2nd June 2023

COVID-19 Genomics Insights Dashboard (CGID) #38

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:

1022*

genomes from cases since the last report
(29th April to 26th May)

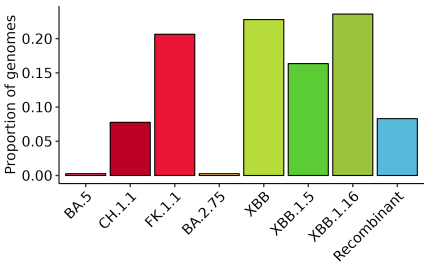
~6500

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.1.16 lineages have risen to 24% of sequenced cases, while FK.1.1 (a newly-designated CH.1.1 descendant) accounts for 20%, XBB.1.5 for 16%, and other XBB lineages make up 24%



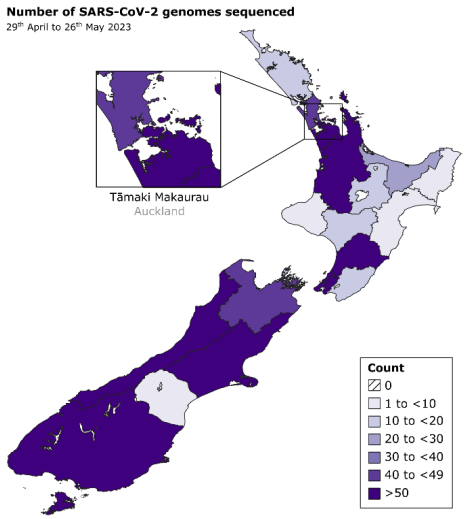
Hospital surveillance:

33% (118 of 358*) of PCR-positive cases with a hospital admission date from 13th to 26th May successfully produced a genome to date. Approximate composition of hospital cases:

<1% BA.2.75
<1% BA.5
3% CH.1.1
23% FK.1.1
30% XBB
14% XBB.1.15
27% XBB.1.16
3% Recombinant

*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:

- XBB.1.16 is now the dominant variant in Aotearoa New Zealand, representing 24% of cases, with a strong growth trajectory expected to continue
- Other tracked variants, such as FK.1.1 and XBB.1.5, remain in circulation
- Wastewater data for week 20 aligns with whole genome data. XBB lineage (including XBB.1.5 & XBB.1.16) accounts for approximately 67%, CH.1.1 lineage (including FK.1.1) represents around 30%, and minor contributions are observed from BA.2.75* (~2%) and BA.4/BA.5 (including BQ.1.1, ~1%)
- There is substantial bias in the age distribution of sequenced cases, which skews towards older individuals compared to the reported cases
- There is little to no evidence of a relationship between age and the frequency of the tracked variant

