

COVID-19 Genomics Insights Dashboard (CGID) #32

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:

399*

genomes from cases reported within the past four weeks (14th - 28th January 2023)

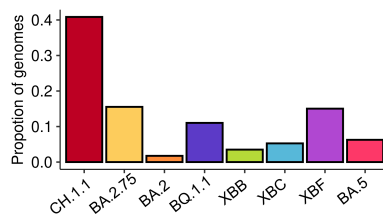
~1,000

genomes reported so far in 2023

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

Variant surveillance:

The formerly dominant variant, BA.5, has been displaced by a complicated blend of variants that can evade the immune system. CH.1.1, a descendant of BA.2.75, is the most common (40% of cases). XBB.1.5 continues to be found in small numbers.



See the next page for the original full-scale annotated figure

Hospital surveillance:

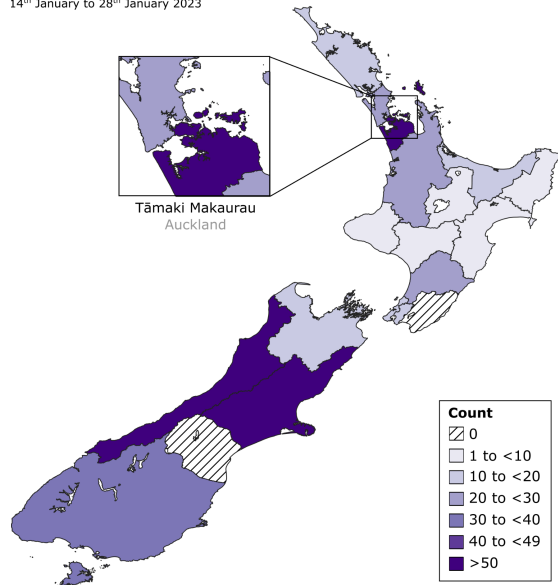
42% (143 of 339) of PCR-positive cases with a hospital admission date from 14th - 28th January successfully produced a genome.

Composition of hospital cases:

- 4% BA.2
- 18% BA.2.75*
- 44% CH.1.1
- 7% BA.5
- 8% BQ.1.1
- <1% XBB
- 6% XBC
- 12% XBF
- <1% Unassigned

Graphical overview showing sample origins

Number of SARS-CoV-2 genomes sequenced
14th January to 28th January 2023



Key Trends & Insights:

- The once dominant variant, BA.5, is now surpassed by a complex blend of variants that can evade the immune system.
- CH.1.1, a descendant of BA.2.75, is the most prevalent variant, accounting for 41% of cases. However, a substantial number of cases are being caused by other BA.2.75 lineages like XBF and BQ.1.1.
- The XBB.1.5 lineage, also known as "Kraken", continues to be found in low amounts with no indications of rapid spread in Aotearoa.
- Around 1.5% of cases reported since the 14th of January 2023, have been sequenced. After a temporary pause over the summer, sequencing has resumed at its typical rate relative to the number of cases.
- During week 4, the primary variants found in wastewater were CH.1.1 (~53%) and BA.2.75* (~32%). There were also smaller contributions from BQ.1.1 (~9%), XBB (which includes XBB.1.5, at ~3%), and XBC (~3%). The BA.4/BA.5 variant was not detected during week 4.

