

COVID-19 Genomics Insights Dashboard (CGID) #24

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:

291

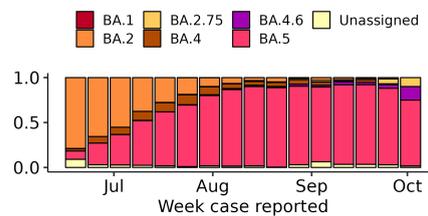
genomes from cases reported within the past two weeks (17th-30th Sept)

~22,000

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) continues to be the dominant Omicron variant across NZ, making up 75% of community cases in the last reporting week. Other variants continue to be detected at low levels. *See the next page for the annotated figure.*



Hospital surveillance:

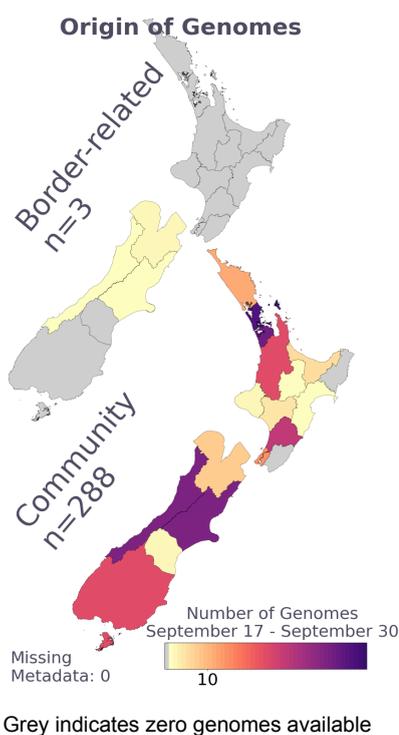
~31%

 (87 of 278)

of PCR positive cases with a hospital admission date from 17th-30th Sept have been genome sequenced. Approximate composition of hospital cases:

- 5% BA.2.75
- 1% BA.4
- 4% BA.4.6
- 90% BA.5
- 1% Unassigned

Graphical overview of sample acquisition (17th-30th Sept)



Key Trends & Insights:

- Omicron BA.5 remains the dominant variant and continues to make up the bulk of community cases. In the last reporting week, BA.5 was > 90% of all community cases
- Changes resulting from the end of the covid protection framework mean border-associated cases can no longer be differentiated from community samples
- As case numbers continue to fall across Aotearoa, recruiting samples for genomic surveillance is becoming more challenging
- We continue to monitor variants identified as having a potential growth advantage over BA.5. In this reporting week, we identify five BQ.1 and one XBB (recombinant) sample. No BQ.1.1 samples have been identified
- BA.4/5 remains the dominant variant in wastewater (aggregate 90%), though detections of BA.2.75 are increasing

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. 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].

