6th April 2023

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:

633*

genomes from cases reported within the previous three weeks (11th-31st March)

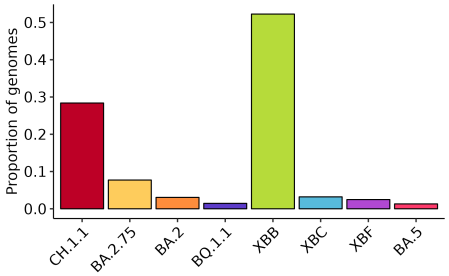
~3,500

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 is now the most common variant in Aotearoa, found in 52% of sequenced cases in the last three weeks. The formerly dominant CH.1.1 remains the second most common variant (33% of cases) while other variants make up less than 10% of sequenced cases



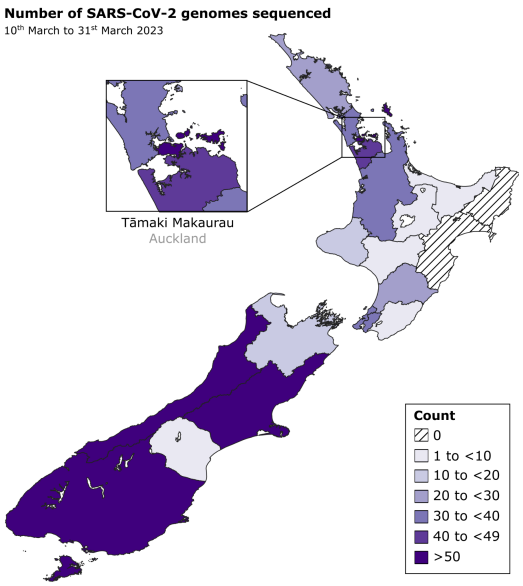
Hospital surveillance:

50% (307 of 612) of PCR-positive cases with a hospital admission date from 27th Feb - 31th Mar successfully produced a genome.

Composition of hospital cases:

- 8% BA.2.75*
- 30% CH.1.1
- 2% BA.5
- 2% BQ.1.1
- 46% XBB
- 5% XBF

Graphical overview showing sample origins



Key Trends & Insights:

- The XBB variant is now the most common, causing more than half of all sequenced cases in the reporting period.
- XBB has been growing because of a specific variant of XBB called XBB.1.5, which is responsible for 36% of all cases. This matches the growth of XBB in other countries.
- Other XBB lineages, including XBB.1.9.1 and XBB.1.16 are present in New Zealand and being tracked.
- The results from testing wastewater match what doctors are seeing in patients. The most common variants found were XBB (includes XBB.1.5, ~65%), CH.1.1 (~24%), BA.2.75* (includes XBF, ~4%), and with minor contributions from BQ.1.1 (~6%), and XBC (~1%).