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

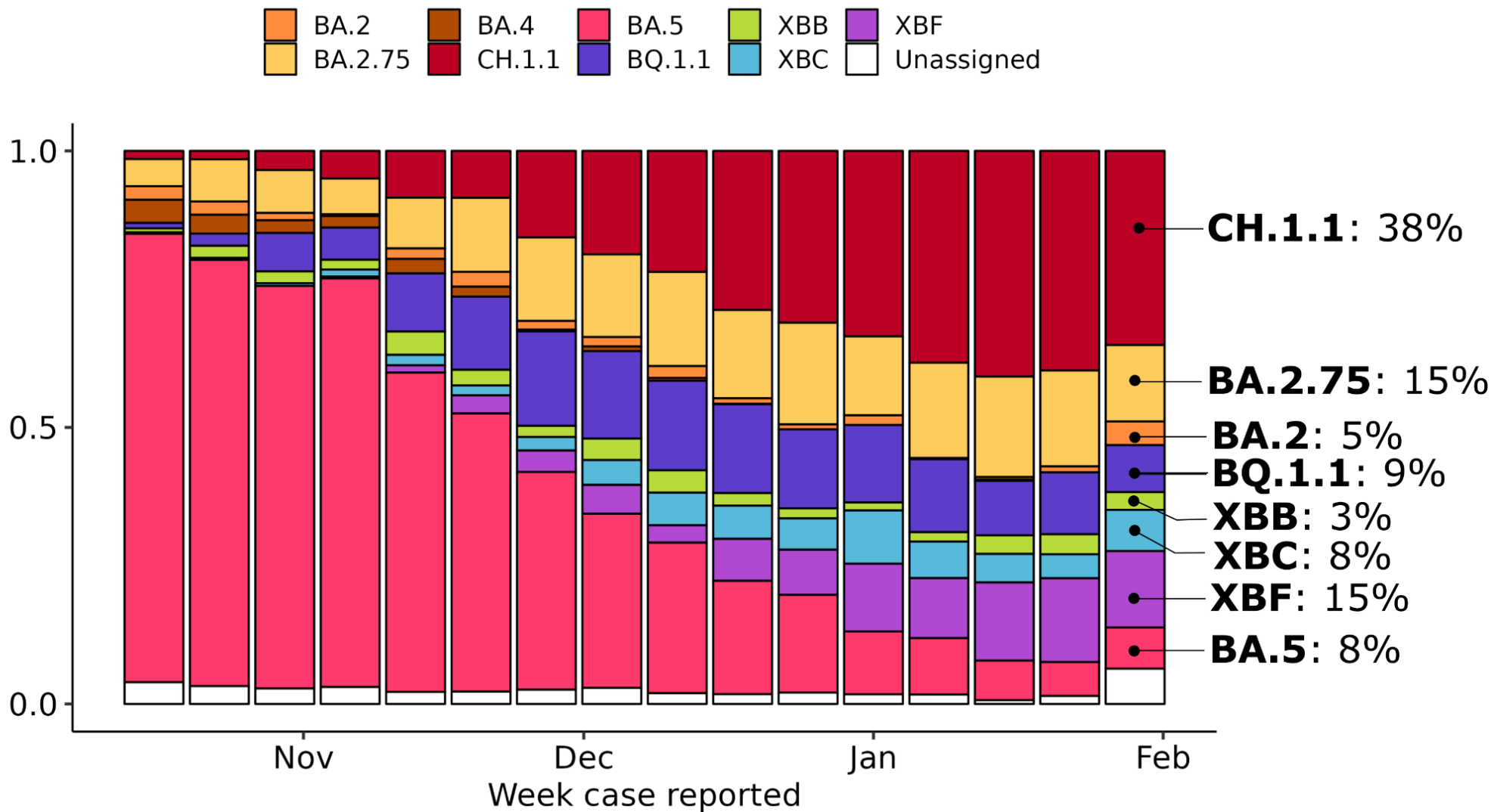


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. *Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period. [The category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

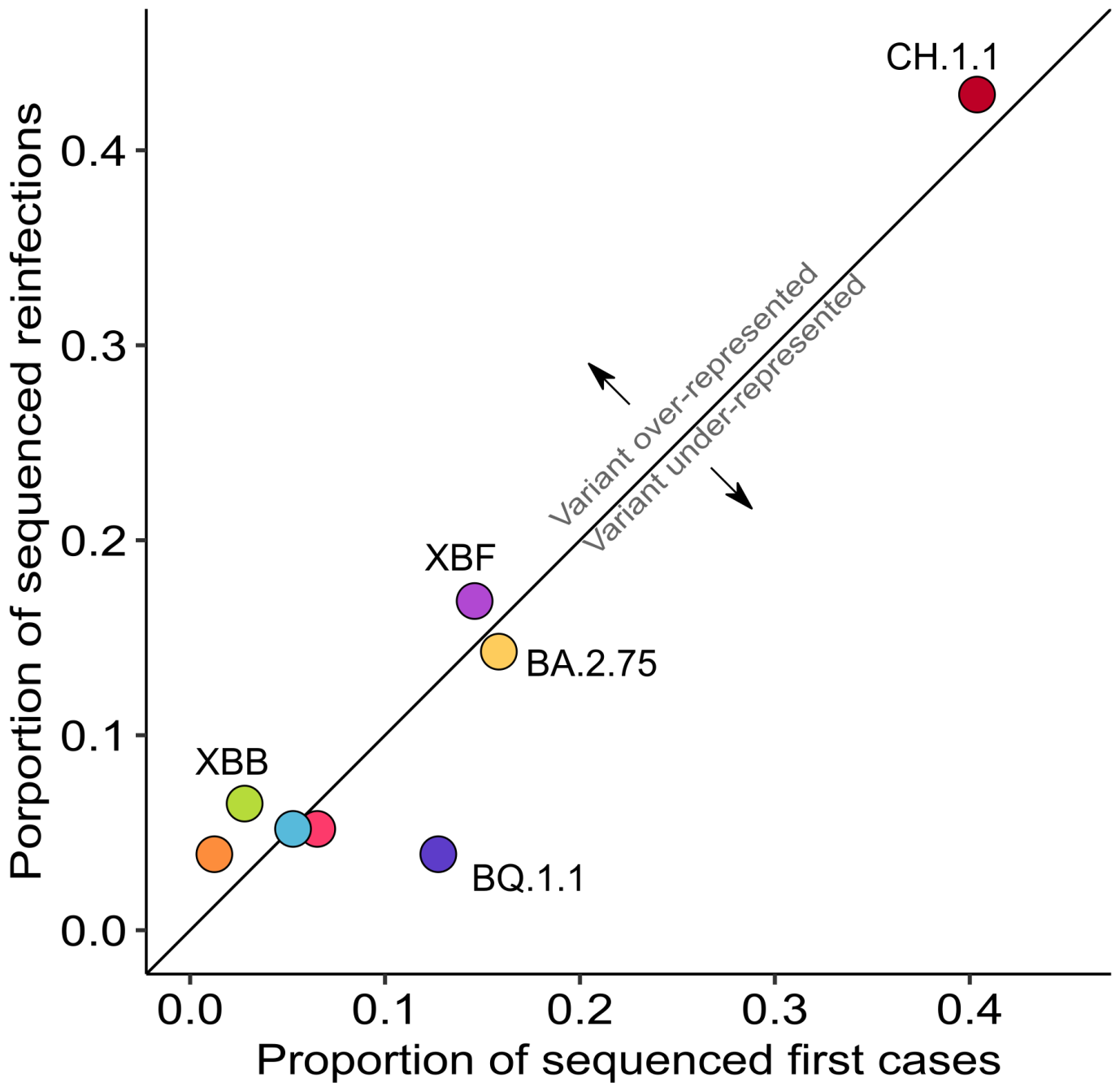


Figure 2: Representation of COVID-19 variants among reinfections and apparent first cases. Each point represents a SARS-CoV-2 variant currently tracked by ESR. The position of points on the Y-axis represents the proportion of all sequenced reinfections associated with this variant, and the position on 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.