

COVID-19 Genomics Insights Dashboard (CGID) #45

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:

1881*

genomes from cases since the last report (December 2024)

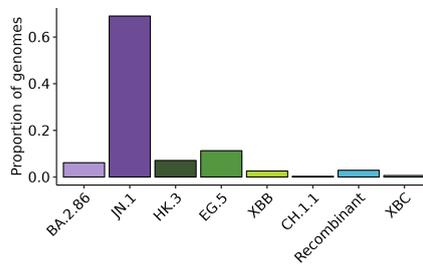
~1,000

genomes reported so far in 2024

* number of successful genomes. Sample no. processed is higher due to failed WGS attempts & cases sequenced multiple times

Variant surveillance:

JN.1 is now the main COVID-19 variant in New Zealand, comprising 68% of recent cases in the last two weeks, with other variants decreasing rapidly



Hospital surveillance:

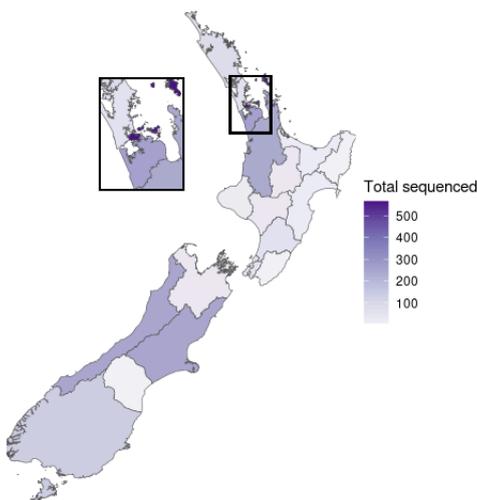
35% (110 of 308*) of PCR-positive cases with a hospital admission date from 12 to 26 Jan have successfully produced a genome to date. The approximate composition of hospital cases:

