

# COVID-19 Genomics Insights Dashboard (CGID) #28

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:

**933**

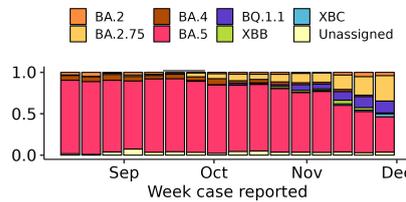
genomes from cases reported within the past two weeks (12<sup>th</sup> - 25<sup>th</sup> Nov)

**~26,000**

genomes reported so far in 2022

### Variant surveillance:

BA.5 (pink) continues to decline across Aotearoa, making up ~49% of cases in the last two-week reporting window. BA.2.75\* is the fastest growing variant, now making up ~25% of cases



See the next page for the full-scale annotated figure

### Hospital surveillance:

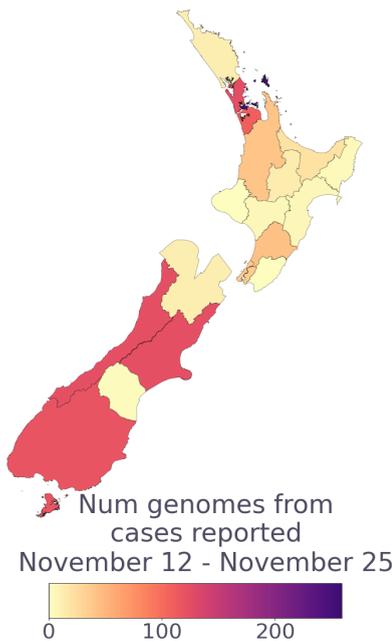
**51%** (202 of 393) of

PCR-positive cases with a hospital admission date from 12<sup>th</sup> - 25<sup>th</sup> Nov have successfully produced a genome.

Composition of hospital cases:

