5th May 2023

COVID-19 Genomics Insights Dashboard (CGID) #37

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:

1058*

genomes from cases since the last report
(1th-28st April)

~5000

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 most prevalent lineages are XBB and CH.1.1 in the last two reporting weeks. Among their subtypes, XBB.1.5 is the most widespread (30% of sequences), followed by FK.1.1 (a newly-designated CH.1.1 descendant, at 22%) and XBB.1.16 (13%), which are also becoming more common
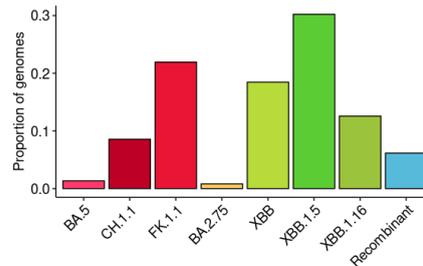
Hospital surveillance:

23% (90 of 397*) of PCR-positive cases with a hospital admission date from 15th - 28th April successfully produced a genome to date.

Composition of hospital cases:
- 2% BA.5
- 13% CH.1.1
- 32% FK.1.1
- 10% XBB
- 26% XBB.1.15
- 10% XBB.1.16
- 6% 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

Number of SARS-CoV-2 genomes sequenced
1st April to 28th April 2023

Tāmaki Makaurau
Auckland

Count
- 0
- 1 to <10
- 10 to <20
- 20 to <30
- 30 to <40
- 40 to <49
- >50
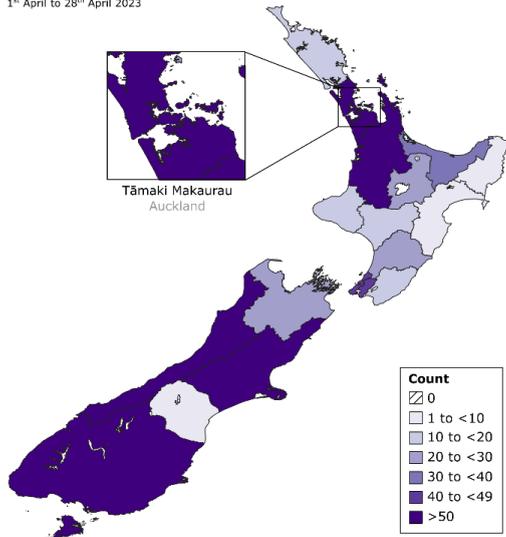
Key Trends & Insights:

- We are providing a more detailed classification of the sublineages that comprise the common COVID-19 variants, XBB and CH.1.1, which are well-established in Aotearoa New Zealand

- The FK.1.1 lineage is descended from CH.1.1 and the majority of early cases were detected in New Zealand

- Among the newly tracked COVID-19 variants, XBB.1.5 is the most prevalent, whereas FK.1.1 and XBB.1.16 are the ones experiencing the most rapid growth

- Wastewater analysis in week 16 confirms the prevalence of the XBB (includes XBB.1.5 & XBB.1.16, ~60%) and CH.1.1 (includes FK.1.1, ~31%) COVID-19 variants, with minor contributions from BA.2.75* (6%) and BA.4/BA.5 (3%). These findings are consistent with the whole genome data