- JN.1: 72%
- EG.5: 9%
- HK.3: 8%
- BA.2.86: 6%
- All others: 5%

*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

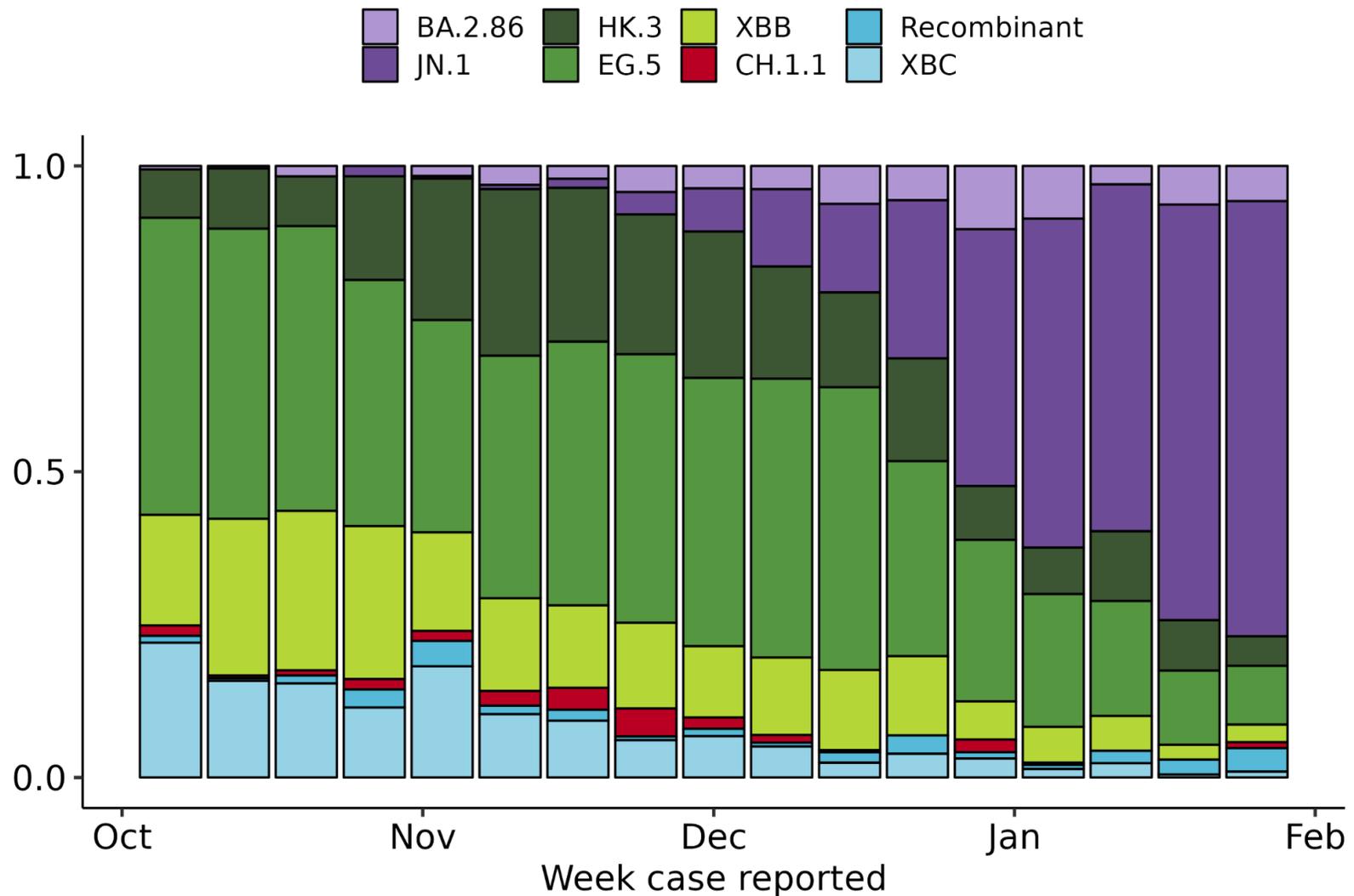
Number of SARS-CoV-2 genomes sequenced



Key Trends & Insights:

- JN.1 has risen rapidly and now makes up 68% of sequenced cases reported in the last two weeks.
- JN.1 is spreading more rapidly than the earlier dominant variants, suggesting the current prevalence could be higher than the reported 68%. We expect 85% of cases on 1st February to be caused by the JN.1 variant.
- JN.1 is now the most common variant, marking the first time since the winter of 2022 (BA.5 wave) that a single variant has quickly become dominant.
- No tracked variant has been able to keep pace with the rise in JN.1. At present, no specific descendant of JN.1 has a growth advantage over its parent.
- Wastewater analysis mirrors the whole genome sequencing results, with JN.1 rapidly replacing all tracked lineages.

