6th October 2023

COVID-19 Genomics Insights Dashboard (CGID) #42

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:

607*

genomes from cases since the last report (8th September)

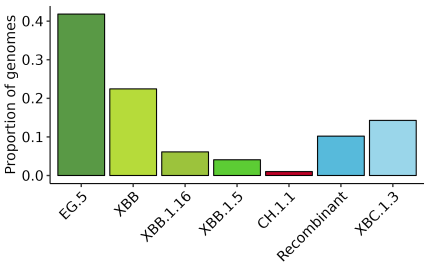
~10,000

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:

An XBB variant called EG.5 has been slowly growing in the past two weeks. EG.5 now makes up 41% of all cases we've looked at. The rest of the cases are primarily other XBB variants (33%), with a smaller portion being XBC.1.3 (14%) and other recombinants (10%)



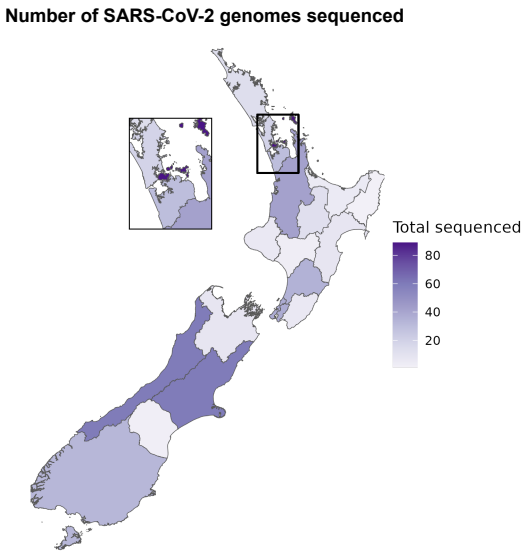
Hospital surveillance:

41% (77 of 186*) of PCR-positive cases with a hospital admission date from 15th -29th Sept successfully produced a genome to date. The approximate composition of hospital cases:

- EG.5: 46%
- XBB: 20%
- XBB.1.16: 13%
- XBC.1.3: 10%

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

Graphical overview showing sample origins



Key Trends & Insights:

- In Aotearoa, we found the BA.2.86 variant in our wastewater monitoring. However, as of September 29th, we haven't identified BA.2.86 in the clinical sequence data we've analysed
- WGS relies on PCR samples, and COVID-19 testing prioritises PCR for hospital and care cases. This means the cases sequenced aren't random, and they mostly involve older individuals
- EG.5 is the most common tracked variant, but its growth rate has slowed in the past few weeks. This could mean that other variants are becoming competitive with EG.5, or that EG.5 has reached its limit
- The top candidates to take EG.5's place right now are HK.3, which comes from EG.5, and FL.2 (XBB)
- Wastewater testing matches clinical samples, showing that EG.5 keeps growing. Only wastewater testing has found BA.2.86 variant, not clinical samples

