

# COVID-19 Genomics Insights Dashboard (CGID) #31

The COVID-19 genomics insights dashboard (CGID) provides a public and high-level overview of viral genomic surveillance across Aotearoa, New Zealand. It aims to explain how whole-genome sequencing (WGS) complements other epidemiological data to support public health decision-making. As SARS-CoV-2, the virus that causes COVID-19, continues to adapt, mutate, and spread, the CGID reports trends and insights gained by our WGS surveillance programme here in Aotearoa New Zealand, and abroad.

## Summary Infographics & Insights:

### Genomes analysed:

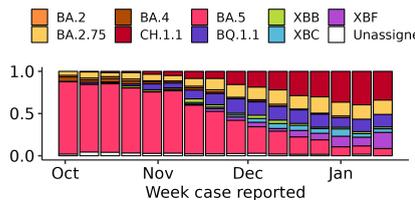
**1783\***

genomes from cases reported within the past four weeks (10<sup>th</sup> December - 13<sup>th</sup> January)

\* number of successful genomes. Sample no. processed is higher due to failed WGS attempts & cases sequenced multiple times

### Variant surveillance:

A complex mixture of immune-evasive variants have replaced the formerly dominant BA.5. Among these lineages CH.1.1 (a descendant of BA.2.75) is the most common, accounting for 30% of sequenced cases. XBB.1.5 has been detected but is present only at low levels currently.



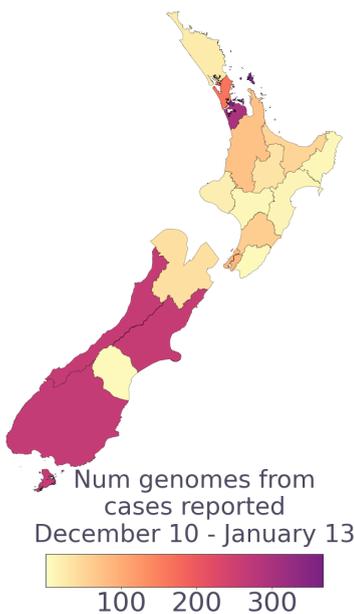
See the next page for the full-scale annotated figure

### Hospital surveillance:

**31%** (522 of 1668) of PCR-positive cases with a hospital admission date from 10<sup>th</sup> December - 13<sup>th</sup> January successfully produced a genome. Composition of hospital cases:

- 1% BA.2
- 17% BA.2.75\*
- 32% CH.1.1
- <1% BA.4
- 18% BA.5
- 16% BQ.1.1
- 2% XBB
- 6% XBC
- 7% XBF
- <1% Unassigned