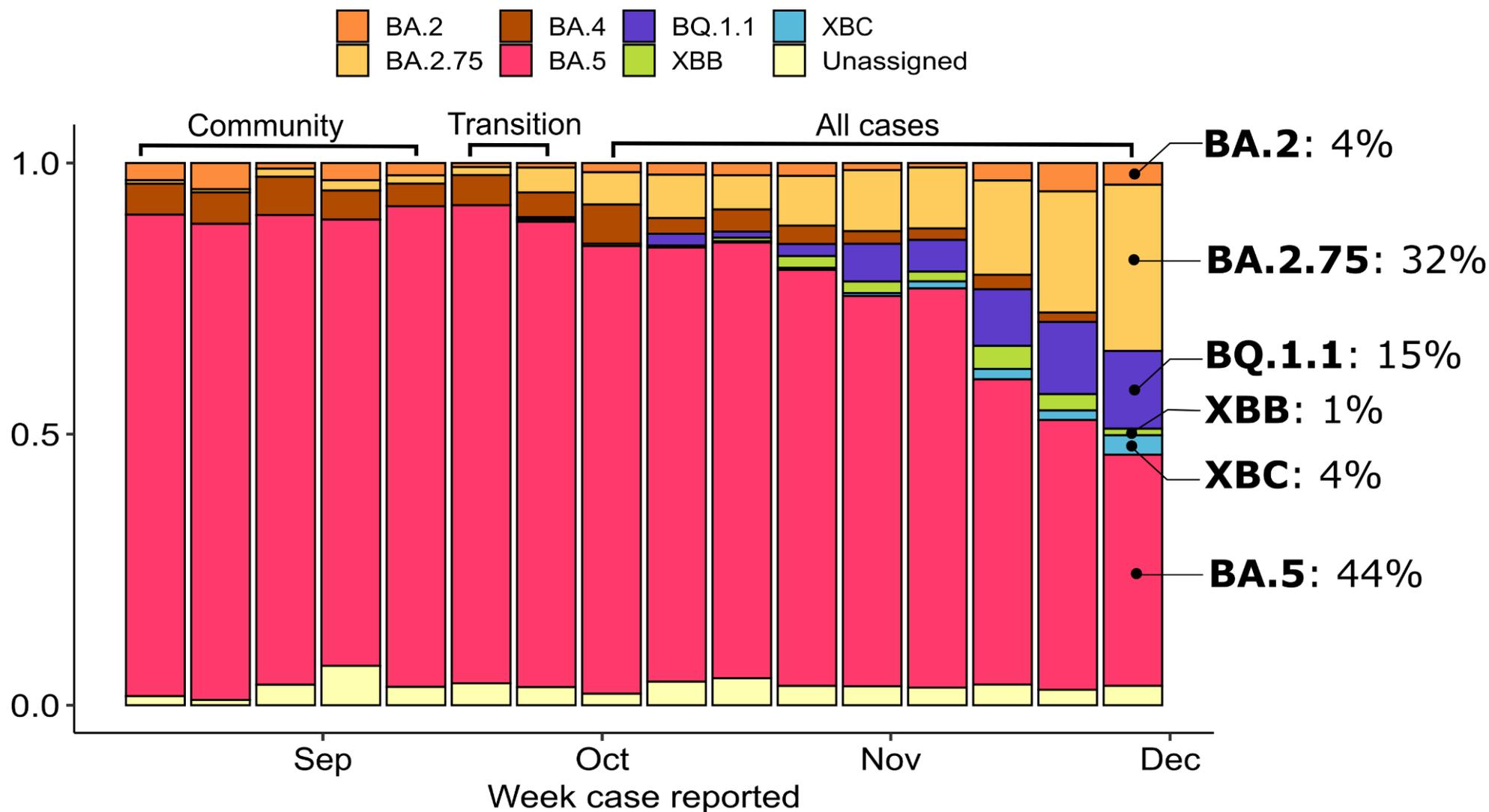
- 3% BA.2
- 22% BA.2.75\*
- <1% BA.4
- 59% BA.5
- 11% BQ.1.1
- 1% XBB
- 2% XBC

Graphical overview showing sample origins (12<sup>th</sup> - 25<sup>th</sup> Nov)



