7th July 2023

COVID-19 Genomics Insights Dashboard (CGID) #39

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:

955*

genomes from cases since the last report
(27th May to 30th June)

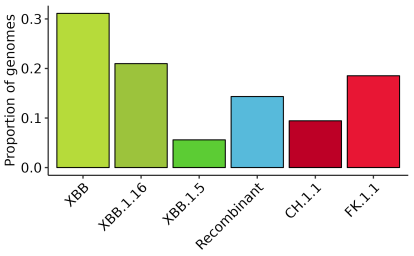
~8,000

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 XBB recombinant lineages remain dominant in Aotearoa, making 58% of sequenced cases. Among tracked XBB sublineages XBB.1.16 has remained steady at 20% of sequenced cases, while XBB (i.e. XBB lineages not specially tracked) has grown to make 32%



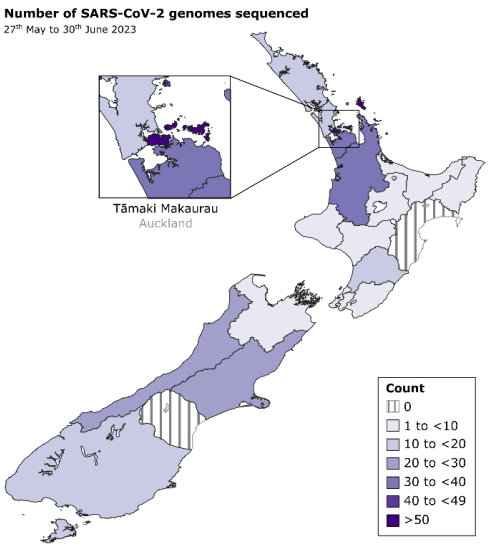
Hospital surveillance:

37% (118 of 321*) of PCR-positive cases with a hospital admission date from 16th - 30th June successfully produced a genome to date. The approximate composition of hospital cases:

- XBB: 30%
- XBB.1.5: 8%
- XBB.1.16: 22%
- FK.1.1: 14%
- Recombinant:17%

*The total number of PCR positive admitted cases includes high Ct samples not suitable for sequencing and cases reported late in the reporting period.

Graphical overview showing sample origins



Key Trends & Insights:

- The XBB variants are still the most common (found in 58% of sequenced cases in the past fortnight). The XBB.1.5 variant is decreasing and now accounts for only 5% of cases. Meanwhile, the XBB.1.16 variant is holding steady, representing ~20% of cases
- Other XBB variants account for 32% of cases, while FK.1.1 and CH.1.1 continue to circulate at 19% and 9% respectively
- Data from wastewater samples collected during weeks 20-24 show that the XBB variants are the most common, accounting for around 60% to 75% of all samples during this time. This matches the findings from clinical samples taken from patients
- There is a notable age bias in the distribution of sequenced cases, with a higher proportion of older individuals than reported cases
- Most of the genomes in the XBB group belong to the XBB.1.9 lineages, which include EG.1 and EG.2 that originate from XBB.1.9.2