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

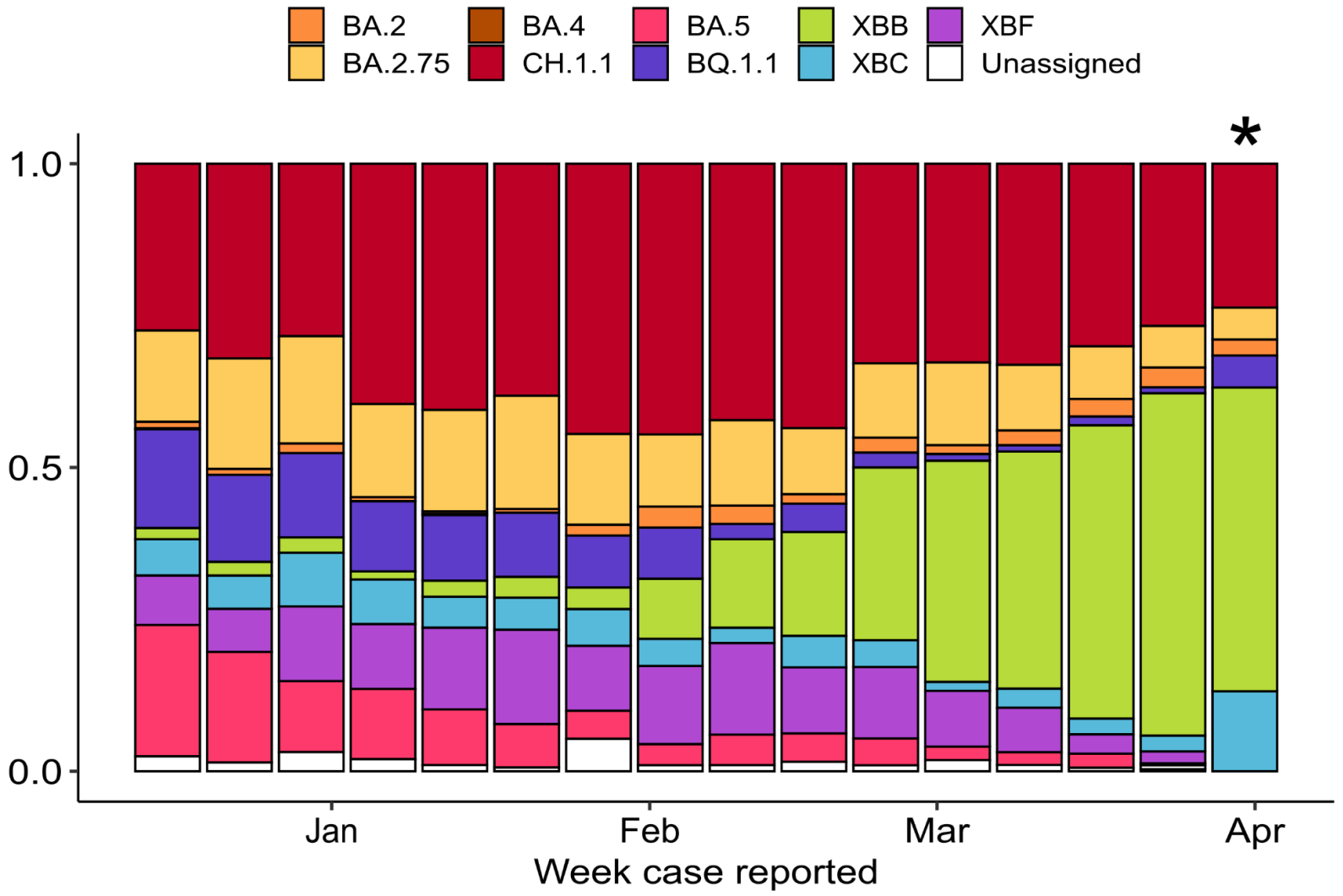


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing*. Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In this case d*ata from the last reporting week (marked with an asterisk) is based on a limited number of genomes (38) as data is still being generated for this week. [The category 'unassigned' is typically where a partial genome has been recovered, and a definitive assignment to a variant was not possible].*

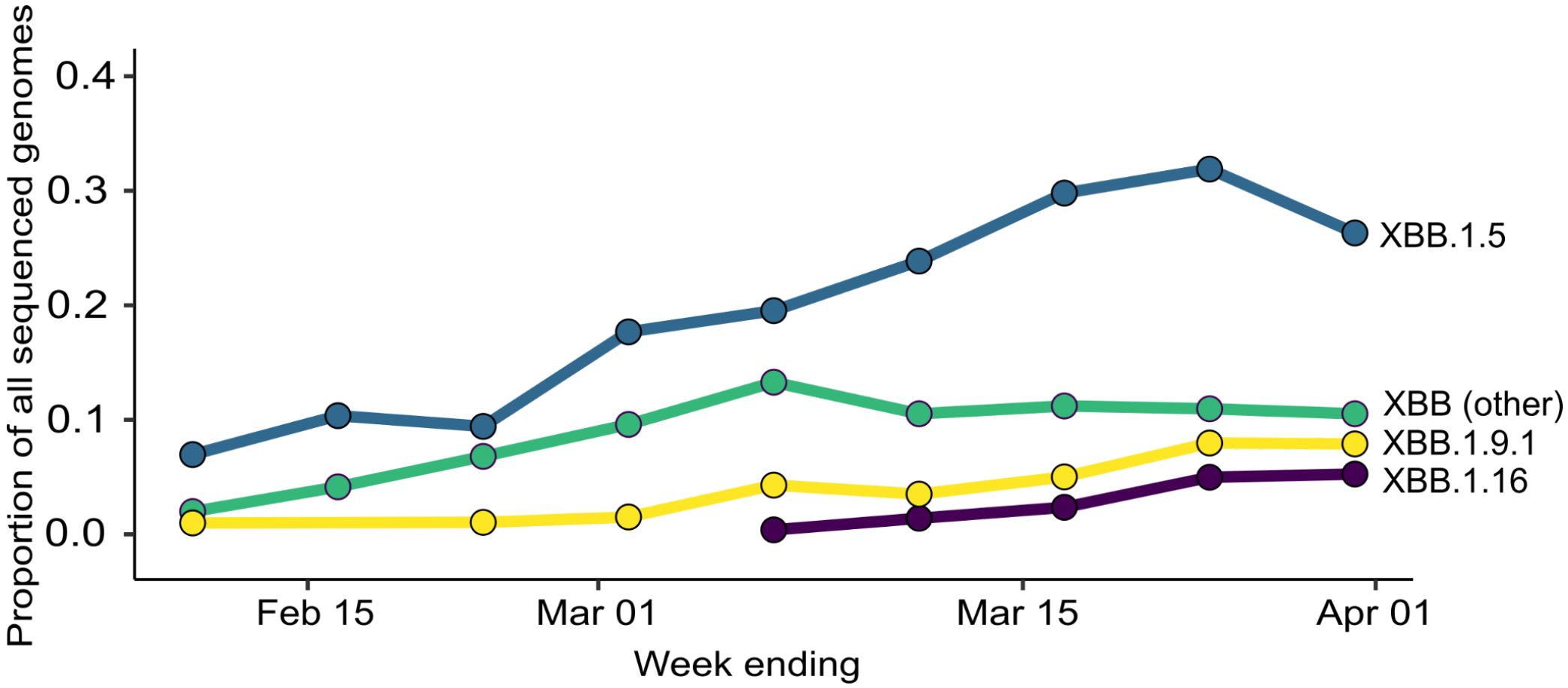


Figure 2: Frequency XBB sublineages over time.