

COVID-19 Genomics Insights Dashboard (CGID) #21

The COVID-19 genomics insights dashboard (CGID) provides a public and high-level overview of viral genomic surveillance across Aotearoa. 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:

1,189

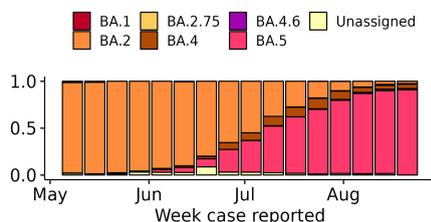
genomes from cases reported within the past two weeks (6th-19thAug)

~18,500

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) continues to be the dominant Omicron variant across NZ, making up >90% of community cases in the last reporting week. BA.2 (orange) is becoming rare, and now represents only 3% of cases. *See next page for annotated figure.*



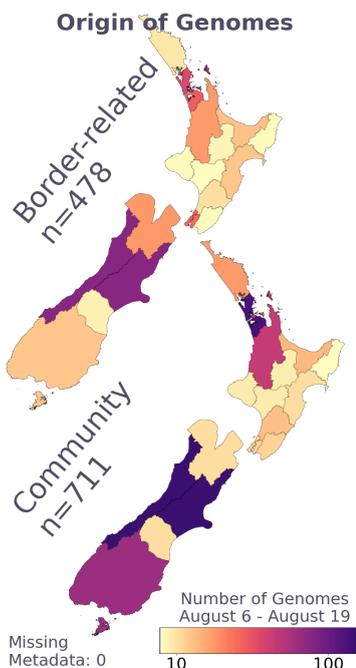
Hospital surveillance:

~25% (145 of 570)

of PCR positive cases with a hospital admission date in the past fortnight (6th-19thAug) have been genome sequenced. Composition of hospital cases:

- 4% BA.2
- <1% BA.2.75
- 9% BA.4
- 86% BA.5

Graphical overview of sample acquisition (6th-19thAug)



Key Trends & Insights

- There is good temporal and spatial coverage within our genomic surveillance system: ~1.2% of all community cases and ~20% of border-related cases are sequenced.
- Omicron BA.5 remains the dominant variant and continues to make up the bulk of cases (community & border). In the last reporting week BA.5 was > 90% of all community cases.
- We continue to monitor a relatively small number of Omicron BA.2.75 (6 cases) and BA.4.6 (10 cases) that are detected within the community. We frequently see BA.4.6 at the border but it seemingly fails to gain traction within the NZ community.
- BA.4/5 was detected at all wastewater sentinel sites. Estimated BA.4/5 levels are at >98% - 16 of the 20 sentinel sites were 100% BA.4/5.
- Variants detected at the border (dominated by BA.5.2) are consistent with international surveillance and trends.
- In this reporting window ~5% of BA.5 cases detected in the community were suspected reinfections

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.

Top: 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.] **Bottom:** The Omicron variant 'infection history' of Aotearoa New Zealand. Indicative percentage of SARS-CoV-2 variants and estimated number of cases for all major Omicron subvariants (see embedded table) across the country in 2022. The proportion of each variant is overlaid on the cumulative 2022 community case numbers as reported by MoH. Note; biases in samples referred for genomic sequencing and case underreporting will be reflected in these projections, accordingly they should be regarded as indicative

