

COVID-19 Genomics Insights Dashboard (CGID) #17

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:

1,221*

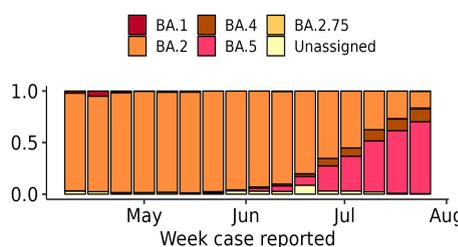
genomes from cases reported within the past two weeks (9th-22nd July)

~14,500*

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) is firmly established as the dominant Omicron lineage across NZ community samples, (~70%) of cases in the last week. BA.4 static at ~10%. See *next page for annotated figure*.



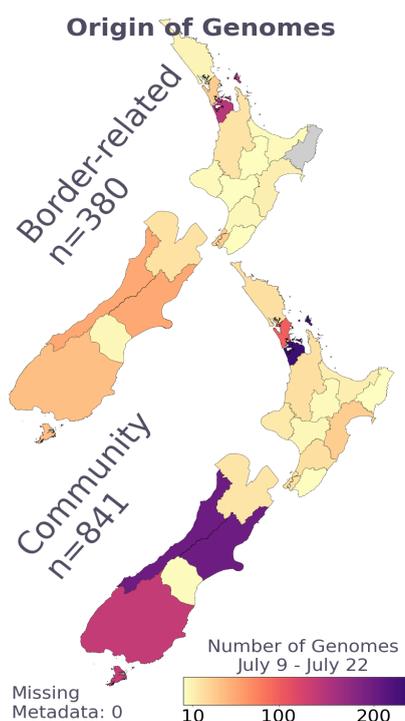
Hospital surveillance:

~25% (190 of 738)

of PCR positive cases with a hospital admission date in the past fortnight (9th-22nd July) have been genome sequenced. Composition of hospital cases:

- 19% BA.2
- <1% BA.2.75
- 14% BA.4
- 66% BA.5

Graphical overview of sample acquisition (9th-22nd July)



Key Trends & Insights

- Omicron BA.5 continues to increase in prevalence. NZ-based models predict it will reach ~90% of all community cases in the next week.
- Seven new cases of the Omicron BA.2.75 variant have been detected, including four community cases. There is growing evidence that this lineage does not have a substantial growth advantage compared to BA.5 and thus is unlikely to significantly impact NZ case numbers.
- BA.4/5, was detected at all wastewater sentinel sites. Aggregated data over the past 5 weeks had BA.4/5 at: 10.5%, 33%, 53%, 73% and now 81%. No BA.2.75 was detected at wastewater sentinel sites.
- Variants detected at the border (dominated by BA.5) are consistent with international surveillance and trends.
- To date, ~2.4% of BA.5 cases detected in the community were suspected reinfections (i.e. occurring in a patient with a previous registered case more than 28 days prior).

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 nationwide sentinel sites in Week 29: ending 24th July. Notes: (i) The level of precision and sensitivity in the percentage estimates can be uncertain. (ii) Covid-19 impacted on the ability to collect and courier samples from four of the regular sentinel sites across Auckland - hence the missing data this week.

