16th December 2022

COVID-19 Genomics Insights Dashboard (CGID) #29

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 here in Aotearoa New Zealand, and abroad.

## Summary Infographics & Insights:

Genomes analysed:

888

genomes from cases reported within the past two weeks (26th Nov - 9th Dec)

~27,000

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) continues to decline in community samples, now making up only 35% of cases in the two-week reporting window. BA.2.75* (yellow) is set to become the dominant subvariant, making 33% of cases in the window and growing rapidly (up to 39% of cases in the last reporting week)
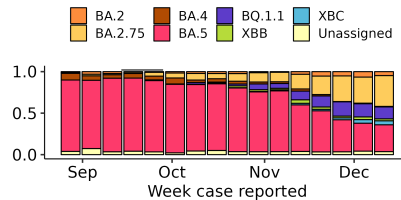

See the next page for the full-scale annotated figure

Hospital surveillance:

39% (208 of 540) of PCR-positive cases with a hospital admission date from 26th Nov - 9th Dec have successfully produced a genome. Composition of hospital cases:

- 3% BA.2
- 34% BA.2.75*
- 1% BA.4
- 38% BA.5
- 17% BQ.1.1
- 2% XBB
- 4% XBC
- 1% Unassigned

Graphical overview showing sample origins
(26th Nov to 9th Dec)

Num genomes from cases reported November 26 - December 9

50   150   250
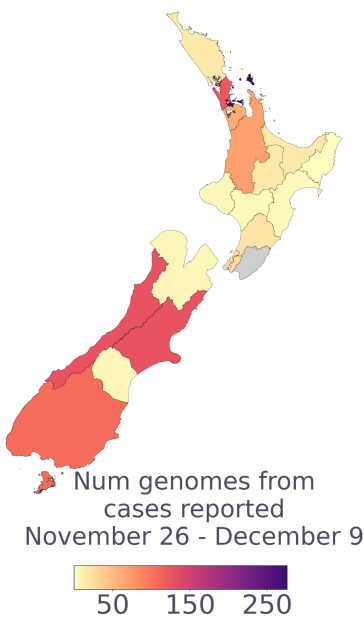
Key Trends & Insights:

- BA.5 continues to decline in frequency, making up 35% of cases in the two-week reporting window (the previous report was 49%).

- BA.2.75* continues to increase amongst the tracked lineages, making up 32% of cases.

- In the past fortnight, ~1.4% of all New Zealand COVID-19 cases were sequenced. There are, however, some locations with emerging variants where genomic surveillance is sub-optimal.

- BA.2.75* (~58%) and BA.4/5 (~19%) are the dominant variants in wastewater. Detections of BQ.1.1 (~18%), XBC (~3%), and XBB (~2%) were steady.

- The rise of BA.2.75 has been driven by specific descendants of the original BA.2.75 variant, notable CH.1.1 and BR.2*.

