

COVID-19 Genomics Insights Dashboard (CGID) #34

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:

236*

genomes from cases reported within the past four weeks (11th - 24th Feb 2023)

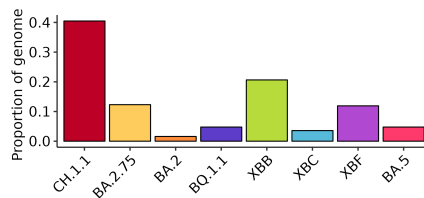
~2,000

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:

XBB cases are increasing and represent 21% of sequenced cases, driven by the XBB.1.5 lineage. XBF, CH.1.1, and BA.2.75* group lineages continue to circulate, while BA.5, XBC, and BQ.1.1 are decreasing.



Hospital surveillance:

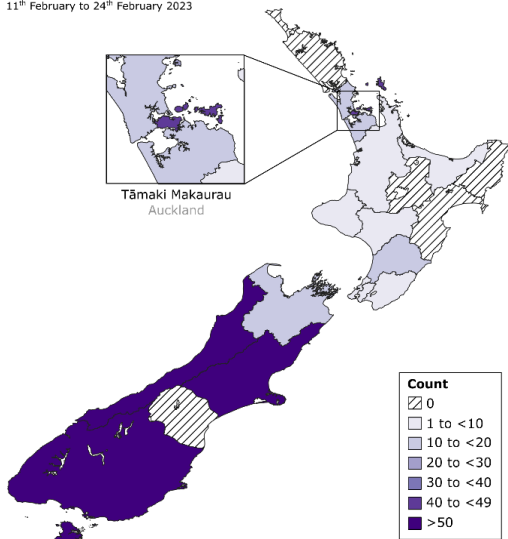
34% (80 of 233) of PCR-positive cases with a hospital admission date from 11th - 24th Feb successfully produced a genome.

Composition of hospital cases:

- 1% BA.2
- 14% BA.2.75*
- 38% CH.1.1
- 6% BA.5
- 4% BQ.1.1
- 20% XBB
- 4% XBC
- 14% XBF

Graphical overview showing sample origins

Number of SARS-CoV-2 genomes sequenced
11th February to 24th February 2023



Key Trends & Insights:

- Severe Tropical Cyclone Gabrielle disrupted several regions in Te Ika-a-Māui (the North Island), such as Northland, Bay of Plenty, and the East Coast, and caused their exclusion from the report, resulting in underrepresentation in these regions
- A complex mixture of immune-evasive variants is circulating Aotearoa New Zealand with no single dominant lineage
- The XBB subvariant continues to grow as a proportion of all cases. The XBB.1.5 lineage accounts for 17% of all sequenced cases in the reporting period
- 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
- Wastewater analysis showed XBB (including XBB.1.5) at 35%, CH.1.1 at 33%, and BA.2.75* at 24%. Minor contributions were BQ.1.1 (2%), BA.4/BA.5 (1%), and XBC (5%).