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

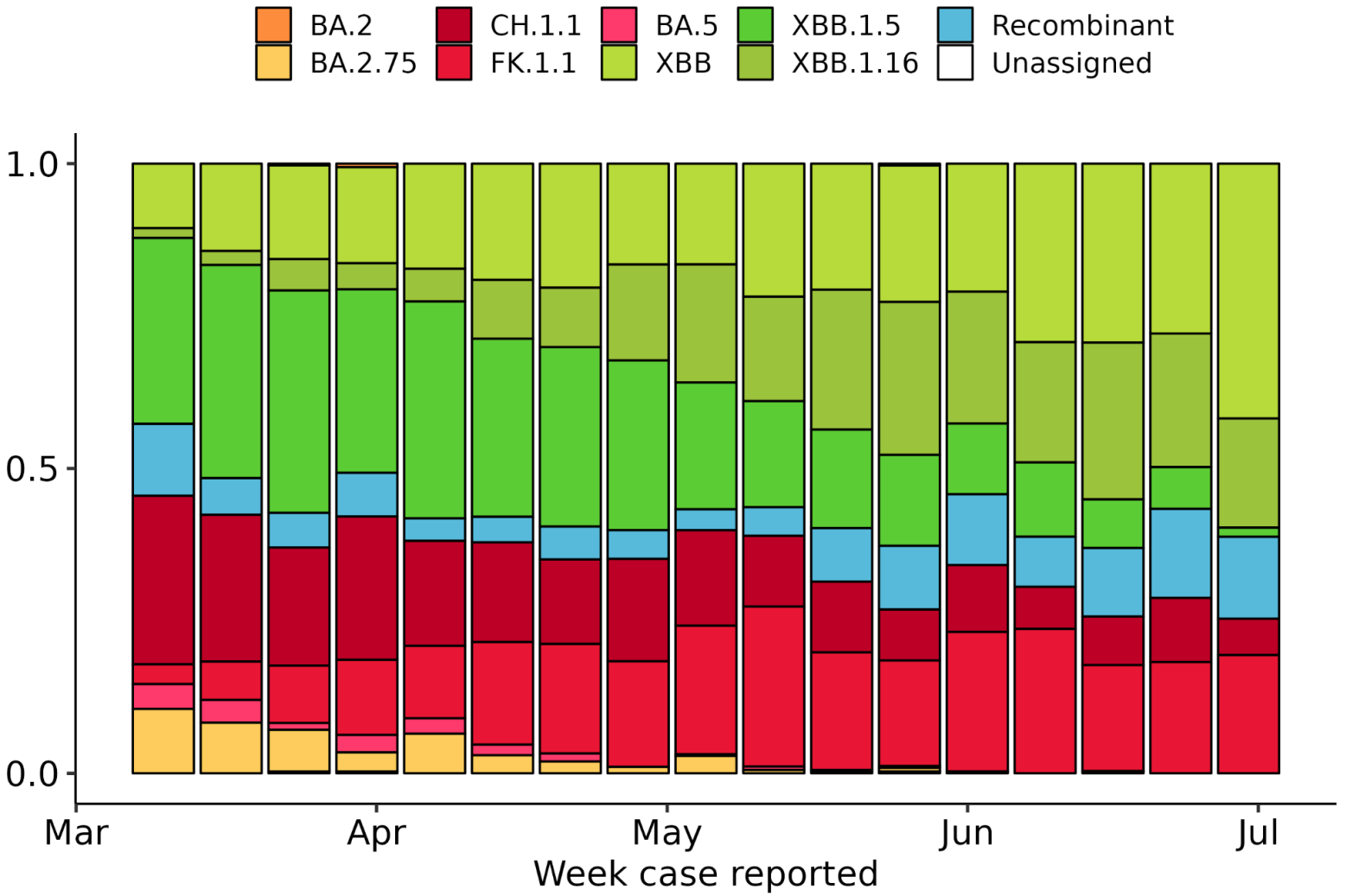


Figure 1: (A) Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. *Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In this case d*ata from the last reporting week is based on a limited number of genomes (101) 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].*

