

COVID-19 Genomics Insights Dashboard (CGID) #40

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:

527*

genomes from cases since the last report (6th July)

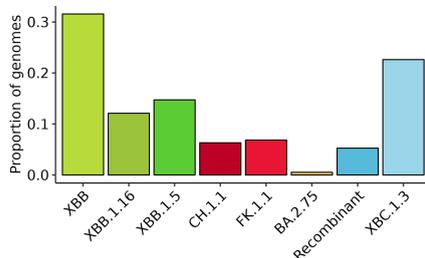
~8,500

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:

XBC.1.3 (previously part of the 'Recombinant' group in the CGI report) accounts for 24% of sequenced cases, showing growth. XBB family variants remain the most common at 59%



Hospital surveillance:

48% (70 of 146*) of

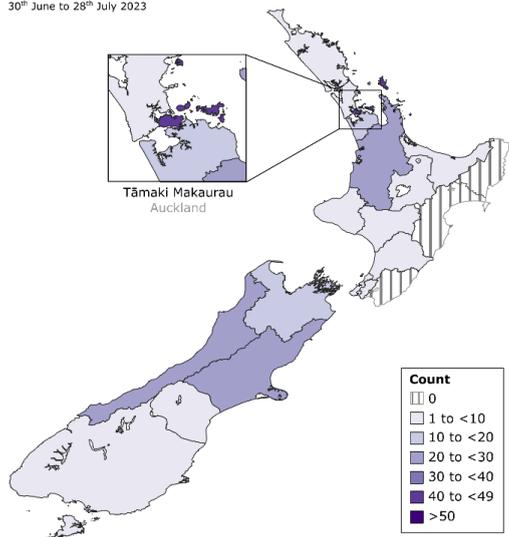
PCR-positive cases with a hospital admission date from 14th - 28th July successfully produced a genome to date. The approximate composition of hospital cases:

- XBB: 30%
- XBB.1.5: 10%
- XBB.1.16: 14%
- XBC.1.3: 26%
- Recombinant: 10%
- FK.1.1: 6%

*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
30th June to 28th July 2023



Key Trends & Insights:

- During this reporting period, the number of reported cases has consistently decreased
- As the total number of cases recorded decreased, the XBC variant has proportionally increased. We are now monitoring XBC.1.3 as well
- The World Health Organization recently labelled the EG.5 (XBB) sublineage as a "Variant Under Monitoring". EG.5 is currently found in Aotearoa New Zealand, and gradually increasing, but not at a rate that would cause a substantial surge in new cases
- Data from wastewater for weeks 25 to 28 align with clinical samples. The XBC variant is on the rise, estimated to be present in 10% to 25% of samples, while the XBB variant remains the most prevalent, found in 40% to 63% of 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