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



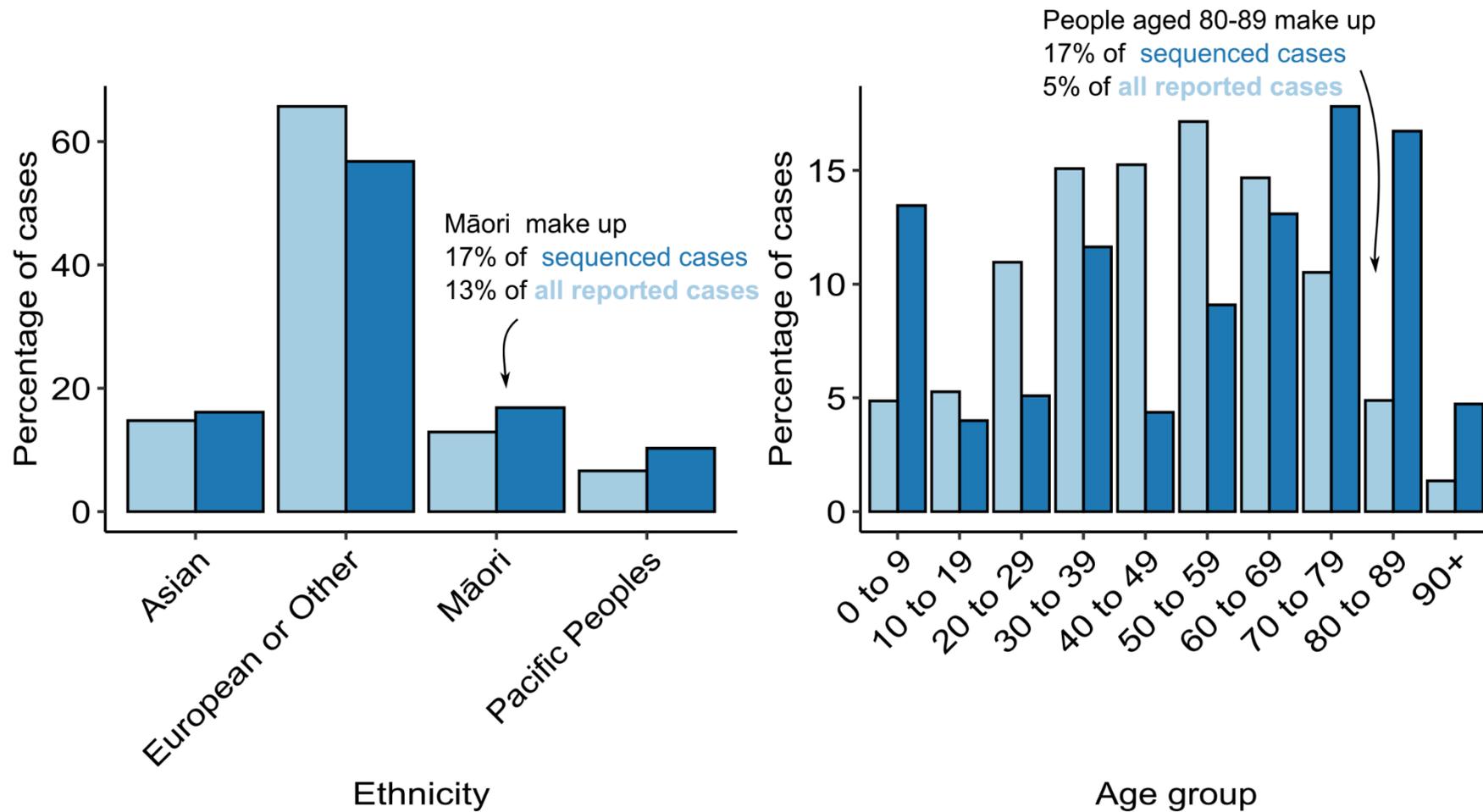


Figure 2: (Left) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (Right) Comparison of age distribution across all reported cases (light blue) and sequenced cases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

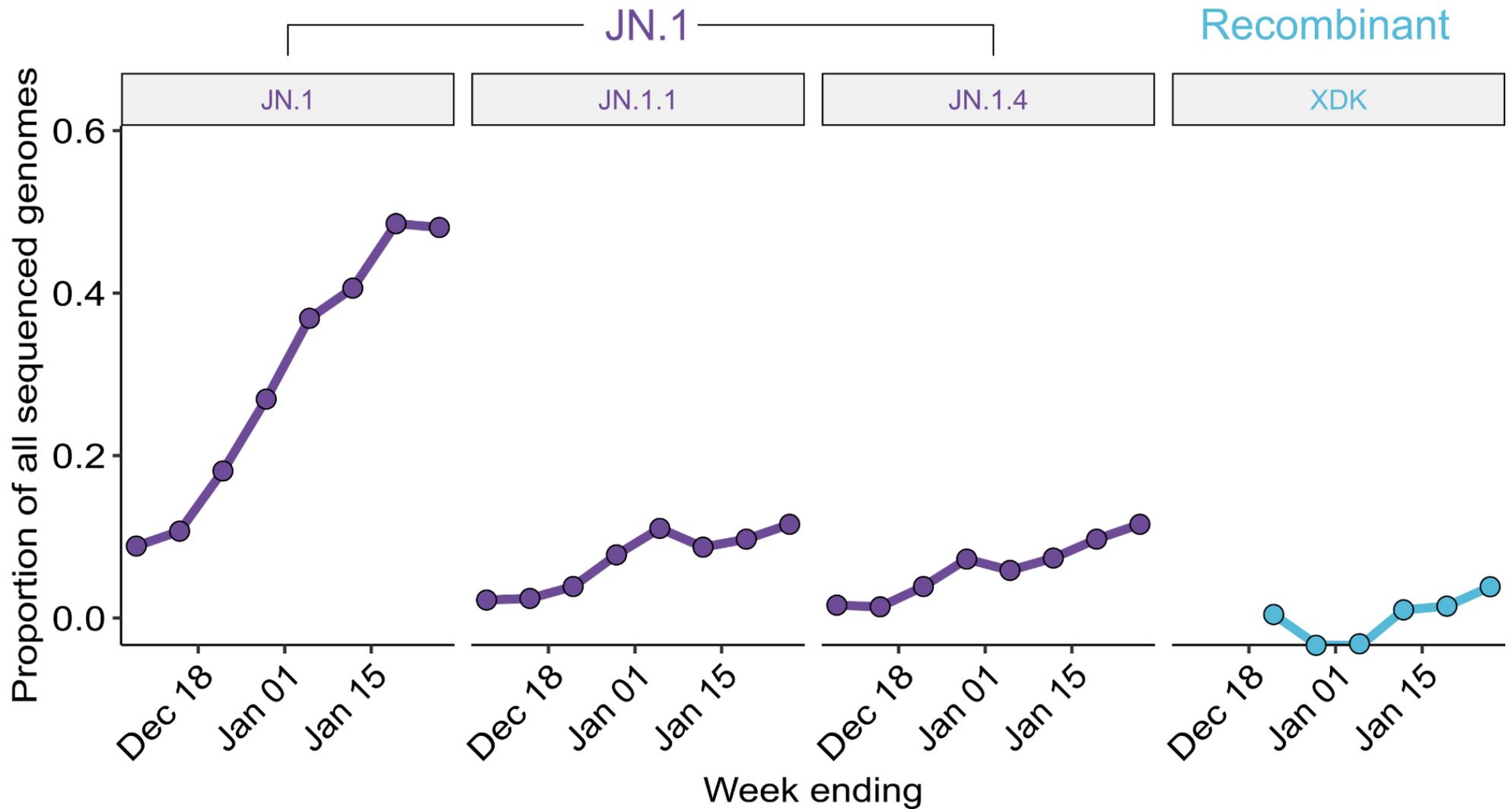


Figure 3: The trajectory of specific sub-lineages in recent weeks. Each subplot represents a single-tracked lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week. The labels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