Supplemental Information:

The origins and potential future of SARS-CoV-2 variants of concern in the evolving COVID-19 pandemic

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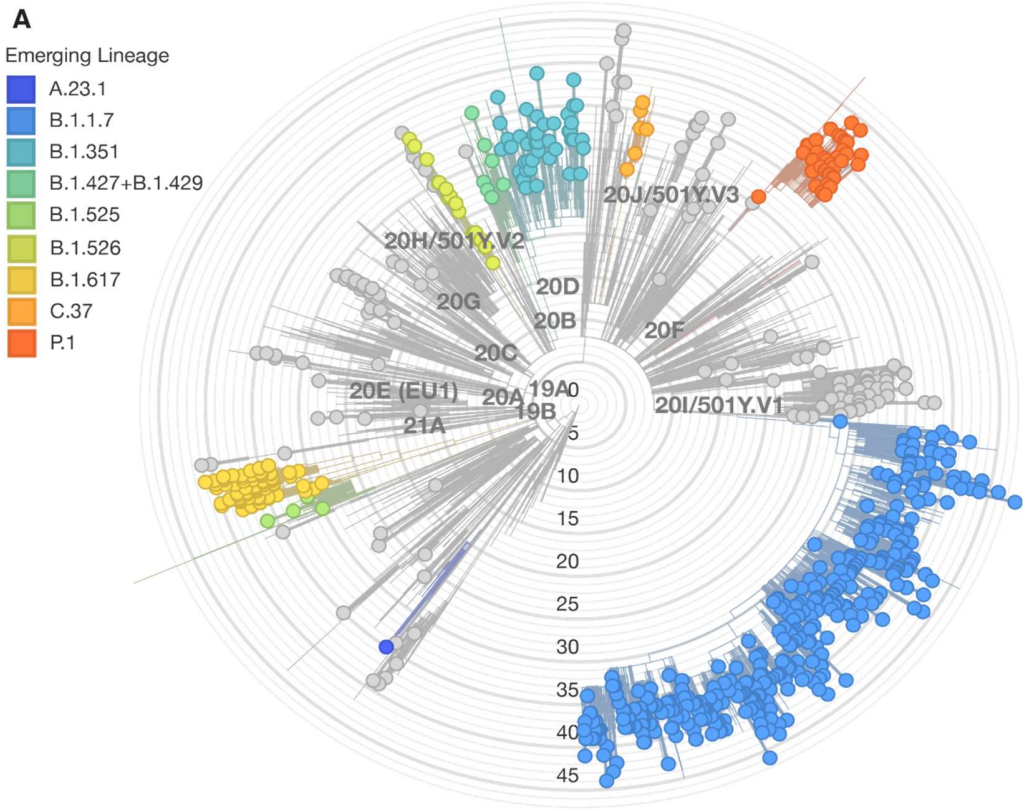
A
Emerging Lineage
A.23.1
B.1.1.7
B.1.351
B.1.427+B.1.429
B.1.525
B.1.526
B.1.617
C.37
P.1
20J/501Y.V3
20H/501Y.V2
20G
20D
20B
20F
20C
20E (EU1)
20A
19A
19B
20I/501Y.V1
21A
0
5
10
15
20
25
30
35
40
45

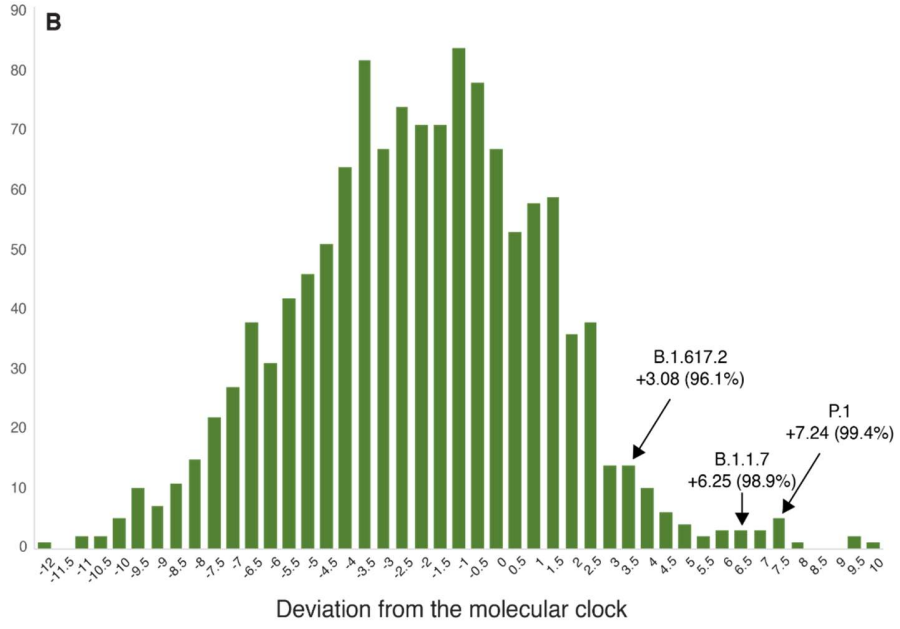
B
B.1.617.2
+3.08 (96.1%)
P.1
+7.24 (99.4%)
B.1.1.7
+6.25 (98.9%)
Deviation from the molecular clock

Figure S1. Phylogenetic analyses show increase in mutation numbers among variants of concern.