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

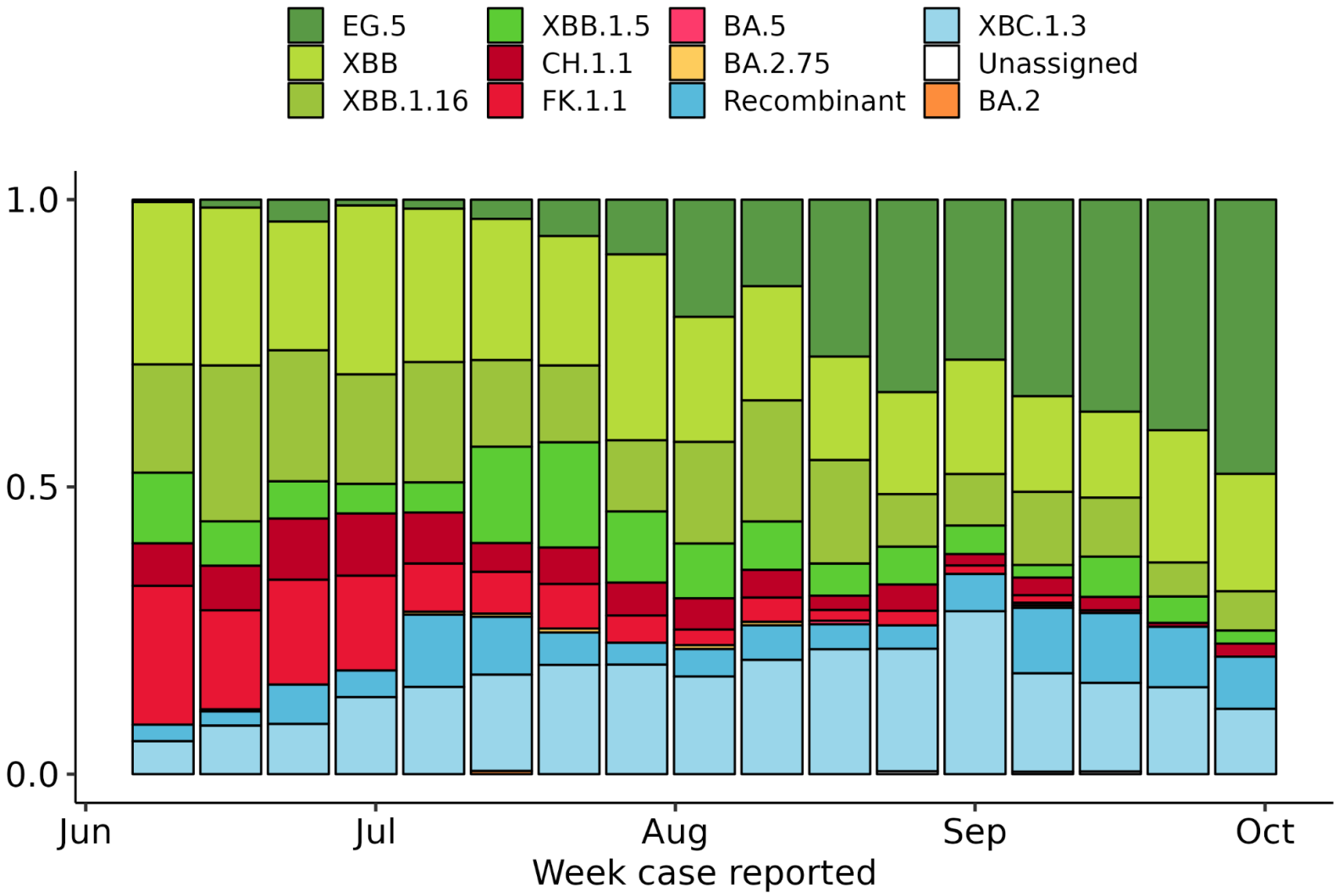


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. *Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In this case d*ata from the last reporting week is based on a limited number of genomes (44) 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].*

