

# COVID-19 Genomics Insights Dashboard (CGID) #36

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 in Aotearoa New Zealand, and abroad.

## Summary Infographics & Insights:

### Genomes analysed:

**214\***

genomes from cases reported within the past four weeks (25<sup>th</sup> Feb – 10<sup>th</sup> Mar 2023)

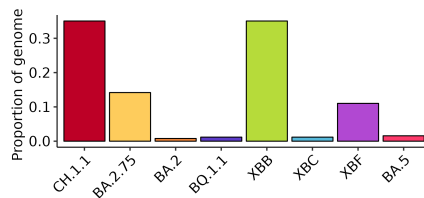
**~2,500**

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:

XBB and CH.1.1 each account for ~35% of reported cases, while BQ.1.1, XBC, and BA.5 variants have decreased to <2% of sequenced genomes. XBB and BA.2.75 lineages are still circulating.



### Hospital surveillance:

**27%** (80 of 264) of

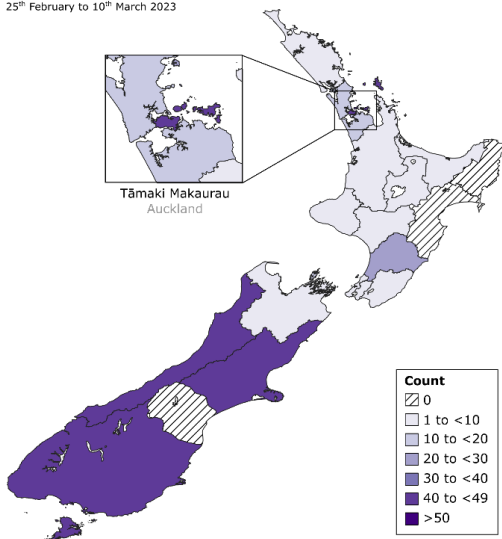
PCR-positive cases with a hospital admission date from 25<sup>th</sup> Feb- 10<sup>th</sup> Mar successfully produced a genome.

Composition of hospital cases:

- 20% BA.2.75\*
- 31% CH.1.1
- 3% BA.5
- 3% BQ.1.1
- 33% XBB
- 10% XBF

### Graphical overview showing sample origins

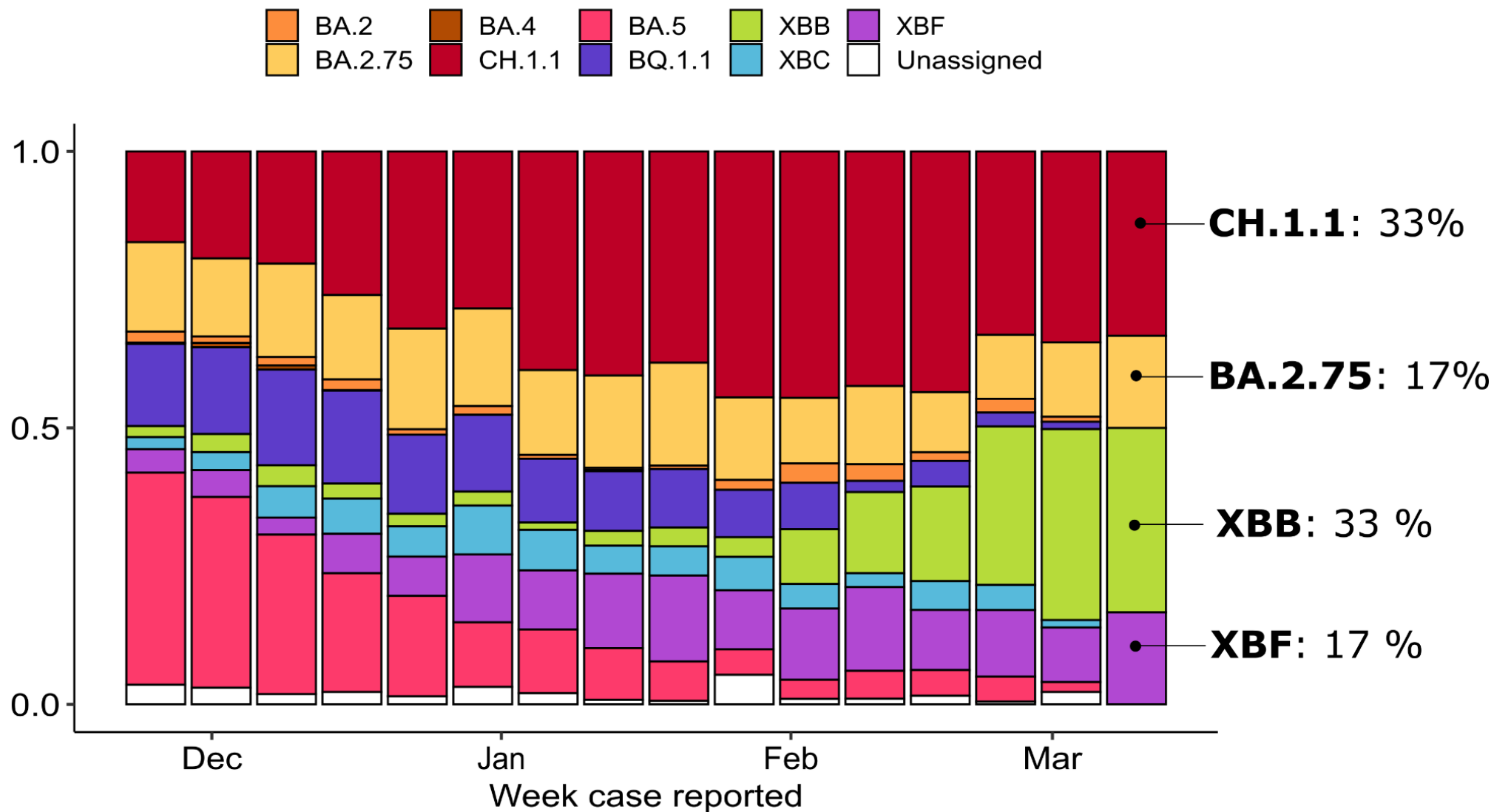
Number of SARS-CoV-2 genomes sequenced  
25<sup>th</sup> February to 10<sup>th</sup> March 2023