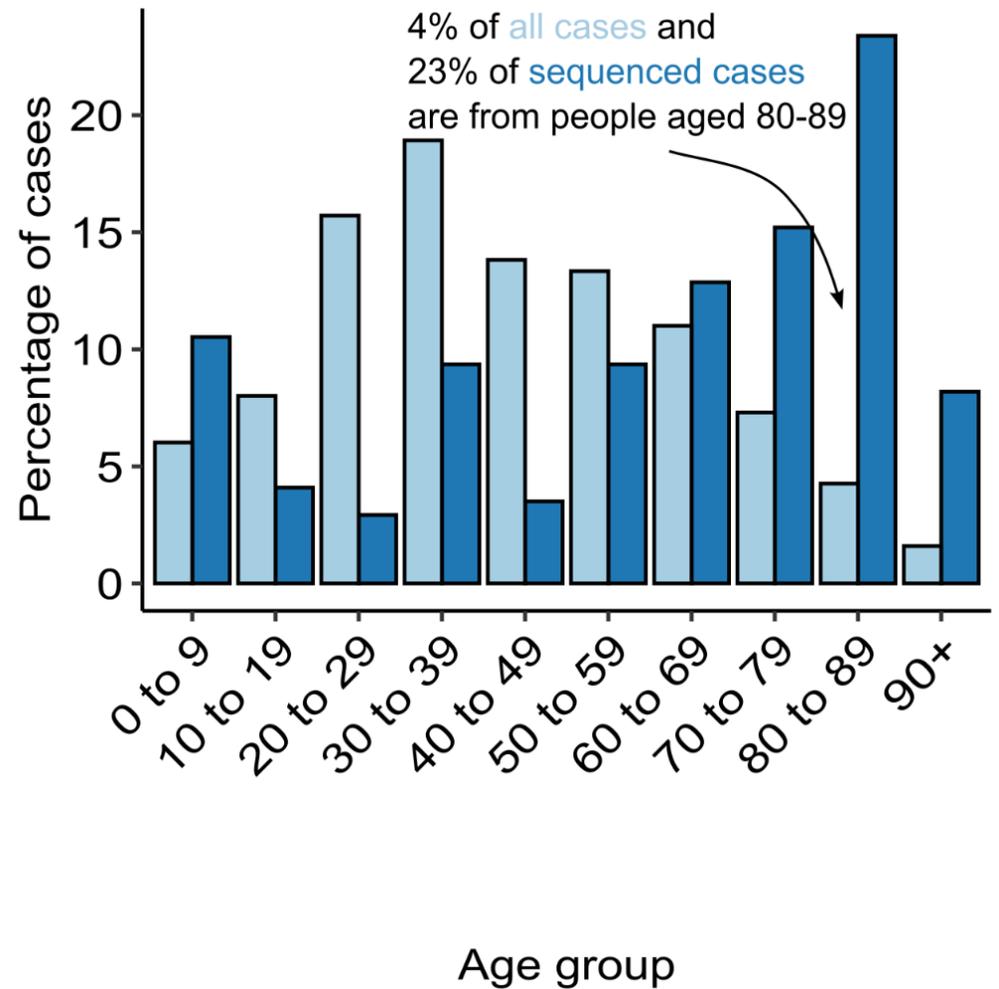
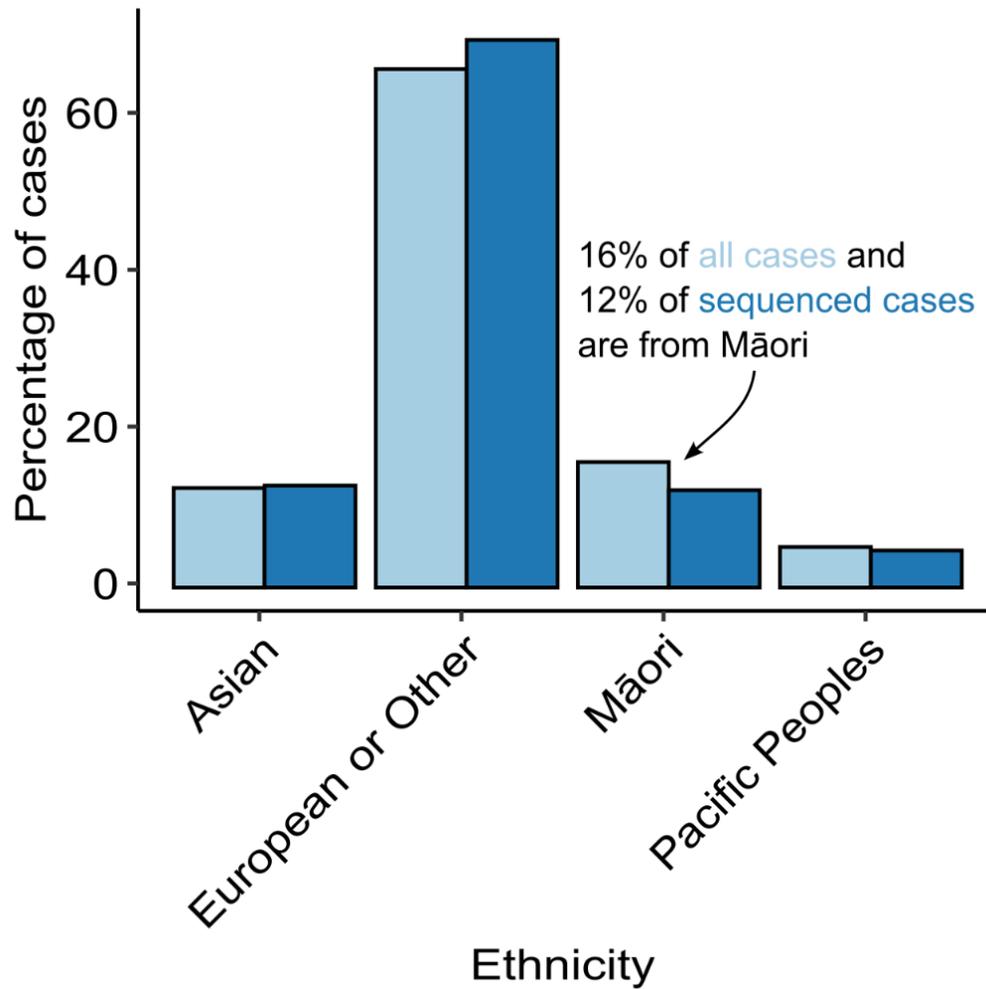