A) Phylogenetic tree built by Nextstrain (https://nextstrain.org[S1]) showing the number of mutational changes in concentric circles relative to the common ancestor at the centre. Phylogeny is limited to samples from April 1–May 22, 2021 (circles, representing 756 of the 3921 genomes in the global build, accessed 22 May 2022), so that samples further from the centre have more mutations than contemporaneous samples. The B.1.617 lineages in yellow (left) have similarly elevated numbers of mutations since the common ancestor as other VOC (35–40 changes relative to the common ancestral genome), including B.1.1.7 (blue at bottom right) and P.1 (orange at top right), whereas the grey circles exhibit fewer changes, on average. B) Deviation from the molecular clock as calculated by CoVizu (https://filogeneti.ca/covizu/)[S2]; B.1.617.2 has undergone a faster rate of change than 96.1% of the 1280 PANGO lineages (CoVizu build: 25 May 2021).

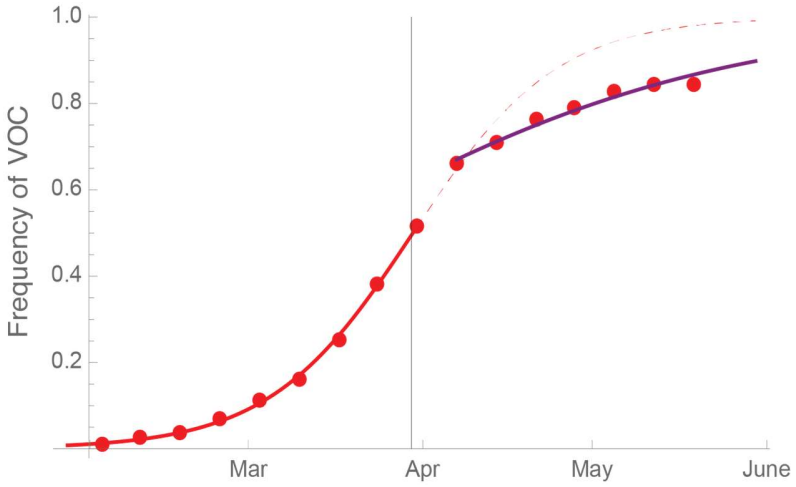

Figure S2. Selective advantage of VOC declines with increasing social restrictions in British Columbia.

The rise in variants of concern was tracked in British Columbia with screening by PCR for the S:N501Y mutation among most COVID-19 cases (data from http://www.bccdc.ca/health-info/diseases-conditions/covid-19/data#variants; accessed 28 May 2021). Whole genome sequencing confirmed that the majority of variant cases were B.1.1.7 or P.1 until the end of April, when B.1.617 variants began to rise in frequency (not detected by this screen). During the time window shown, there was only one major change in restrictions, a 'circuit breaker' on 30 March 2021 (vertical line: closing indoor dining, gym closures, travel within the province restricted). Prior to the circuit breaker, the data (dots) showed the characteristic S-shaped trajectory of evolution (red curve), with a selective advantage of s = 0.078 (95% CI: 0.074–0.082 from a non-linear logistic model fit). This selective advantage declined significantly during the circuit breaker (s = 0.028; 95% CI: 0.021–0.034; s = 0.033; 95% CI: 0.021–0.044, excluding May data points when B.1.617 spread), consistent with prediction that breaking chains of transmission lowers the benefit of these variants. (The selective differences between P.1 and B.1.1.7 cannot be distinguished with these data.)

Supplemental References

S1. Hadfield, J., Megill, C., Bell, S.M., Huddleston, J., Potter, B., Callender, C., Sagulenko, P., Bedford, T., and Neher, R.A. (2018). Nextstrain: real-time tracking of pathogen evolution. Bioinformatics *34*, 4121–4123.

S2. Roux-Cil, F., Wong, E., Wade, K., Liu, M., Muñoz Baena, L., Gugan, G., Olabode, A.S., and Poon, A.F.Y. (2021). CoVizu: Rapid analysis and visualization of the global diversity of SARS-CoV-2 genomes. Virological.org (https://virological.org/t/covizu-rapid-analysis-and-visualization-of-the-global-diversity-of-sars-cov-2-genomes/678; accessed May 27, 2021).