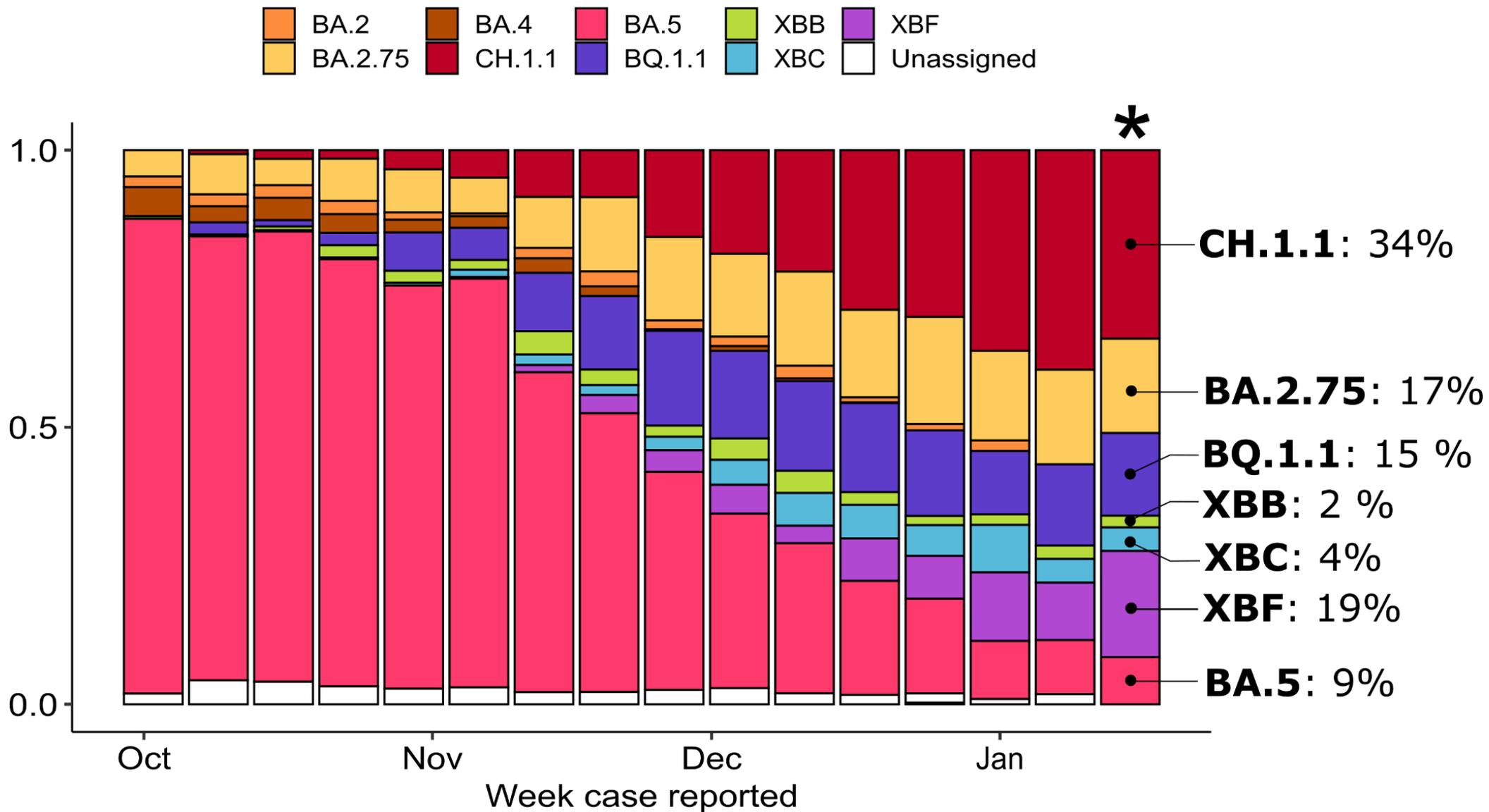
### Graphical overview showing sample origins