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

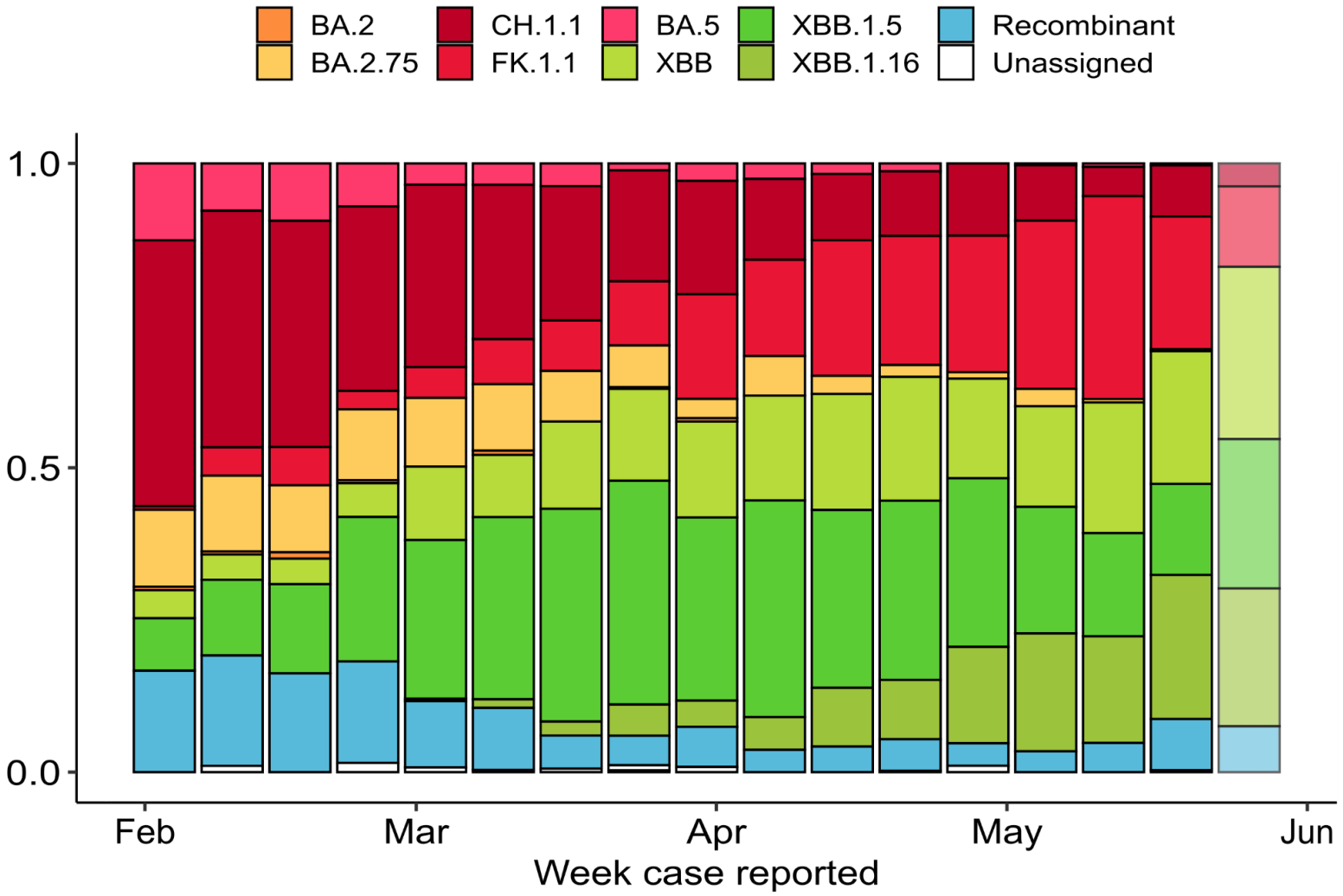


Figure 1: (A) Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing*. Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In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