Figure 2: (Left) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (Right) Comparison of age distribution across all reported cases (light blue) and sequenced cases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

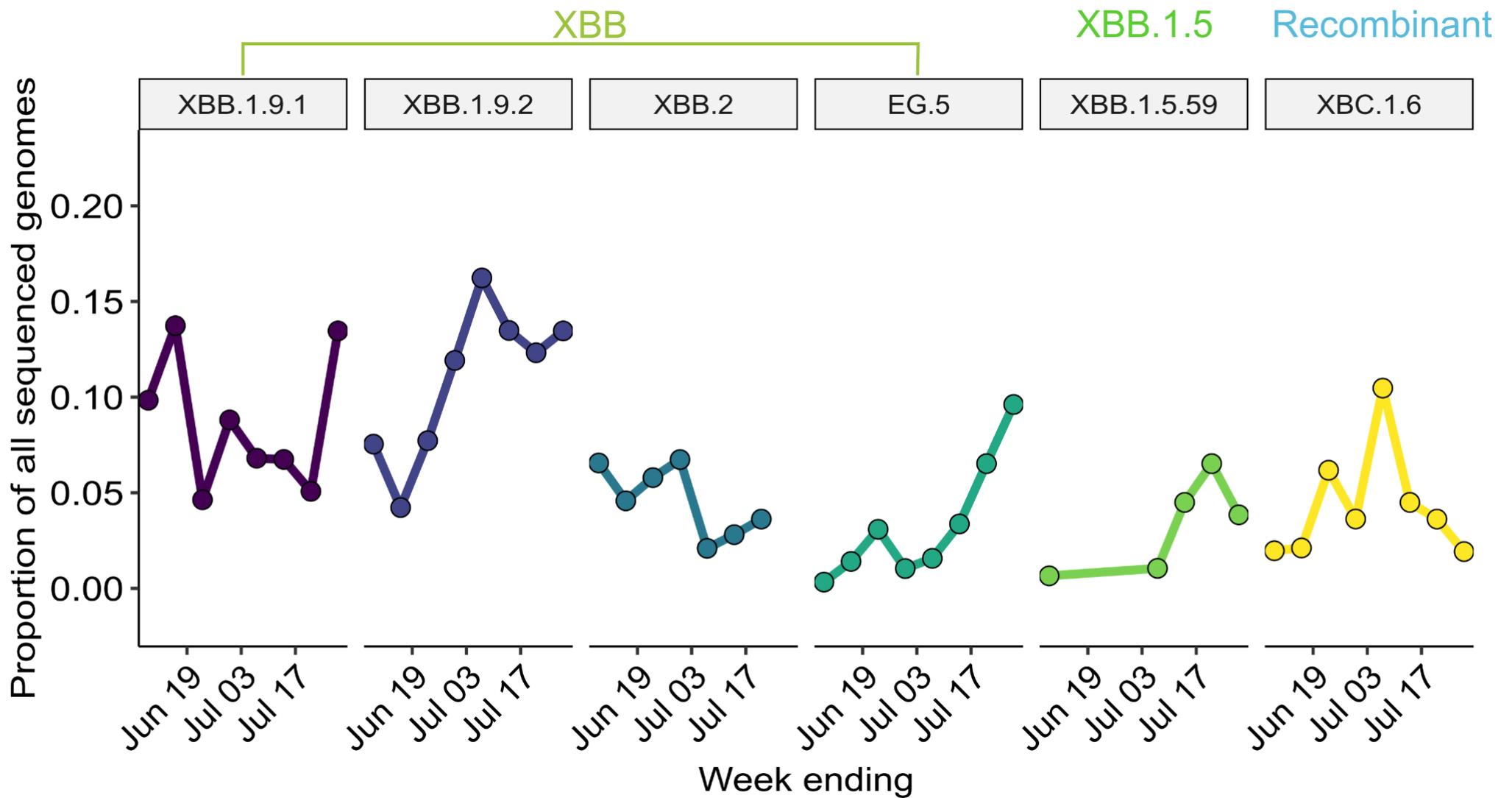


Figure 3: The trajectory of specific sub-lineages included in the “XBB” category. Each subplot represents a lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week.