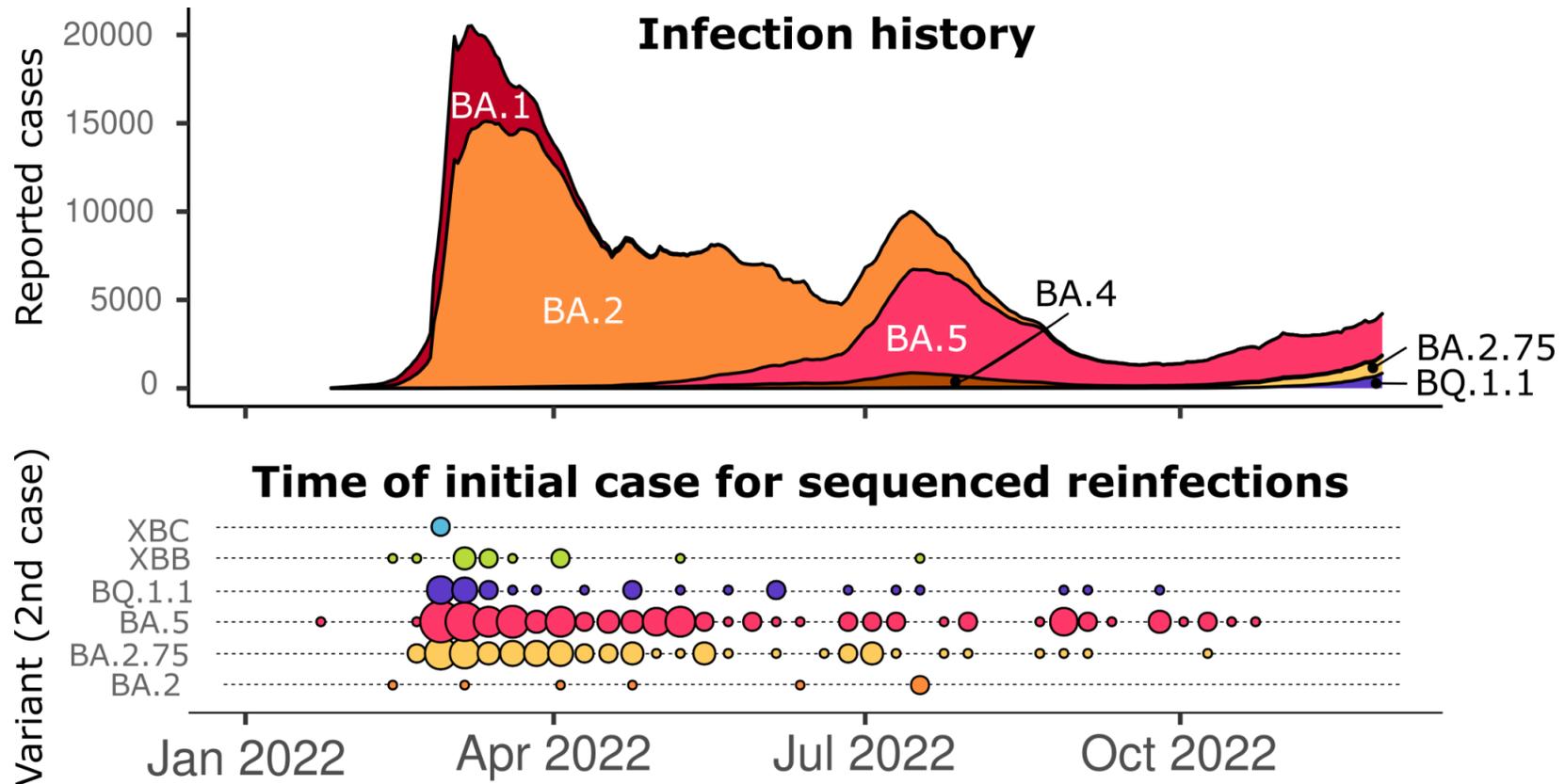
### Key Trends & Insights:

- BA.5 declines in frequency, making up only 49% of cases in the two-week reporting window.
- BA.2.75\* is the second most common of the tracked lineages, making up 25% of cases.
- In the past fortnight, ~1.9% of all New Zealand COVID-19 cases were sequenced. There are, however, some locations with emerging variants where genomic surveillance is sub-optimal.
- At least 11% of the genomes sequenced in this two-week reporting window are from reinfections (i.e., a new positive test more than 28 days following a previously reported COVID-19 case). Currently, there is no substantial difference in circulating variants concerning the time between infections.
- BA.4/5 (~40%) and BA.2.75\* (~39%), are the dominant variants in wastewater. Detections of BQ.1.1 (~12%) and XBB (~3%) were steady, and XBC (~7%) was detected for the first time.
- There remain challenges tracking the growth and locations of new Omicron variants such as BQ.1.1, XBB, and XBC due to the relatively low number of samples currently available for genomic surveillance.



**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.

Rates of reinfection in the community are increasing. As such, we want to understand better which variants are causing reinfection and whether the time between infections differs concerning the variant responsible for the second case. Genomic sequence data can help with this. Most people with reinfections sequenced in this reporting period had their initial case between February and June 2022. This was early in the Omicron wave when BA.2 and BA.1 were the dominant variants in Aotearoa. Although XBB and BA.2.75 are overrepresented among reinfections, there is no substantial difference in the time between infections.



**Figure:** Top panel; 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). Bottom panel; Timing of initial case for sequenced reinfections, broken down by variant responsible for reinfection. Circle size is proportional to the number of initial infections in reporting week that went on to become sequenced reinfections.