- Cases from the lower North Island are slightly under-represented this week due to technical problems at the ESR centre handling these samples. The problem has been fixed, and the backlog of samples has been processed, with results to be included in future reports.
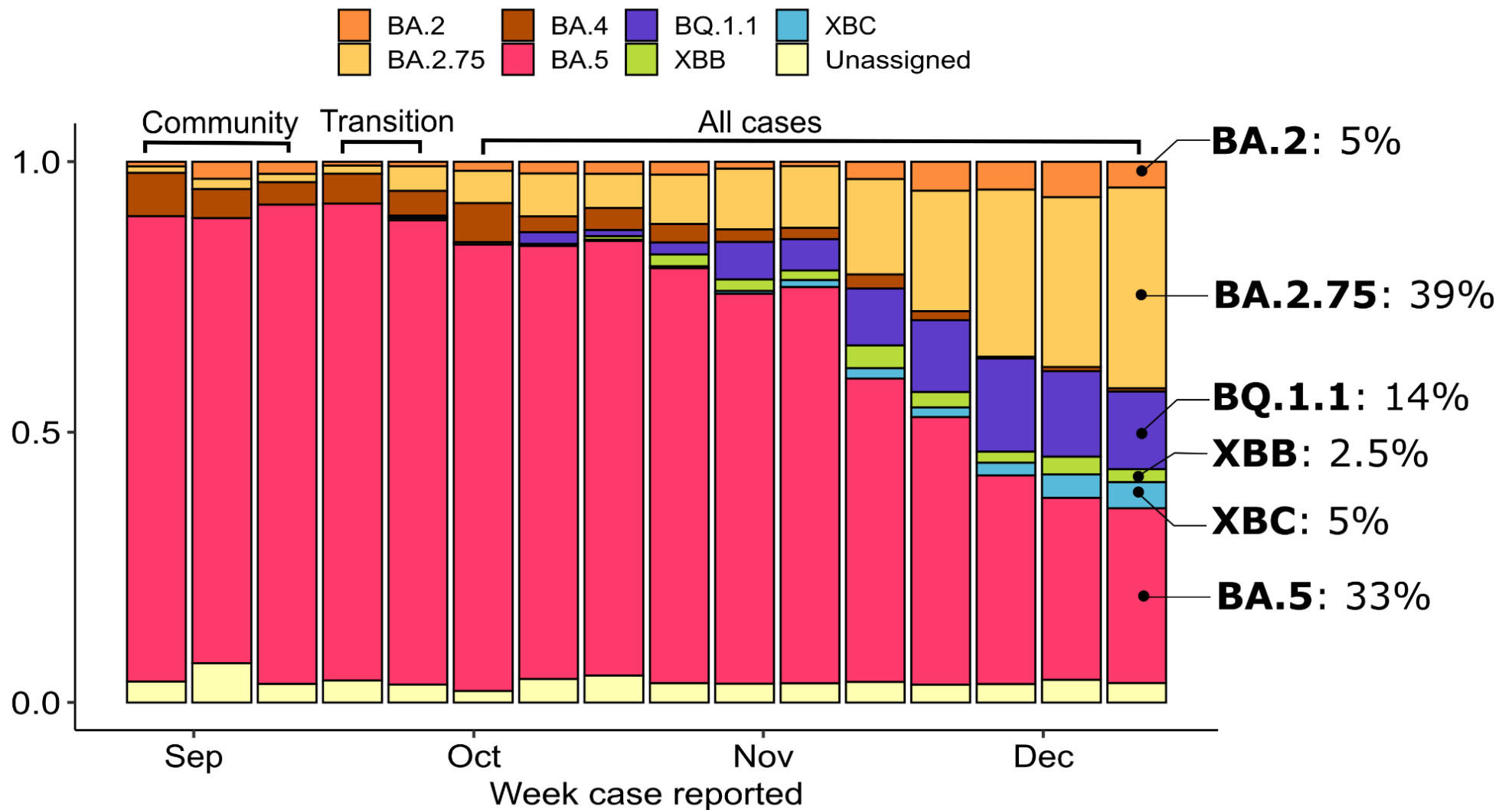
Figure: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. *Only variants with a frequency above 1% are shown*. Data is subject to change as samples may still be added to the most recent two-week period. [The category 'unassigned' is typically where a partial genome has been recovered, and a definitive assignment to a variant is not possible]. For weeks before the end of the COVID-19 Protection Framework, only data from community cases were used. In the period marked as "transition", cases known to be associated with the border are removed, but not all such cases can be reliably identified. Data from all New Zealand cases are used since October.
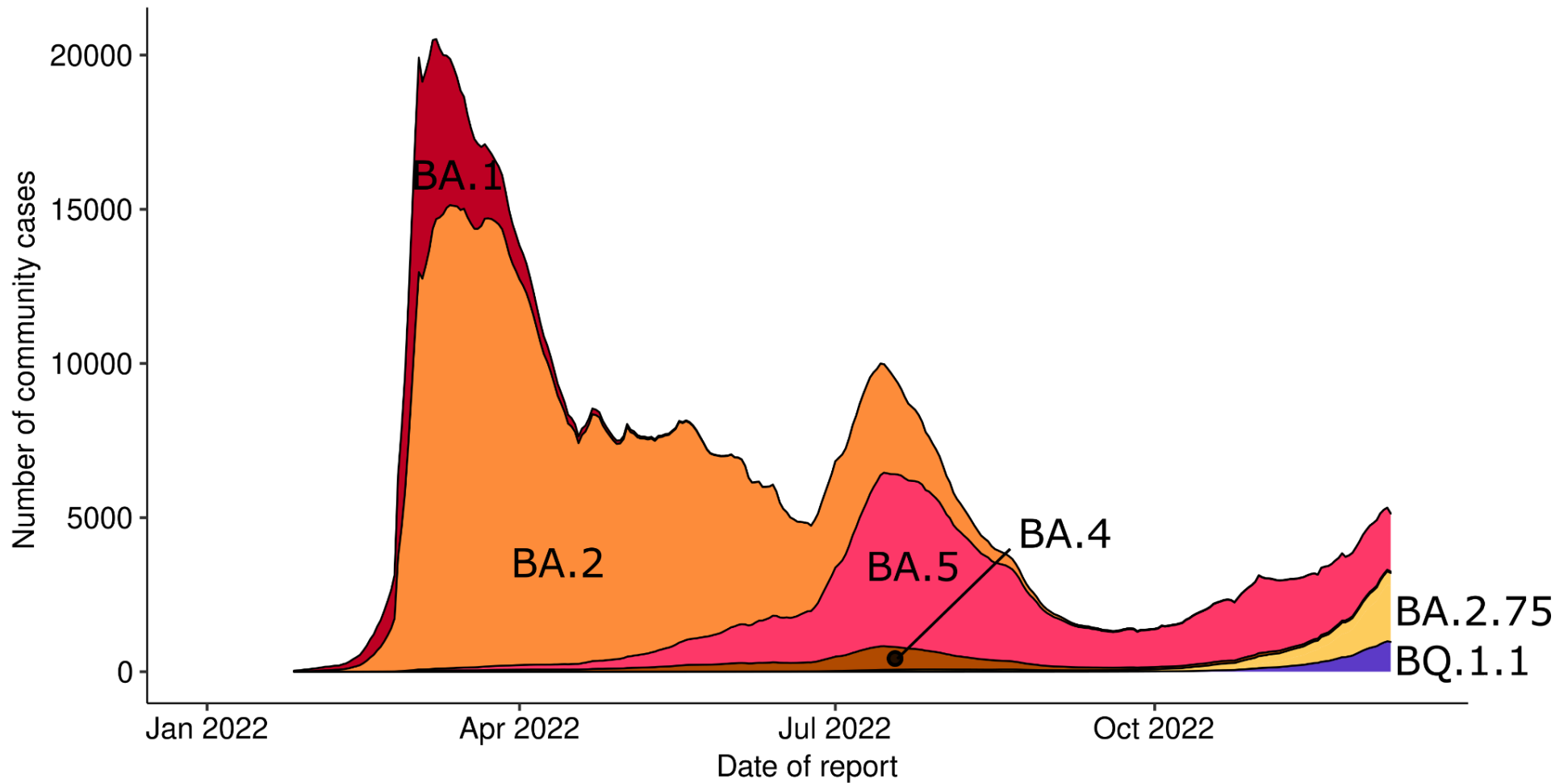
Figure: Omicron variant 'Infection history' of community cases across Aotearoa, New Zealand in 2022. *Estimates are calculated by projecting Omicron variant frequencies (as determined by WGS) onto the 7-day rolling average of cases (y-axis).*