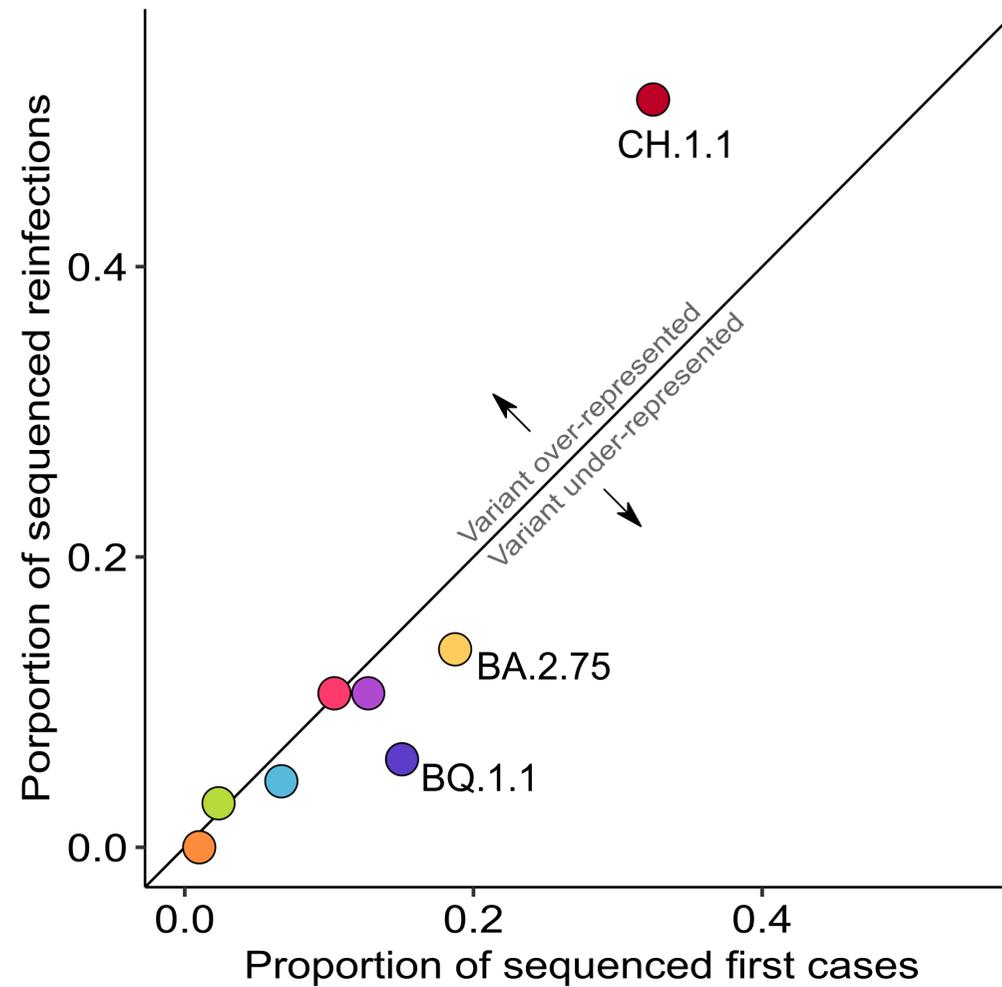
### Key Trends & Insights:

- BA.5 continues to decline in frequency, making up 18% of cases in the two-week reporting window (the last report in December reported 35%)
- CH.1.1 (a BA.2.75 derivative) is now the most common variant (>30% of samples). However, a substantial number of cases are being caused by BQ.1.1, recombinant lineages, and other BA.2.75\* lineages
- The XBB.1.5 lineage (sometimes called “Kraken”) has been detected in Aotearoa but is currently present at low frequencies
- ~1.2% of cases reported since the 10<sup>th</sup> of December 2022 have been sequenced. A summer hiatus in sequencing means fewer genomes are available from the most recent reporting weeks than is typical. Sequencing has now resumed at normal levels
- The main variants detected in wastewater were CH.1.1 (~55%), and the BA.2.75\* constellation (~22%) (includes BM.4, BR.2, XBF, and BA.2.75). Detections of XBB (includes XBB.1.5, ~3%) and XBC (~7%) were steady. BQ.1.1 and BA.4/BA.5 declined to ~10% and ~7%, respectively

The CGID report is produced ‘at pace’ by ESR in collaboration with Massey University, University of Auckland, and University of Otago. Data & insights are subject to change and correction



**Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing.** Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period. Frequencies from the last reporting week represent 47 samples [The category 'unassigned' is typically where a partial genome has been recovered, and a definitive assignment to a variant is not possible].



**Figure 2: Representation of COVID-19 variants among reinfections and apparent first cases.** Each point represents a SARS-CoV-2 variant currently tracked by ESR. The position of points on the Y-axis represents the proportion of all sequenced reinfections associated with this variant, and the position on the x-axis represents the proportion of apparent first cases. Reinfections are defined as a positive COVID-19 test greater than 28 days following an initial positive test.