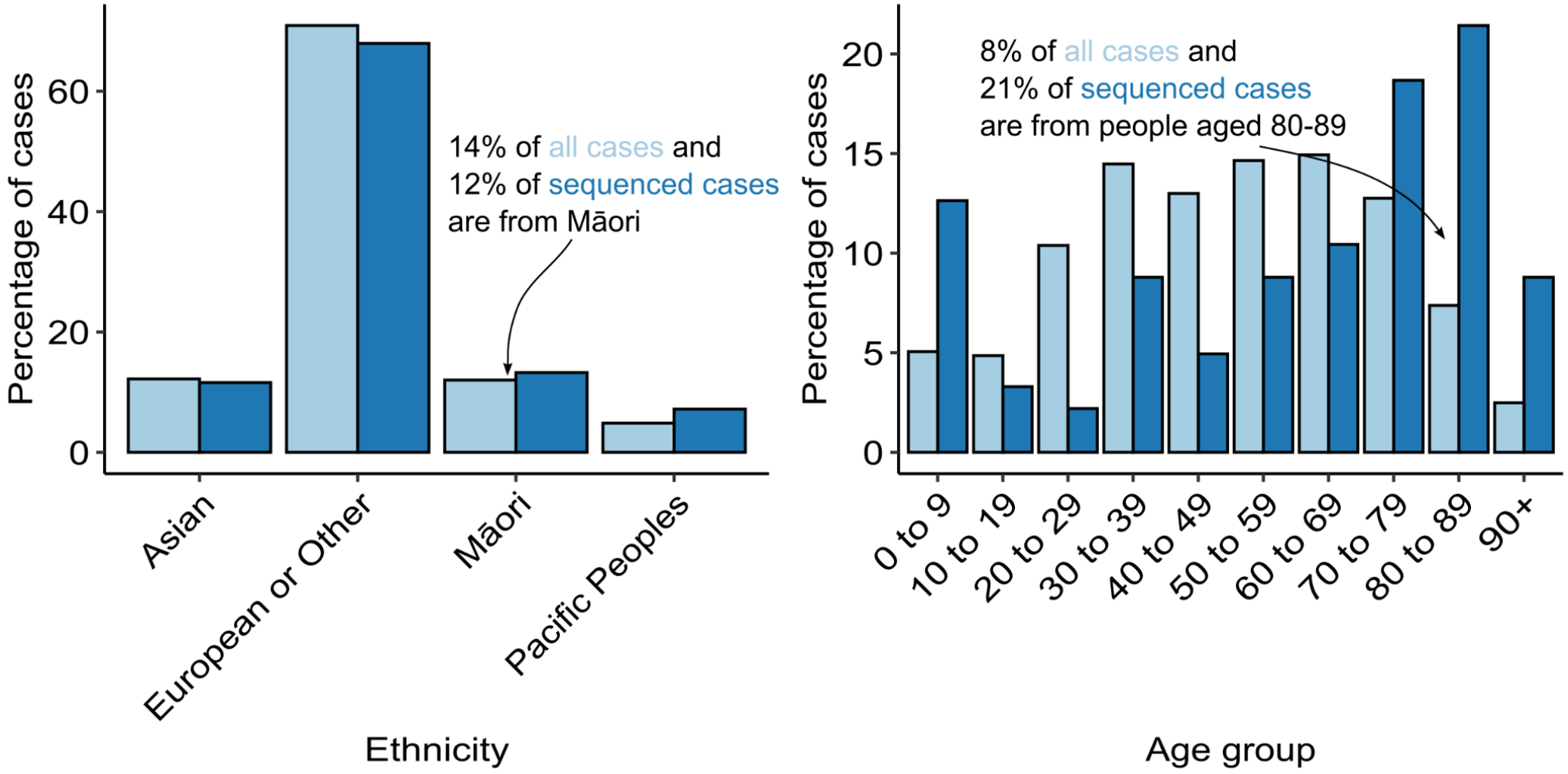


Figure 2: *(**Left**) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (**Right**) Comparison of age distribution across all reported cases (light blue) and sequenced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

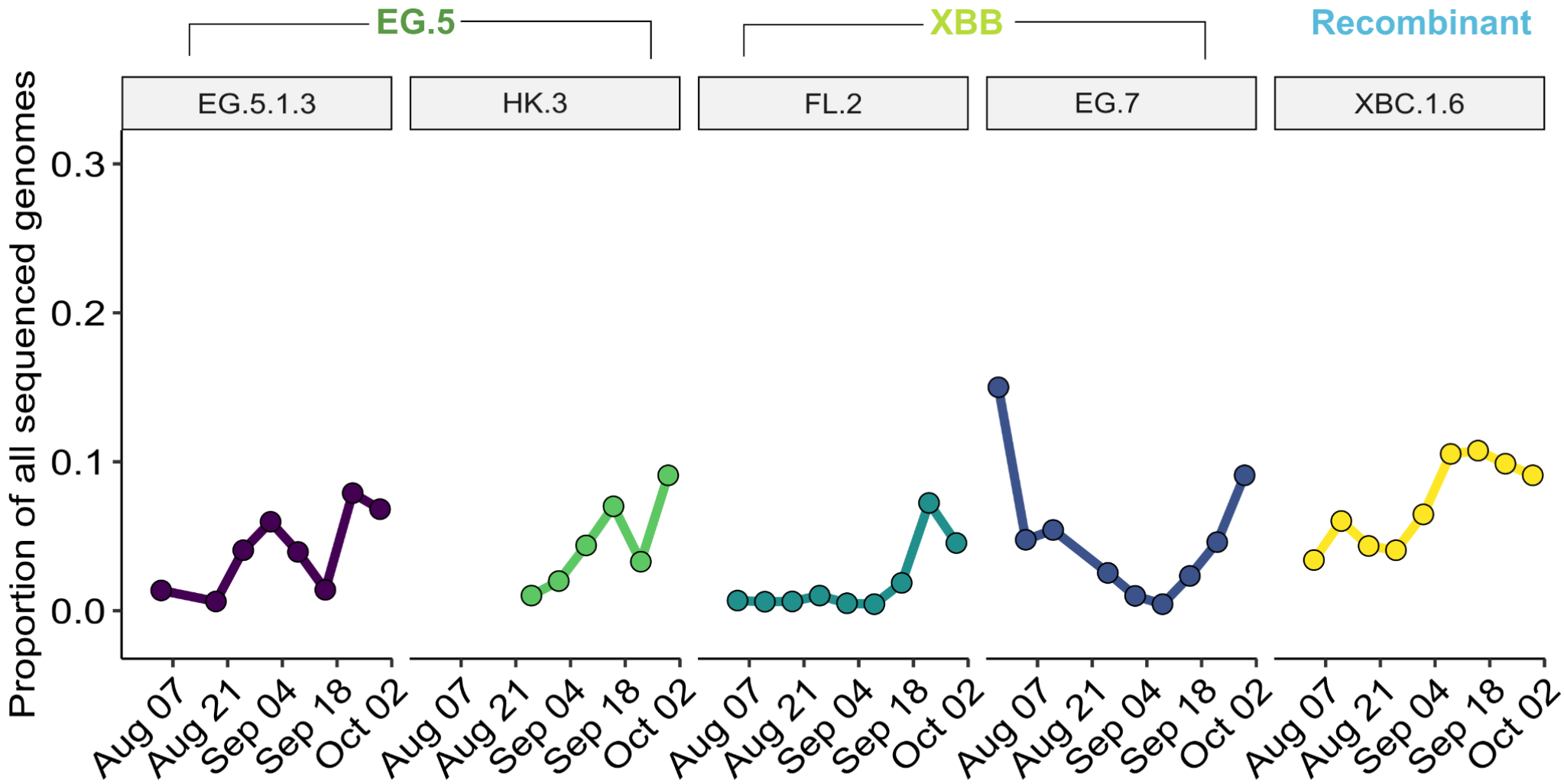


Figure 3: *The trajectory of specific sub-lineages. Each subplot represents a lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week.* The labels above the subplot describe which variant each lineage is reported under in Figure 1.