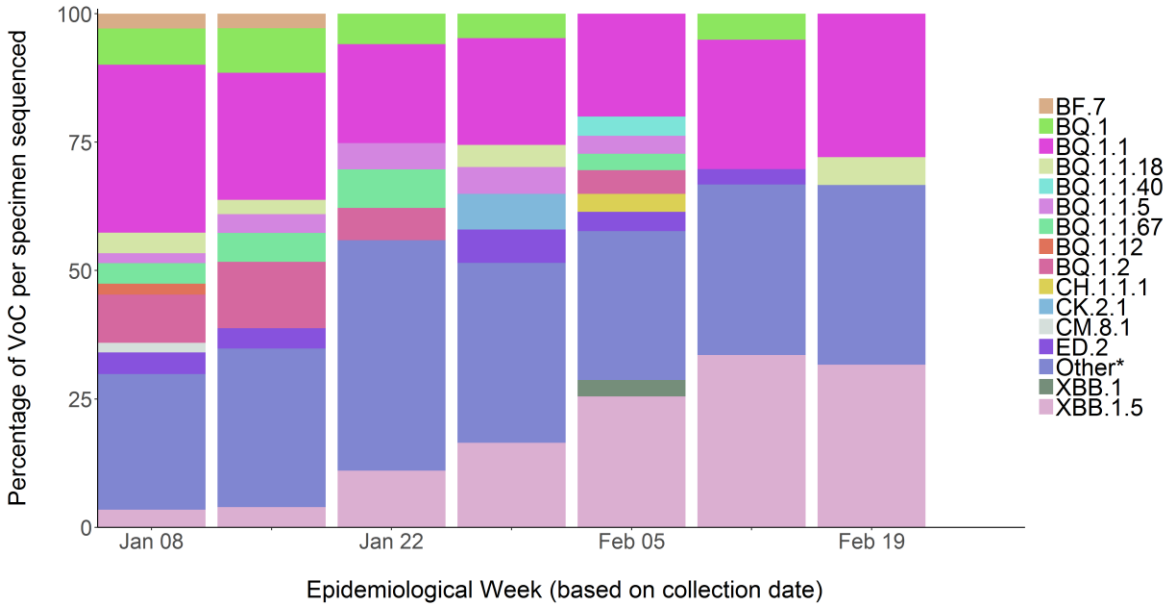


Whole genome sequencing (WGS)

Whole genome sequencing (Illumina only) was performed on 187,513 specimens up to epi week 8 (February 19 - February 25) in BC. Figure 4 above illustrates BC's whole genome sequencing strategy of COVID cases.

The VOCs represent a cumulative 87.3% of all the variants that were detected in the province since the start of the pandemic (see WGS frequency of lineages table on BCCDC website). The Delta (n = 57,837) and Omicron (n = 77,988) variants account for largest proportion of the VOCs. Omicron includes B.1.1.529, the parent lineage, and BA sub-lineages (Figure 5 and appendix Table).

Figure 5. Distribution of Omicron sublineages in the past 6 weeks**

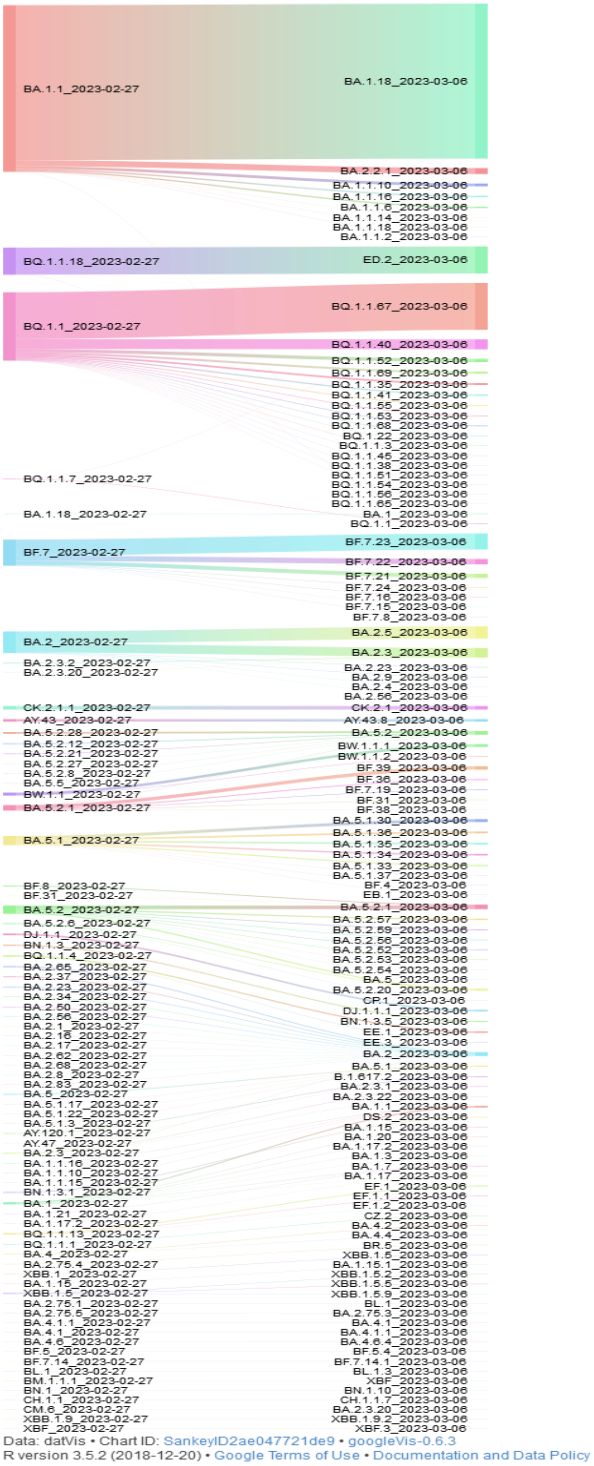


*Lineages with less than 10 samples sequenced a week are binned into `Other*`

*** These counts represent the total number of samples (not cases) sequenced.*

BCCDC Public Health Laboratory updates the lineage assignment tool (Pangolin), on an at least weekly basis, to reflect current lineage classification changes as shown in Figure 6.

Figure 6. Lineage assignment changes* in Pangolin



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.*
Omicron**	B.1.1.529, BA.*, BA, BC, BD, BE, BF, BG, BH, BJ, BK, BL, BM, BN, BP, BQ, BR, BS, BT, BU, BV, BW, BY, BZ, CA, CB, CC, CD, CE, CF, CG, CH, CJ, CK, CL, CM, CN, CP, CQ, CR, CS, CT, CU, CV, CW, CY, CZ, DA, DB, DC, DD, DE, DF, DG, DH, DJ, DK, DL, DM, DN, DP, DQ, DR, DS, DT, DU, DV, DW, DY, DZ, EA, EB, EC, ED, EE, EF, XE, XG, XH, XJ, XK, XL, XM, XN, XP, XQ, XR, XT, XU, XV, XW, XY, XZ, XAA, XAB, XAC, XAD, XAE, XAF, XAG, XAH, XAJ, XAK, XAL, XAM, XAN, XAP, XAQ, XAR, XAS, XAT, XAU, XAV, XAZ, XBG, XBH, XBJ

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

*** Lineages starting with X indicate a recombination of Omicron variants.*

**** 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.*