

COVID-19 Genomics Insights Dashboard (CGID) #33

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:

243*

genomes from cases reported within the past four weeks (28th Jan - 10th Feb 2023)

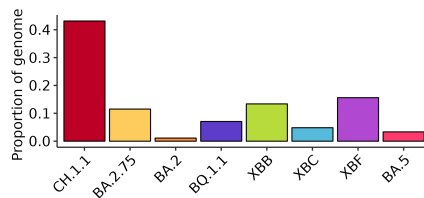
~1,500

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:

A complex mixture of immune-evasive variants has replaced the formerly dominant BA.5. The trend of more immune evasive variants dominating the New Zealand landscape continues in this reporting window.



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

Hospital surveillance:

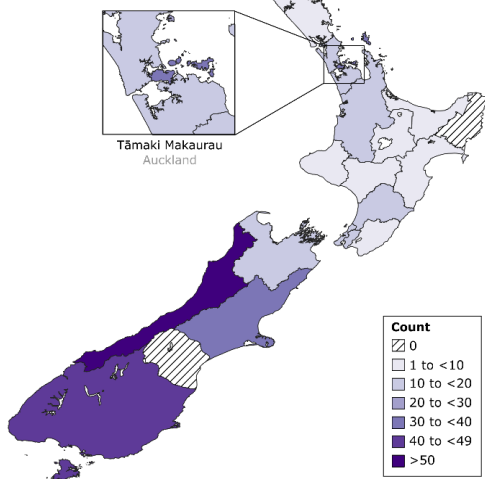
33% (72 of 220) of

PCR-positive cases with a hospital admission date from 28th January - 10th February successfully produced a genome. Composition of hospital cases:

- 21% BA.2.75*
- 39% CH.1.1
- 4% BA.5
- 4% BQ.1.1
- 8% XBB
- 7% XBC
- 15% XBF
- 1% Unassigned

Graphical overview showing sample origins

Number of SARS-CoV-2 genomes sequenced
28th January to 10th February 2023



Key Trends & Insights:

- Currently, in Aotearoa New Zealand, there is a complex mixture of variants circulating that are known to be more immune-evasive
- Although CH.1.1, a derivative of BA.2.75, is the most prevalent variant accounting for 42% of cases, there are substantial numbers of cases caused by other lineages like XBF, BQ.1.1, and additional BA.2.75* group lineages
- Over the past few weeks, the XBB variant has increased in proportion relative to all cases, with both the XBB.1.5 and XBB.1.9 lineages contributing to its growth
- Due to disruptions this week, no wastewater data is available for this particular CGID. However, all the wastewater results, including variant detection, will be included in the upcoming wastewater reports