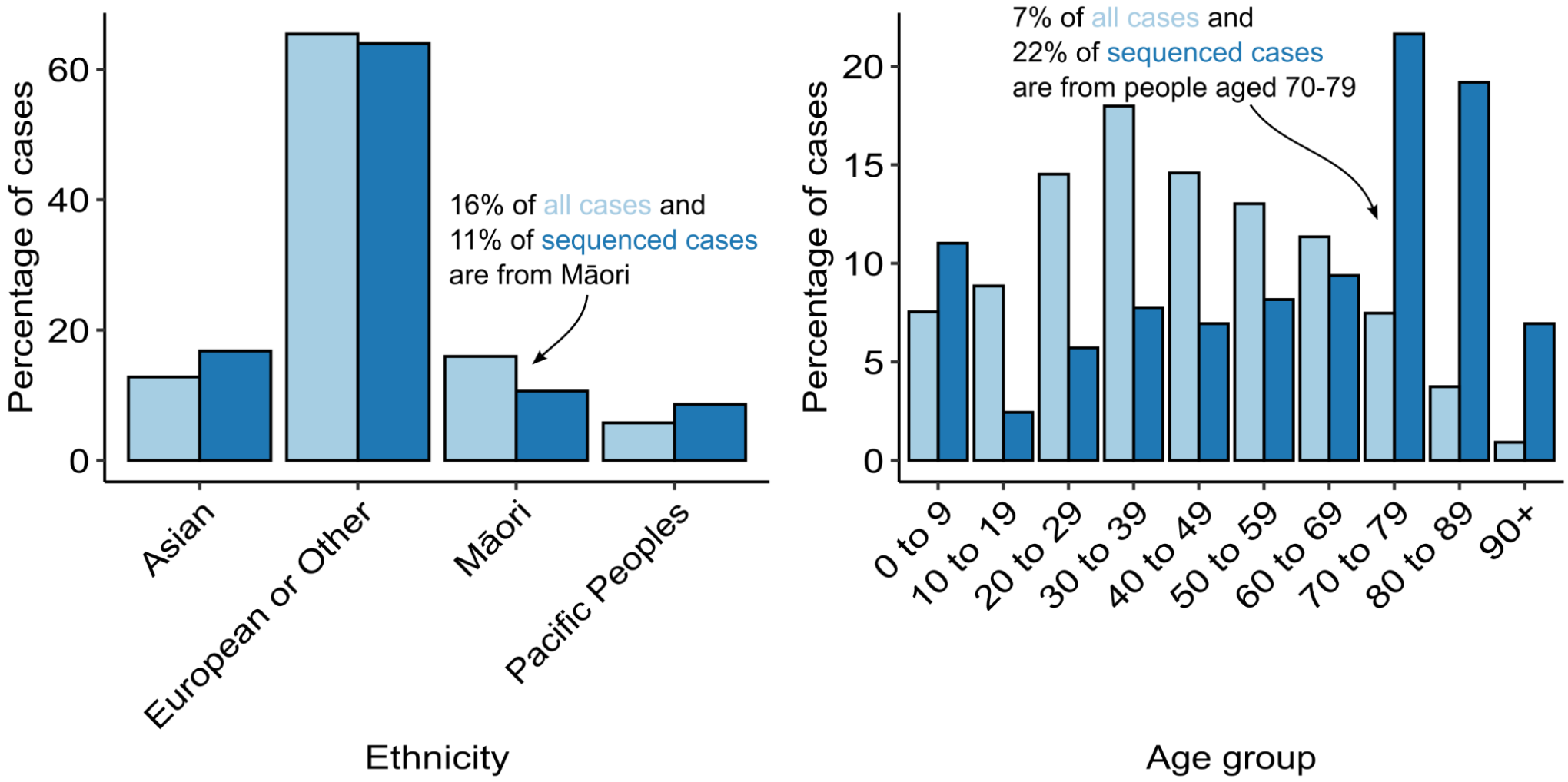


Figure 2: *(**Left**) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (**Right**) Comparison of age distribution across all reported cases (light blue) and sequenced cases (dark blue).*

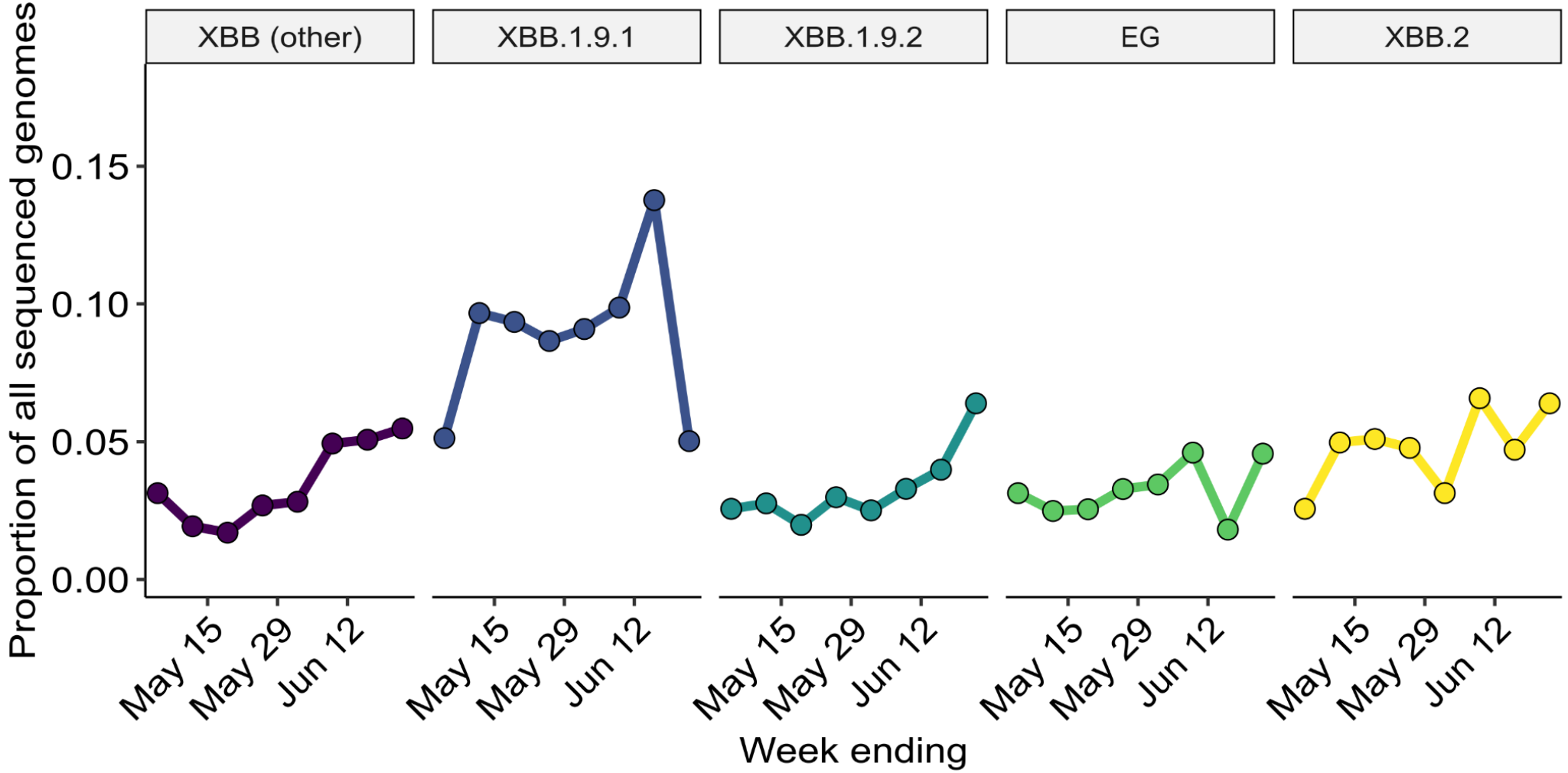


Figure 3: *Trajectory of specific sub-lineages included in the "XBB" category. Each subplot represents a lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week.*