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
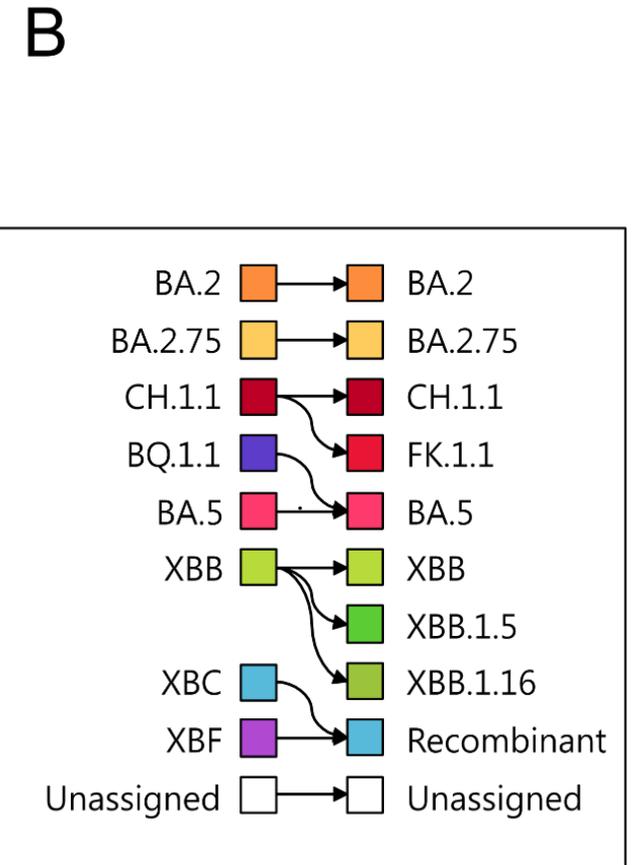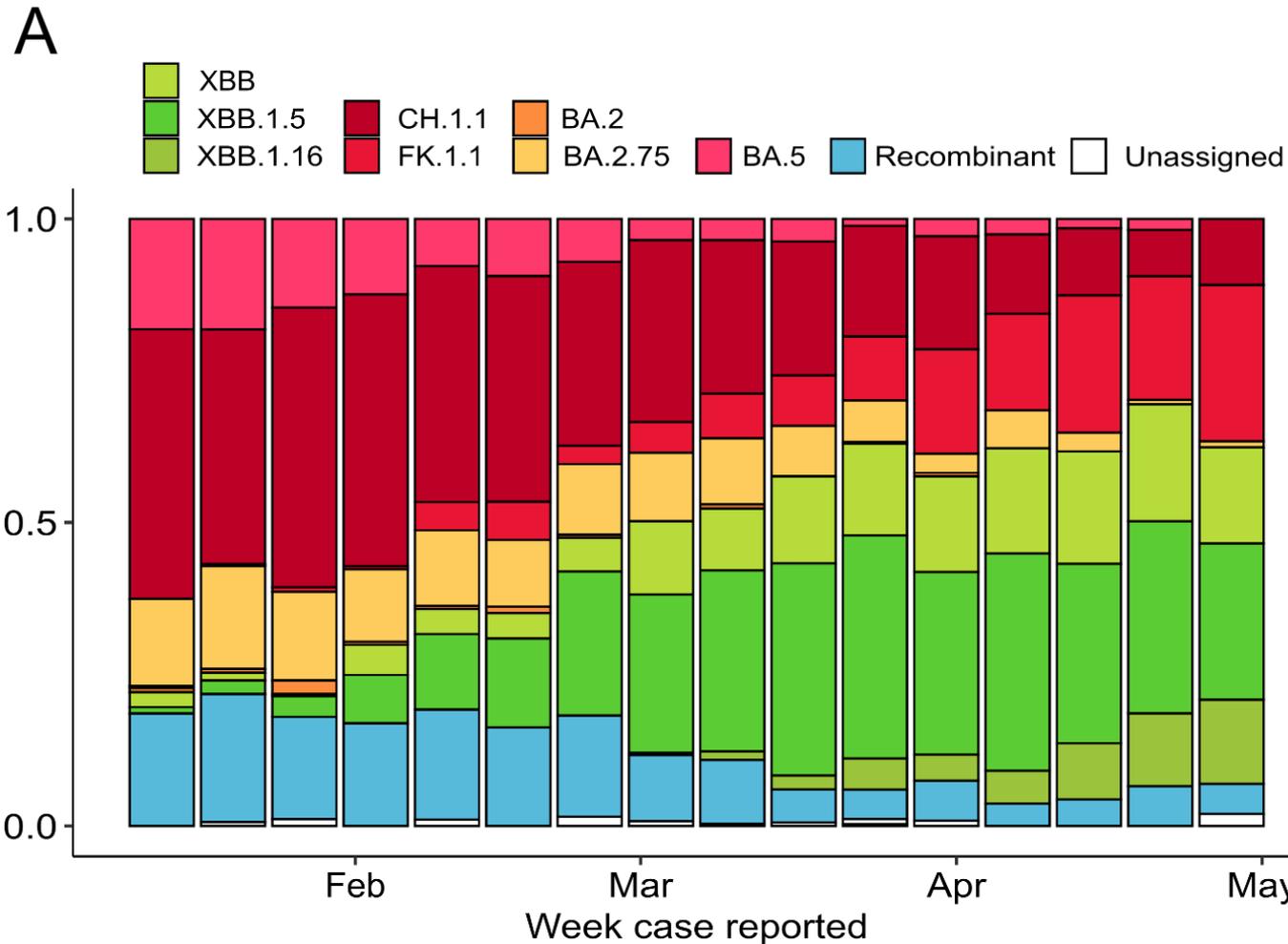
Figure 1: (A) Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. <u>Only variants with a frequency above 1% are shown</u>. Data is subject to change as samples will still be added to the most recent two-week period. In this case data 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**
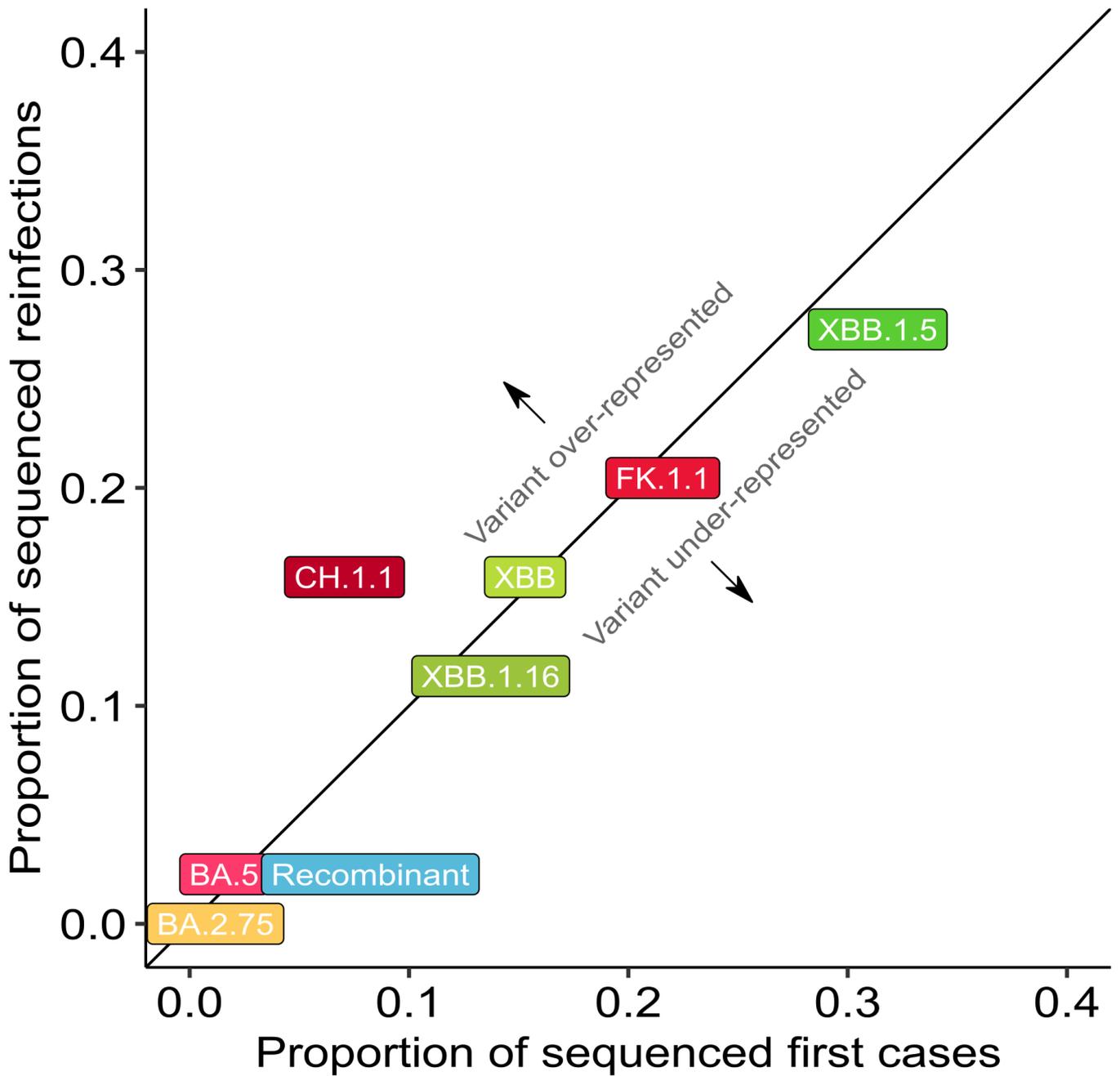
Figure 2: Representation of COVID-19 variants among reinfections and apparent first cases. *Each point represents a SARS-CoV-2 variant currently tracked by ESR. The position of points on the Y-axis represents the proportion of all sequenced reinfections associated with this variant, and the position on the x-axis represents the proportion of apparent first cases. Reinfections are defined as a positive COVID-19 test greater than 28 days following an initial positive test.*