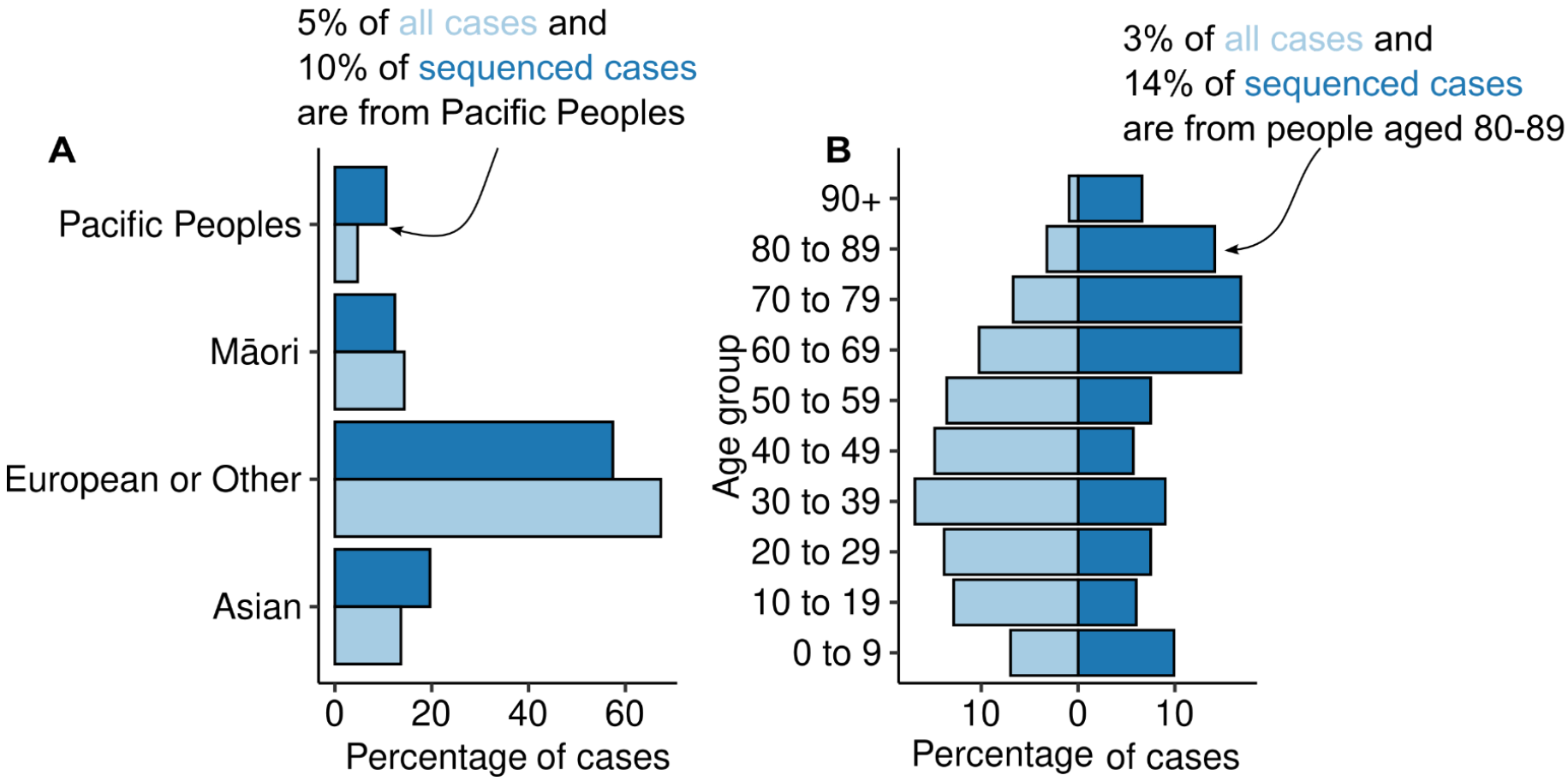


Figure 2: *(**A**) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (**B**) Comparison of age distribution across all reported cases (light blue) and sequenced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

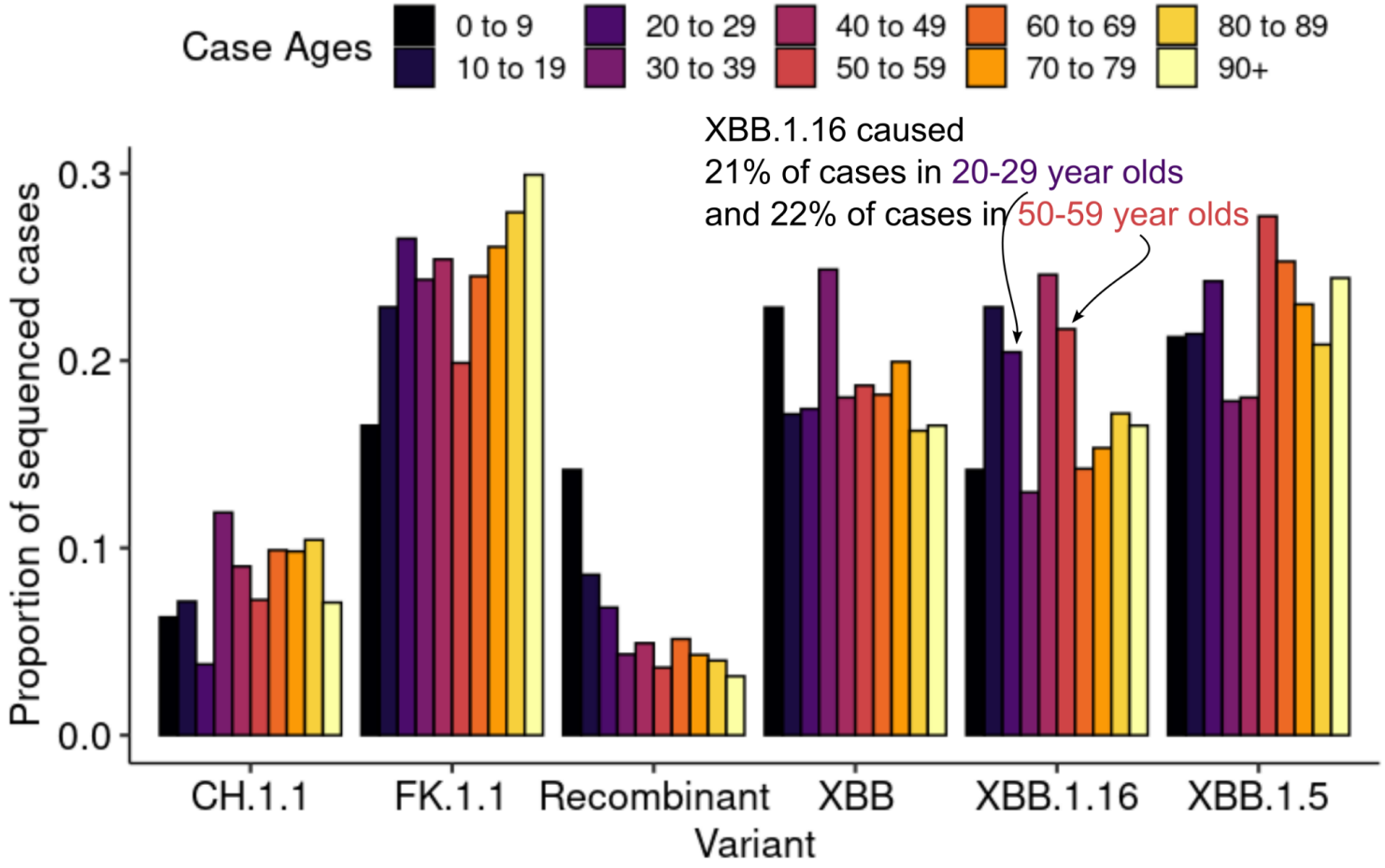


***Figure 3**: Proportion of sequenced cases caused by each of the most common tracked variants over the last six reporting weeks, broken down by age group.*