### Key Trends & Insights:

- The XBB variant is becoming more common and now makes up 36% of all cases, which is the same proportion as the CH.1.1 variant.
- XBB has been growing because of a specific variant of XBB called XBB.1.5, which is responsible for 22% of all cases. This matches the growth of XBB in other countries.
- While BA.2.75 and XBF are still present, other lineages that were circulating with CH.1.1 are decreasing rapidly.
- CH.1.1 (a BA.2.75\* group derivative) is the most common variant (42% of cases), followed by XBB, XBF, and other BA.2.75 lineages.
- The results from testing wastewater match what doctors are seeing in patients. The most common variants found were XBB, which includes XBB.1.5 and accounts for ~43% of cases, followed by CH.1.1 at ~28% and BA.2.75 (which includes XBF) at ~25%. There were also smaller amounts of BQ.1.1 at ~2% and XBC at ~2%.

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 was not possible].**

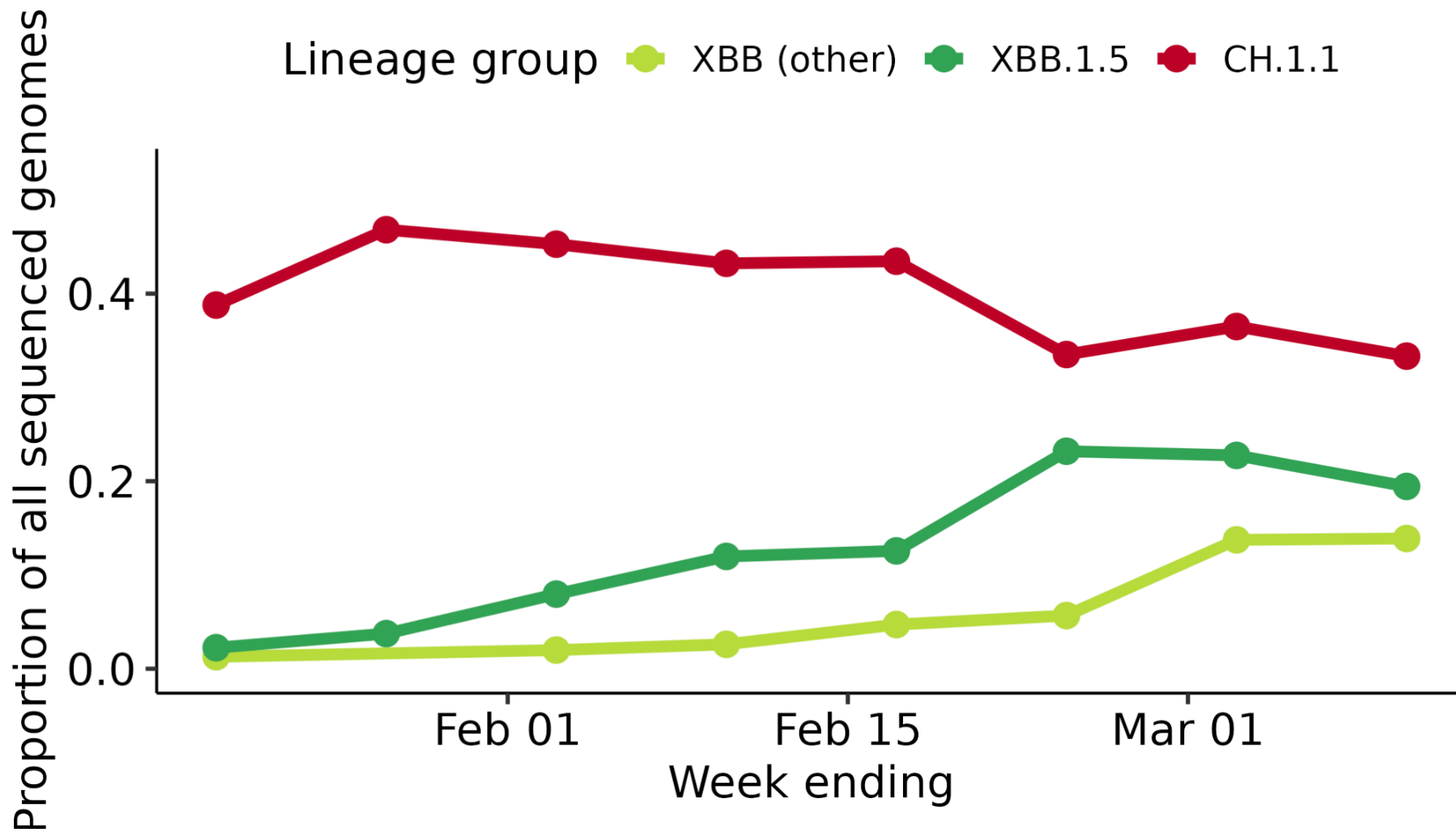


Figure 2: Frequency XBB lineages over time. Data for CH.1.1, the most commonly tracked variant over this time, is provided for context.