Breakdown of BA.2.75 lineages

The growth of BA.2.75* in recent weeks is driven by several distinct descendants of the original BA.2.75 lineage, including CH.1.1, BN*, BR.2* (Figure). These fast-growing lineages mean BA.2.75 may quickly become the dominant subvariant in Aotearoa. However, at present, it is unclear if BQ.1.1, XBC or newly emerging lineages will be displaced or be able to co-circulate with BA.2.75.
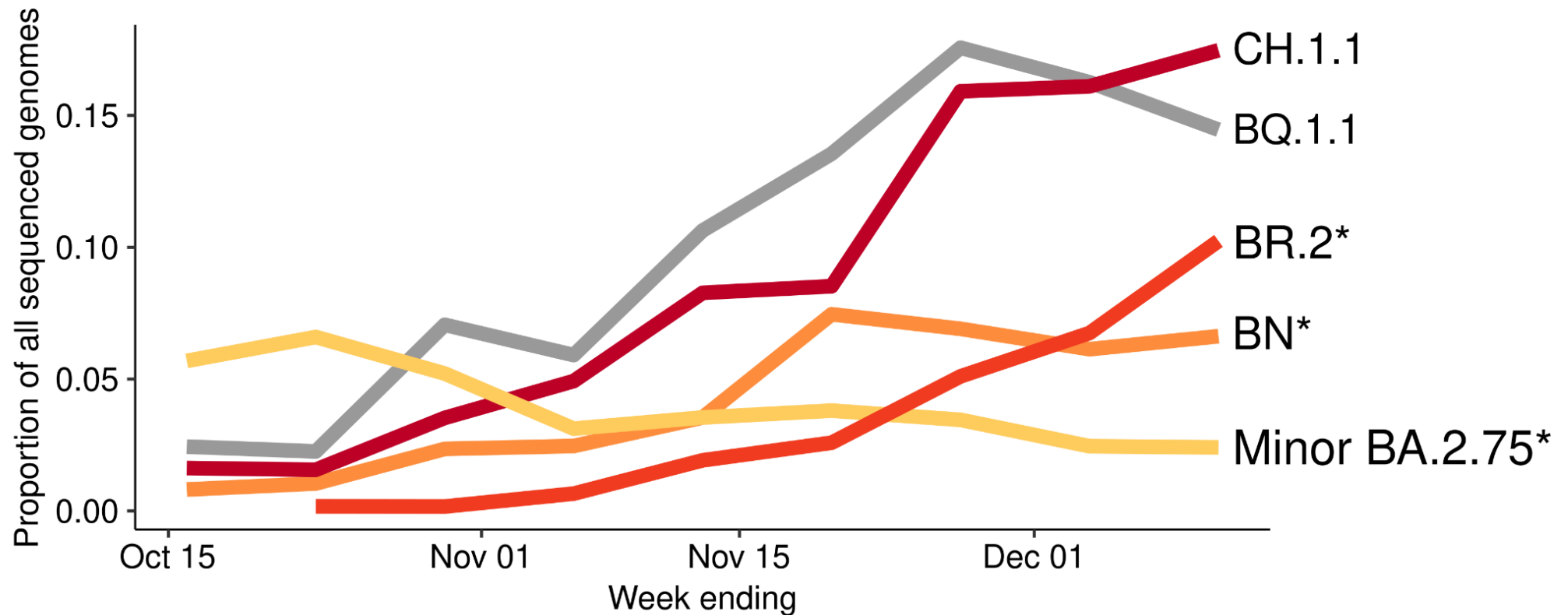

Figure: Frequency of specific BA.2.75 lineages in sequenced cases. *Data from the BQ.1.1 lineage (which is not included in BA.2.75) is presented to allow comparison between individual lineages and watchlist variants.*