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

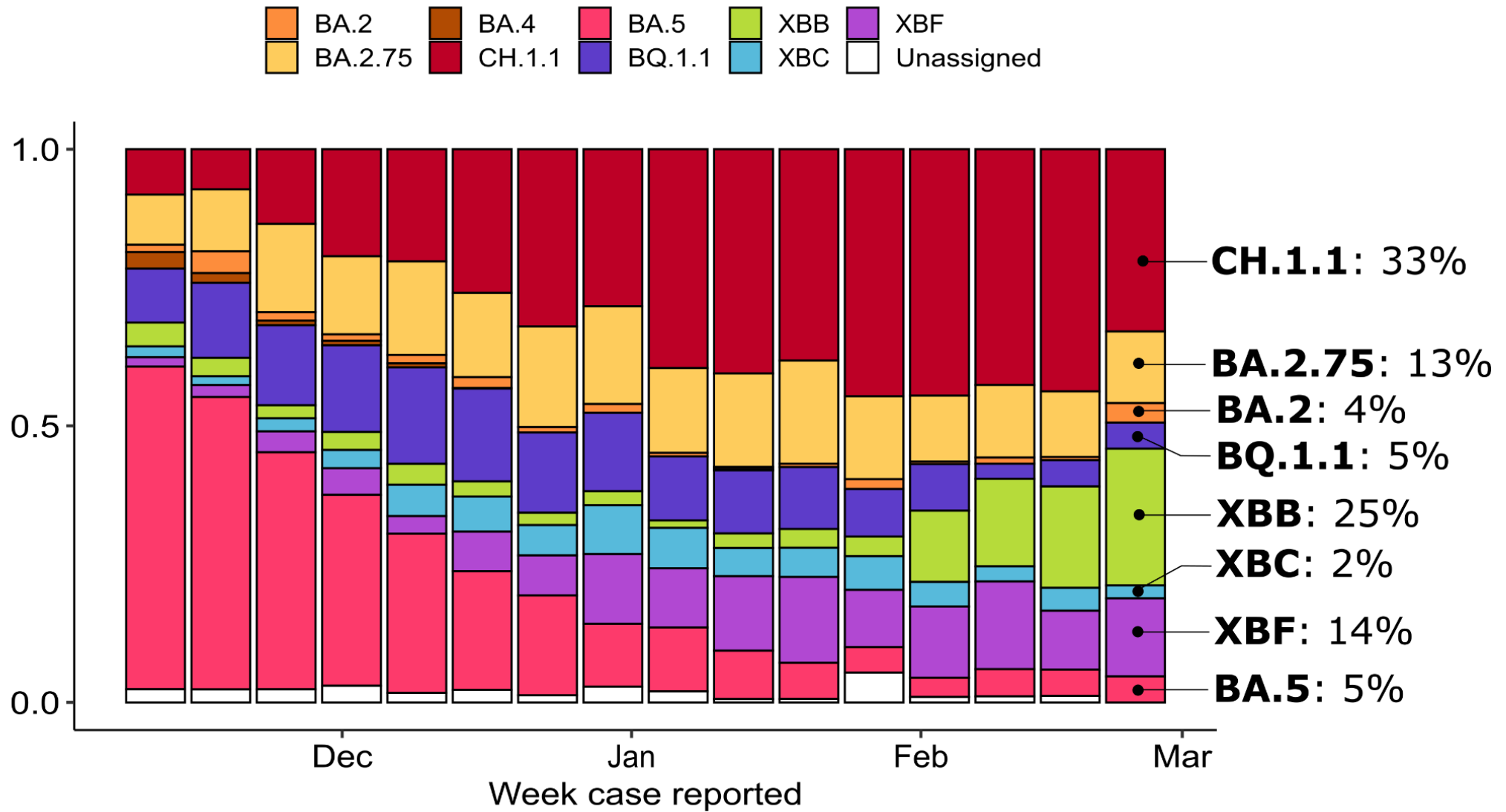


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period. [The category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

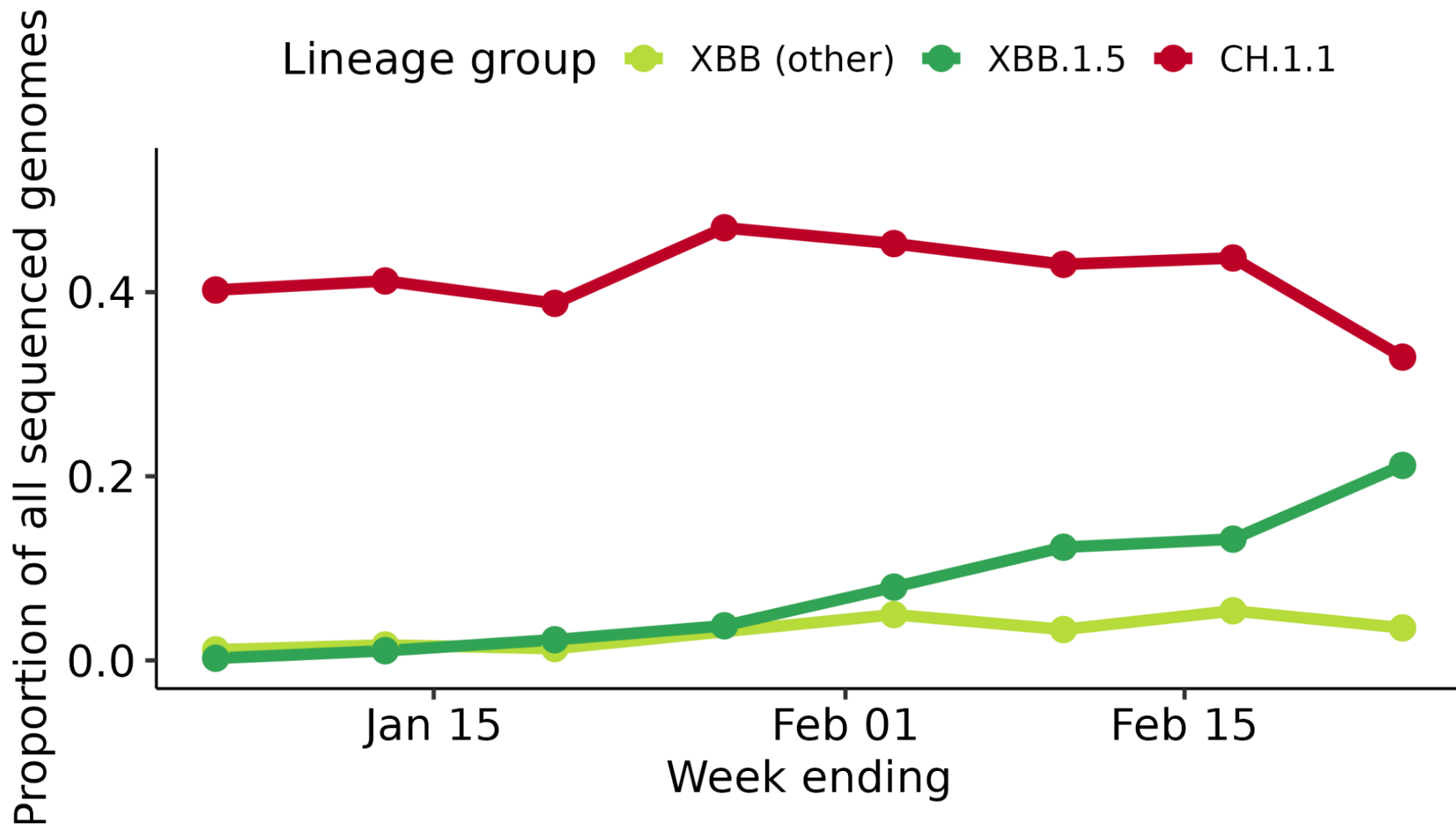


Figure 2: Frequency XBB lineages over time. Data for CH.1.1, the most commonly tracked variant over this time, is provided for context.