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

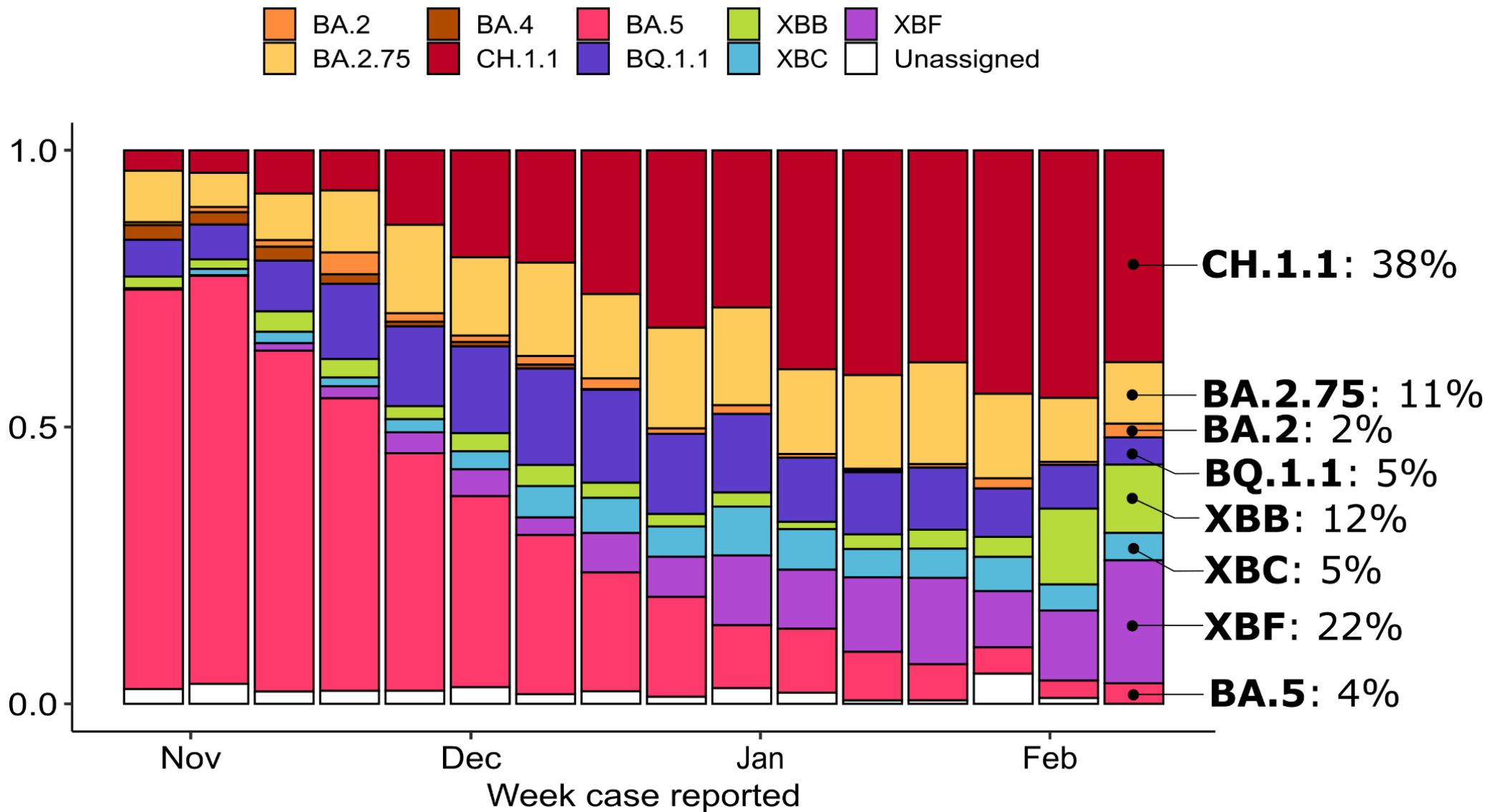


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period. [The category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

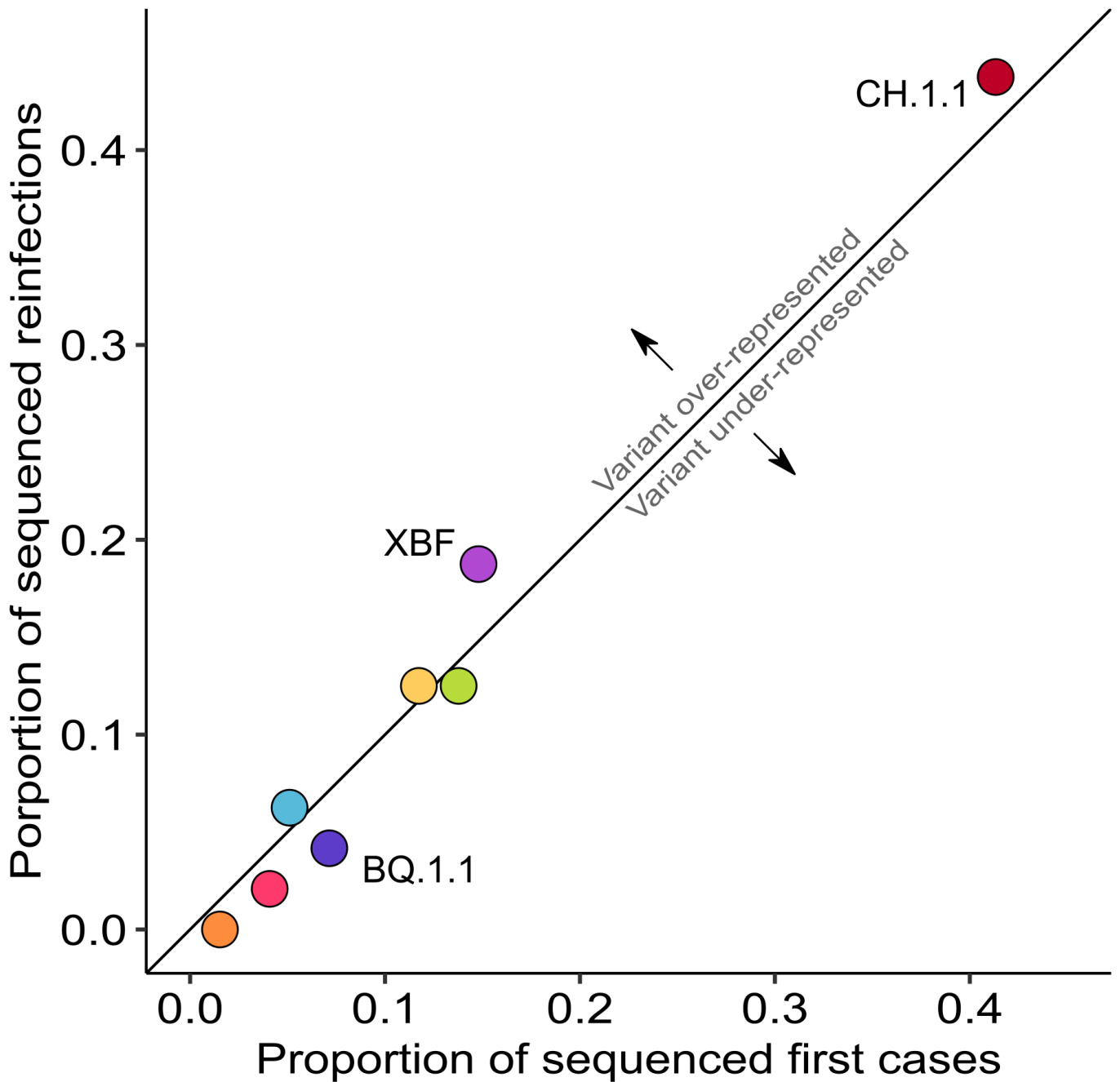


Figure 2: Representation of COVID-19 variants among reinfections and apparent first cases. Each point represents a SARS-CoV-2 variant currently tracked by ESR. The position of points on the Y-axis represents the proportion of all sequenced reinfections associated with this variant, and the position on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