

COVID-19 Genomics Insights Dashboard (CGID) #19

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:

1,593

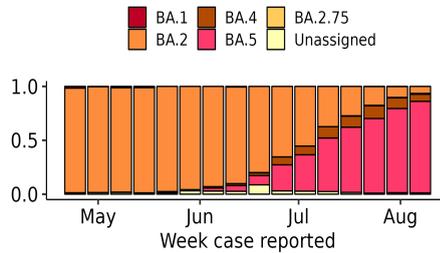
genomes from cases reported within the past two weeks (23rd Jul - 5th Aug)

~17,000

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) continues to be the dominant Omicron variant across NZ, making up 86% of community cases in the last reporting week. BA.4 (brown) is now even with BA.2 (orange) at 7%. *See next page for annotated figure.*



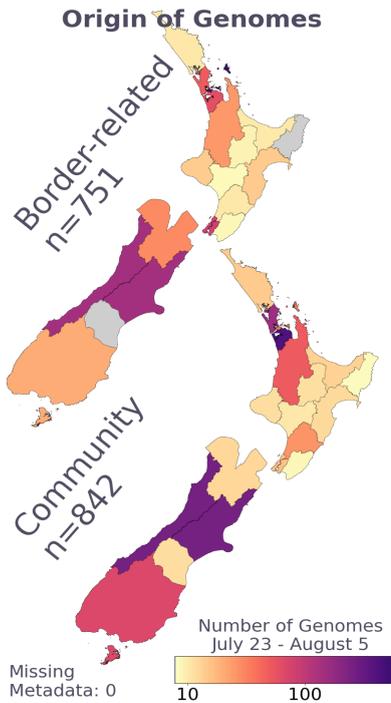
Hospital surveillance:

~30% (193 of 655)

of PCR positive cases with a hospital admission date in the past fortnight (23rd Jul - 5th Aug) have been genome sequenced. Composition of hospital cases:

- 13% BA.2
- 6% BA.4
- 81% BA.5

Graphical overview of sample acquisition (23rd Jul - 5th Aug)



Key Trends & Insights

- The Omicron BA.5 variant continues to increase in prevalence. In the last reporting week it was ~86% of all sequenced cases. The BA.5.2 subvariants (e.g. BA.5.2.1) now make up >50% of all community cases
- A small number of Omicron BA.2.75 variants continue to be detected in the community (n=4), this week we began monitoring the spread of BA.4.6 which is trending up globally.
- BA.4/5 was detected at all wastewater sentinel sites. Estimated BA.4/5 levels are at 93% (up from 90% last week)
- Based on genomic surveillance, coupled with the ~1.62 million total cases reported so far in 2022, we estimate Aotearoa has seen ~280,000 cases with BA.4 or BA.5. This number should be considered a lower bound and is subject to sampling error and under reporting of cases.
- In this reporting window ~3.7% of BA.5 cases detected in the community were reinfections (i.e. a registered case >28 days prior).

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:** In collaboration with [Wilderlab](#), ESR generated SARS-CoV-2 variant data from a set of 21 nationwide sentinel sites in Week 31: ending 7th August. Note: (i) The level of precision and sensitivity in the percentage estimates can be uncertain. (ii) The 'Auckland Combined' site is missing this week.

